### **HIV Molecular Immunology 2002**

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### **Preface**

### Scope and Purpose of the HIV Molecular Immunology Database

HIV Molecular Immunology is a companion volume to Human Retroviruses and AIDS Genetic Sequence Compendium. This publication, the 2002 issue, is the printed version of the Web-based HIV Immunology Database (http://hiv-web.lanl.gov/immunology). The web interface for this relational database has many search options, as well as interactive tools to help immunologists design reagents and interpret their results.

The data included in this database is extracted from the HIV immunology literature. HIV-specific B-cell and T-cell responses are summarized and annotated. Immunological responses are divided into three sections, CTL, T helper, and antibody. Within these sections, defined epitopes are organized by protein and binding sites within each protein, moving from left to right through the coding regions spanning the HIV genome. We include human responses to natural HIV infections, as well as vaccine studies in a range of animal models and human trials. Responses that are not specifically defined, such as responses to whole proteins or monoclonal antibody responses to discontinuous epitopes, are summarized at the end of each protein sub-section. Studies describing general HIV responses to the virus, but not to any specific protein, are included at the end of each section.

The annotation includes information such as cross-reactivity, escape mutations, antibody sequence, TCR usage, functional domains that overlap with an epitope, immune response associations with rates of progression and therapy, and how specific epitopes were experimentally defined. Basic information such as HLA specificities for T-cell epitopes, isotypes of monoclonal antibodies, and epitope sequences are included whenever possible. All studies that we can find that incorporate the use of a specific monoclonal antibody are included in the entry for that antibody. A single T cell epitope can have multiple entries, generally one entry per study.

Finally, maps of all defined linear epitopes relative to the HXB2 reference proteins are provided. Alignments of CTL, helper T-cell, and antibody epitopes are available through the search interface on our web site at http://hiv-web.lanl.gov/immunology.

Only responses to HIV-1 and HIV-2 are included in the database. CTL responses to SIVs have been periodically summarized in our review section by Dr.

Dave Watkins and colleagues. (For their most recent review, please see: Where Have All The Monkeys Gone?: Evaluating SIV-Specific CTL in the Post-Mamu-A\*01 Era David H. O'Connor, Todd M. Allen, and David I. Watkins, in the 2001 HIV Immunology compendium). Dr. Christian Brander and colleagues annually provide a concise listing of optimal CTL epitopes. Additional reviews that our editorial board deems of general interest to the HIV research immunology community are solicited each year. This year's reviews are printed in the first section of this database; reviews from previous years can be found at: http://www.hiv.lanl.gov/content/hiv-db/REVIEWS/reviews.html.

Comments on the database or requests for the hard copy can be sent via email to immuno@t10.lanl.gov.

### Citing the Database

This publication may be cited as

HIV Molecular Immunology 2002. Bette T. M. Korber, Christian Brander, Barton F. Haynes, Richard Koup, Carla Kuiken, John P. Moore, Bruce D. Walker, and David I. Watkins, editors. Publisher: Los Alamos National Laboratory, Theoretical Biology and Biophysics, Los Alamos, New Mexico. LA-UR 03-5816.

### **About the Cover**



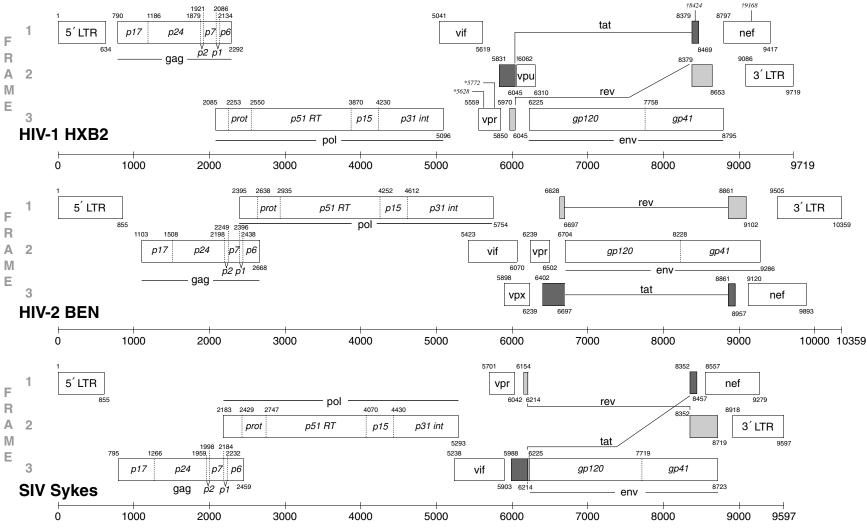
The illustration used for the cover of this year's immunology compendium highlights the location of the most variable amino acids in gp41, and was extracted from the review: Mutational Analyses and Natural Variability of the gp41 Ectodomain, by Rogier W. Sanders, Bette Korber, Min Lu, Ben Berkhout, and John P. Moore (this volume).

Preface About the PDF

### **About the PDF**

The complete *HIV Molecular Immunology 2002* is available in Adobe Portable Document Format (PDF) from our website, http://hiv-web.lanl.gov/immunology. The PDF version is hypertext enabled and features 'clickable' table-of-contents, indexes, references and links to external web sites.

Genome Maps Preface



Landmarks of the HIV-1, HIV-2, and SIV genomes. The gene start, indicated by the small number in the upper left corner of each rectangle normally records the position of the a in the atg start codon for that gene while the number in the lower right records the last position of the stop codon. For *pol*, the start is taken to be the first t in the sequence tttttag which forms part of the stem loop that potentiates ribosomal slippage on the RNA and a resulting -1 frameshift and the translation of the Gag-Pol polyprotein. The *tat* and *rev* spliced exons are shown as shaded rectangles. In HXB2, \*5628 and \*5772 mark positions of frameshifts in the *vpr* gene; !6062 indicates a defective acg start codon in *vpu*; †8424 and †9168 mark premature stop codons in *tat* and *nef*. See Korber *et al.*, Numbering Positions in HIV Relative to HXB2CG, in *Human Retroviruses and AIDS*, 1998, p. 102. Available from http://hiv-web.lanl.gov/HTML/reviews/HXB2.html.

Preface HIV/SIV Proteins

### **HIV/SIV Proteins**

Name	Size	Function	Localization
Gag MA	p17	membrane anchoring; env interaction; nuclear transport of viral core. (myristylated protein)	virion
CA	p24	core capsid	virion
NC	p7	nucleocapsid, binds RNA	virion
	p6	binds Vpr	virion
Protease (PR)	p15	gag/pol cleavage and maturation	virion
Reverse Transcriptase (RT)	p66, p51	reverse transcription	virion
RNase H	(heterodimer)	RNAse H activity	virion
Integrase (IN)		DNA provirus integration	virion
Env	gp120/gp41	external viral glycoproteins bind to CD4 and chemokine co-receptors	plasma membrane, virion envelope
Tat	p16/p14	viral transcriptional transactivator	primarily in nucleolus/nucleus
Rev	p19	RNA transport, stability and utilization factor (phosphoprotein)	primarily in nuleolus/nucleus shuttling between nucleolus and cytoplasm
Vif	p23	viral infectivity factor, inhibits minus-strand viral DNA hypermutation	cytoplasm (cytosol, membranes), virion
Vpr	p10-15	promotes nuclear localization of preintegration complex, inhibits cell division, arrests infected cells at G2/M	virion nucleus (nuclear membrane?)
Vpu	p16	promotes extracellular release of viral particles; degrades CD4 in the ER; (phosphoprotein only in HIV-1 and SIVcpz)	integral membrane protein
Nef	p27-p25	CD4 and class I downregulation (myristylated protein)	plasma membrane, cytoplasm, (virion?)
Vpx	p12-16	Vpr homolog present in HIV-2 and some SIVs absent in HIV-1	virion (nucleus?)
Tev	p28	tripartite tat-env-rev protein (also named Tnv)	primarily in nucleolus/nucleus

**Abbreviations** Preface

### **Abbreviations**

Common abbreviations used in this database.

Abbrev.	Meaning			
Ab	Antibody			
ADCC	Antibody-Dependent Cell-medicated Cytotoxicity			
ADE	Antibody-Dependent Enhancement			
APC	Antigen Presenting Cell			
AZT	Azidothymidine			
CD4BS	CD4 Binding Site			
CD4i	Antibody that has enhanced binding to gp120 in the			
	presence of SCD4 (CD4 induced)			
CSF	Cerebrospinal Fluid			
CTL	Cytotoxic T Lymphocyte			
CTLp	CTL precursor			
DTT	Dithiothrietol			
EIA	Enzyme Immuno Assay			
ELISA	Enzyme Linked ImmunoSorbent Assay			
ER	Endoplasmic reticulum			
Fabs	Fragment Antigen Binding-univalent antibody			
	fragment			
FIV	Feline Immunodeficiency Virus			
gp	Glycoprotein			
HIV	Human Immunodeficiency Virus			
HLA	Human Leukocyte Antigens			
HLA-MHC	Human Leukocyte Antigens-Major			
	Histocompatibility Complex			
IFN	Interferon			
IL	Interleukin			
IN	Integrase			

Abbrev.	Meaning		
Ig	Immunoglobulin		
MAb	Monoclonal Antibody		
MHC	Major Histocompatibility Complex		
MRC	Medical Research Council, UK		
NAb	Neutralizing Antibody		
NIBSC	National Institute for Biological Standards and		
	Control, UK		
NIH	National Institutes of Health		
PBLs	Peripheral Blood Lymphocyte		
PBMC	Peripheral Blood Mononuclear Cell		
PR	Protease		
RAC	Ricin A Chain		
rec/r	recombinant		
RIP	Recombinant Identification Program		
RIPA	Radio Immuno Precipitation assay		
rsgp160	recombinant soluble gp160		
RT	Reverse Transcriptase		
sCD4	soluble CD4		
SDS	Sodium Duodecyl Sulfate		
SIV	Simian Immunodeficiency Virus		
Th	T-helper cell		
TNF	Tumor Necrosis Factor		
VLP	Virus like particle, assembled from p55 gag		
VV	Vaccinia virus		
WB	Western Blot		

### Part I

### **Review Articles**

## Total Assessment of HIV-Specific CTL Responses: Epitope Clustering, Processing Preferences, and the Impact of HIV Sequence Heterogeneity

Nicole Frahm<sup>1</sup>, Philip J.R. Goulder<sup>1,2</sup>, and Christian Brander<sup>1</sup>

<sup>1</sup>Partners AIDS Research Center, Massachusetts General Hospital, Boston, USA. <sup>2</sup>The Peter Medawar Building for Pathogen Research, Oxford, UK.

The HIV Immunology database at the Los Alamos National Laboratory has collected data on HIV-specific cellular immune responses for over 8 years now and the list of targeted regions within the HIV protein sequences has been growing steadily. These compiled data and our own studies using comprehensive sets of overlapping peptides indicate that almost all parts of the viral protein sequence can be targeted by virus-specific T cells, especially CTL [Addo2003, Frahm2003]. HIV is the pathogen that has been characterized most extensively in terms of T-cell epitope distribution and the well-defined epitope landscape of HIV has allowed for a number of studies beyond assessing CTL activity in relation to HIV disease progression [Brander2002].

### **Targets of HIV-specific CTL**

Whilst in the early years of HIV CTL epitope mapping, attention was focused on structural proteins, more recent studies have included regulatory and accessory proteins as well [Tomiyama1999a, Altfeld2001a, van Baalen1997, Addo2001, Addo2002b]. High-throughput assays such as intracellular cytokine staining (ICS), and the Elispot assay are now routinely used to assess genome wide immune responses to HIV [Edwards2002, Frahm2003, Betts2001, Addo2003, Novitsky2001, Novitsky2002]. This is especially true for the characterization of CD8+ CTL responses, but newer data also include the identification of Th cell activity. Studies from several labs, including ours, using overlapping peptide sets spanning the entire HIV protein sequence have now shown that at least 90% of these peptides can be targeted by HIV-specific CTL, indicating

that all viral proteins undergo appropriate antigen processing *in vivo* and that epitopes from all HIV proteins can be effectively presented to CD8 T cells [Addo2003, Frahm2003]. However, there are specific patterns among these responses which will impact HIV vaccine design and which can potentially help to address more fundamental aspects of antigen processing, antigen presentation and T-cell repertoire development [Yusim2002].

Of special interest for these extended studies, but also for questions of CTL escape and (sub-unit)-vaccine development, is the identification of optimally defined CTL epitopes. Since 1995, largely through the voluntary contributions of unpublished data from many laboratories, regularly updated lists of "optimal CTL epitopes" have been made accessible through the Los Alamos National Laboratory's HIV database [Brander1995]. This year's update again adds a number of new epitopes whilst some others were removed as they were erroneously included before (mainly some HLA-A\*0201 restricted epitopes from our own lab which were based on epitope prediction only and which were not defined with the same stringency as the other epitopes in this list). While the earliest reports clearly focused on alleles common in individuals infected early in the US epidemic, more attention is now given to individuals of non-Caucasian descent [Frahm2003, Sabbaj2003]. In addition, epitopes from non-clade B infections are increasingly identified [Novitsky2002, Novitsky2003, Bond2001, Fukada2002, Lynch1998, Sriwanthana2001, Goulder2001]. The identification of these epitopes provides valuable information for vaccine development in non-Caucasians and non-clade B infection.

In addition, these new epitopes, when characterized in full detail, can provide important insights into HLA binding motifs for these less well characterized alleles; again facilitating the design of a potential HIV vaccine. To support this work, the HIV database offers additional tools such as *EPILIGN*:

http:

//hiv-web.lanl.gov/content/hiv-db/EPILIGN/EPI.html,
PeptGen:

http://hiv-web.lanl.gov/content/hiv-db/PEPTGEN/
PeptGenSubmitForm.html

In *HIV Molecular Immunology* 2002. Bette T. M. Korber, Christian Brander, Barton F. Haynes, Richard Koup, Carla Kuiken, John P. Moore, Bruce D. Walker, and David I. Watkins, editors. Publisher: Los Alamos National Laboratory, Theoretical Biology and Biophysics, Los Alamos, New Mexico. LA-UR 03-5816. pp. 3–21.

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MotifScan:
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http://hiv-web.lanl.gov/content/hiv-db/MOTIFSCAN/
MotifScanner.html

as well as valuable links to other sites, including the *SYFPEITHI HLA binding motifs database*:

http://www.syfpeithi.de/

and others:

http://hiv.basic.nwu.edu/HLA,

http://bimas.dcrt.nih.gov/cgi-bin/molbio/ken\_parker\_

comboform,

http://www.jenner.ac.uk/JenPep/

Clearly, these databases and prediction softwares can profit from each other and facilitate the future identification of T-cell targets in HIV and other infections.

### Immunodominant regions in HIV protein sequences

As mentioned above, the described optimal CTL epitopes are not evenly distributed over the entire viral genome. Rather, there are regions where many epitopes overlap. This phenomenon has been described as early as 1993 and various explanations have been put forward [Goulder2000a, Buseyne1993]. Two factors that seem to significantly contribute to this epitope clustering appear to be viral sequence heterogeneity and processing preferences [Yusim2002].

Sequence heterogeneity affects all HIV proteins, albeit to variable degrees. Relatively conserved regions in Gag and Nef have been identified as immunodominant regions in a study of more than 150 individuals of different ethnicities [Frahm2003]. Independently of the HLA background, these clade B infected individuals made strong responses to the peptides spanning these regions. When comparing the sequence heterogeneity in published clade B sequences, these data also show that peptides with low sequence entropy (more conserved) are targeted more frequently than epitopes with higher entropy. It is likely that these differences are due to the fact that the average phylogenetic distance of the test reagent (consensus B sequence) to an individual's autologous viral sequence is larger in higher variable regions than in more conserved ones and thus, responses against the less conserved peptides are not detected due to differences between test reagent and inoculum sequence [Yusim2002, Gaschen2002].

In addition to sequence incompatibility between test reagent and autologous virus, certain regions of the HIV protein sequence may not be processed and presented very effectively. Although 86% of our overlapping peptide sets used in the study above were targeted by at least one individual in the cohort of 150

people, there are still some relatively conserved peptides that do not seem to induce a detectable CTL response in natural HIV infection [Frahm2003]. These peptides may lie within stretches of viral proteins that are relatively resistant to proteasomal digestions or may lack adequate "Transporter associated with Antigen Processing" (TAP) binding motifs [Brander2002, Yusim2002]. The HIV Immunology database provides valuable web links to software where sequences of choice can be analyzed for proteasomal processing preferences (NetChop by C. Kesmir *et al.*, http://www.cbs.dtu.dk/services/NetChop/). Recent work by Yusim *et al.*, demonstrates the accuracy and predictive potential of this algorithm and its usefulness in identifying CTL epitopes [Yusim2002].

Together, these studies indicate that CTL epitope clustering may reflect the biased detection of these responses in rather conserved regions and that processing preferences may play an important role in providing processed antigen. In addition, sequence variability may not only affect CTL recognition but could also have an effect on processing of viral proteins [Yellen-Shaw1997]. Although we have been unable to show such an effect for the flanking regions of the immunodominant, HLA-A\*0201 restricted CTL epitope SL9 (SLYNTVATL) in HIV Gag p17, other studies outside the HIV field suggest that escape from processing may be an effective means of immune evasion [Yellen-Shaw1997, Kuckelkorn2002, Gileadi1999, Brander1999]. These studies also highlight the importance of defining T-cell targets in maximal detail, so that prediction algorithm such as NetChop and binding motif algorithms can be optimized by a precisely characterized training set of defined epitopes. In addition, in order to discriminate between processing escape and escape from T-cell receptor recognition or HLA binding, the boundaries of targeted epitopes need to be optimally determined. The present listing is designed to provide these data specifically for HIV derived epitopes and we therefore still separate CTL epitopes in a list of optimally and suboptimally defined epitopes. We hope that this discrimination continues to provide support for the HIV immunologists and laboratories involved in antigen processing and presentation, who want to take advantage of the exceptionally well defined epitope landscape of HIV.

As every year, we would like to express our gratitude to the large number of researchers in the field who continuously contribute to this database. We very much welcome any criticism, comments and additions to this list since we are sure that some epitopes will unintentionally escape our attention, despite close monitoring of the literature. Also, pertinent information, such as resources for single HLA allele expressing cell lines, HLA subtype information and new technologies for CTL epitope mapping could be listed or referenced in this list, providing additional help to problems encountered by investigators.

### Acknowledgments

The mostly unpublished data added to this years update stemming from the AIDS Research Center at Massachussetts General Hospital have been largely funded by an NIH contract (#NO1-A1-15442) supporting HLA typing and HIV CTL epitope definition in non-Caucasian populations and non-clade B HIV infection.

Please write or call us with any comments you may have at:

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Table 1: Best Defined HIV CTL Epitopes

HLA	Protein	AA	S	equence	Reference
A*0101 (A1)	gp160	787–795	RRGW	EVLKY	[Cao2002]
A*0201 (A2)			2	6 C	[Falk1991, Barouch1995]
		1° anc		L	
		20	. M	V	
A *0201 (A2)	17	2° anc		V	[I-b1001 Park1002 Park1004]
A*0201 (A2)	p17	77–85		ITVATL	[Johnson1991, Parker1992, Parker1994]
A*0201 (A2) A*0201 (A2)	p1 RT	1–10 33–41		WPSYK	[Yu2002b] [Haas1998, Haas1999]
' '	RT			CICTEM	[Harrer1996a]
A*0201 (A2) A*0201 (A2)	RT	179–187 309–317		YMDDL PVHGV	[Walker1989, Tsomides1991]
A*0201 (A2) A*0201 (A2)	Vpr	59–517 59–67			[Altfeld2001a, Altfeld2001b]
A*0201 (A2) A*0201 (A2)	ург gp160	311–320		RILQQL RAFVTI	[Alterd2001a, Alterd2001b] [Alexander-Miller1996]
A*0201 (A2) A*0201 (A2)	gp160 gp160	813–822		TDIAV	[Dupuis1995]
A*0201 (A2) A*0201 (A2)	Nef	136–145		GWCYKL	[Haas1996, Maier1999]
A*0201 (A2)	Nef	180–143		RFDSRL	[Haas1996, Maier1999]
A 0201 (A2)	INCI	100-109	VILVE	TUSKL	[11aas1990, Walc11999]
A*0202 (A2)			2	С	[Barouch1995]
			L	L	
				v	
A*0202 (A2)	p17	77–85	SLYN	ITVATL	[Goulder1999]
A*0205 (A2)	p17	77–85	CT VN	דיי איז דיי	[Goulder1999]
A*0205 (A2) A*0205 (A2)	gp41	335–343		ITVATL	[Sabbaj2003]
A · 0203 (A2)	gp41	333–343	KIKČ	GLERA	[Sa00aj2003]
A*0207 (A2)	p24	164–172	YVDF	RFYKTL	[Currier2002]
A *02 (A 2)	DT	72. 92			FX 2002 1
A*03 (A3)	RT	73–82		'RELNK	[Yu2002a]
A*03 (A3)	RT	356–366	RMRGAH		[Yu2002a]
A*03 (A3)	Integrase	179–188		INFKRK	[Yu2002a]
A*03 (A3)	Vif	28–36		SKKAK	[Yu2002a]
A*03 (A3)	Vif	158–168	KTKPPI		[Yu2002a]
A*03 (A3)	Rev	57–66		TYLGR	[Addo2002a, Yu2002a]
A*03 (A3)	Nef	84–92	AVDI	SHFLK	[Yu2002a]

Table 1 (cont.): Best Defined HIV CTL Epitopes

HLA	Protein	AA	Sequence	Reference
A*0301 (A3)			2 C	[DiBrino1993, Rammensee1995]
			L K	
			V Y	
			M F	
A*0301 (A3)	p17	18–26	KIRLRPGGK	[Harrer1996b]
A*0301 (A3)	p17	20-28	RLRPGGKKK	[Goulder1997a, Culmann1999, Lewinsohn1999b,
				Wilkes1999b]
A*0301 (A3)	p17	20-29	RLRPGGKKKY	[Goulder2000b]
A*0301 (A3)	RT	33–43	ALVEICTEMEK	[Haas1998, Haas1999]
A*0301 (A3)	RT	93-101	GIPHPAGLK	[Yu2002a]
A*0301 (A3)	RT	158-166	AIFQSSMTK	[Threlkeld1997]
A*0301 (A3)	RT	269-277	QIYPGIKVR	[Yu2002a]
A*0301 (A3)	Vif	17–26	RIRTWKSLVK	[Altfeld2001a, Yu2002a]
A*0301 (A3)	gp160	37–46	TVYYGVPVWK	[Johnson1994a]
A*0301 (A3)	gp160	770–780	RLRDLLLIVTR	[Takahashi1991]
A*0301 (A3)	Nef	73–82	QVPLRPMTYK	[Koenig1990, Culmann1991]
A*1101 (A11)			2 C	[Zhang1993, Rammensee1995]
			K	
			V	
			I	
			F	
			Y	
A*1101 (A11)	p17	84–92	TLYCVHQRI	[Harrer1998]
A*1101 (A11)	p24	217–227	ACQGVGGPGHK	[Sipsas1997]
A*1101 (A11)	RT	158–166	AIFQSSMTK	[Johnson1994b, Zhang1993, Threlkeld1997]
A*1101 (A11)	RT	341–350	IYQEPFKNLK	[Culmann1999]
A*1101 (A11)	RNase	80–88	QIIEQLIKK	[Fukada1999]
A*1101 (A11)	Integrase	179–188	AVFIHNFKRK	[Fukada1999]
A*1101 (A11)	gp160	199–207	SVITQACPK	[Fukada1999]
A*1101 (A11)	Nef	73–82	QVPLRPMTYK	[Buseyne1999]
A*1101 (A11)	Nef	75–82	PLRPMTYK	[Culmann1991]
A*1101 (A11)	Nef	84–92	AVDLSHFLK	[Culmann1991]
A*23 (A23)	gp41	74–82	RYLKDQQLL	[Cao2003]

Table 1 (cont.): Best Defined HIV CTL Epitopes

HLA	Protein	AA	Sequence	Reference
A*2402 (A24)			2 C	[Maier1994]
			YI	
			L	
			F	
A*2402 (A24)	p17	28–36	KYKLKHIVW	[Ikeda-Moore1998, Lewinsohn1999a]
A*2402 (A24)	p24	162–172	RDYVDRFFKTL	[Dorrell1999, Rowland-Jones1999]
A*2402 (A24)	gp160	52–61	LFCASDAKAY	[Lieberman1992, Shankar1996]
A*2402 (A24)	gp160	585–593	RYLKDQQLL	[Dai1992]
A*2402 (A24)	Nef	134–141	RYPLTFGW	[Goulder1997b, Ikeda-Moore1998]
A *2501 (A 25)	2.4	13–23		[V
A*2501 (A25)	p24		QAISPRTLNAW	[Kurane 1999]
A*2501 (A25)	p24	71–80	ETINEEAAEW	[Klenerman1996, van Baalen1996]
A*2601 (A26)			12 6 C	[Dumrese1998]
			V Y	
			T F	
			I	
			L	
			F	
			D I	
			E L	
			V	
A*2601 (A26)	p24	35–43	EVIPMFSAL	[Goulder1996a]
A*2601 (A26)	Pol	604–612	ETKLGKAGY	[Sabbaj2003]
A*2902 (A29)	gp160	209–217	SFEPIPIHY	[Altfeld2000a]

Table 1 (cont.): Best Defined HIV CTL Epitopes

HLA	Protein	AA	Sequence	Reference
A*3002 (A30)			12 C	[Rammensee1999]
			Y Y	
			F	
			L	
			v	
A #2002 (A 20)	. 17	76.06	R	[C. 11, 2001]
A*3002 (A30)	p17 RT	76–86 173–181	RSLYNTVATLY	[Goulder2001]
A*3002 (A30) A*3002 (A30)	RT	263–271	KQNPDIVIY	[Goulder2001] [Goulder2001]
A*3002 (A30) A*3002 (A30)	RT	356–365	KLNWASQIY RMRGAHTNDV	[Sabbaj2003]
A*3002 (A30) A*3002 (A30)		219–227		[Sabbaj2003] [Sabbaj2003, Addo2002c]
A*3002 (A30) A*3002 (A30)	Integrase gp160	704–712	KIQNFRVYY	[Sabbaj2003, Addo2002c] [Goulder2001]
A*3002 (A30) A*3002 (A30)	gp100 gp120	310–318	IVNRNRQGY HIGPGRAFY	[Sabbaj2003]
A*3002 (A30) A*3002 (A30)	gp120 gp41	283–291		[Goulder2001]
A · 5002 (A30)	gp41	263-291	KYCWNLLQY	[Goulde12001]
A*3101 (A31)			2 C	[Falk1994, Rammensee1999]
			R	
			L	
			V	
			Υ	
A #2101 (A 21)	1.60	770 700	F	FG 6':1004 G 6':100413
A*3101 (A31)	gp160	770–780	RLRDLLLIVTR	[Safrit1994a, Safrit1994b]
A*3201 (A32)	RT	392-401	PIOKETWETW	[Harrer1996b]
A*3201 (A32)	gp160	419–427	RIKQIINMW	[Harrer1996b]
, , ,				
A*3303 (A33)	gp41	187–196	VFAVLSIVNR	[Hossain2001]
A*3303 (A33)	gp41	320–327	EVAQRAYR	[Hossain2001]
A*3303 (A33)	Vpu	29–37	EYRKILRQR	[Addo2002b]
A*3303 (A33)	Nef	133–141	TRYPLTFGW	[Cao2002]
A*6801 (A68)	Tat	39–49	ITKGLGISYGR	[Oxenius2002]
A*6802 (A68)	Protease	3–11	ITLWQRPLV	[Rowland-Jones1999]
A*6802 (A68)	Protease	30–38	DTVLEEWNL	[Rowland-Jones1999]
A*6802 (A68)	gp160	777–785	IVTRIVELL	[Wilkes1999a]
, ,				
A*7401 (A19)	Protease	3–11	ITLWQRPLV	[Rowland-Jones1999]

Table 1 (cont.): Best Defined HIV CTL Epitopes

HLA	Protein	AA	Sequence	Reference
B*07 (B7)	p24	84–92	HPVHAGPIA	[Yu2002a]
B*0702 (B7)			123 C	[Englehard1993, Rammensee1999]
			P L	
			A R	
			R K	
B*0702 (B7)	p24	16–24	SPRTLNAWV	[Lewinsohn1999a]
B*0702 (B7)	p24	48–56	TPQDLNTML	[Wilson1999a, Wilkes1999c, Jin2000,
				Wilson1997]
B*0702 (B7)	p24	223–231	GPGHKARVL	[Goulder1999]
B*0702 (B7)	Vpr	34–42	FPRIWLHGL	[Altfeld2001a]
B*0702 (B7)	Vif	48–57	HPRVSSEVHI	[Altfeld2001a]
B*0702 (B7)	gp160	298-307	RPNNNTRKSI	[Safrit1994b]
B*0702 (B7)	gp160	843-851	IPRRIRQGL	[Wilkes1999b]
B*0702 (B7)	Nef	68–77	FPVTPQVPLR	[Haas1996, Maier1999]
B*0702 (B7)	Nef	68–76	FPVTPQVPL	[Bauer1997, Frahm2002]
B*0702 (B7)	Nef	71–79	TPQVPLRPM	[Goulder1999]
B*0702 (B7)	Nef	77–85	RPMTYKAAL	[Bauer1997]
B*0702 (B7)	Nef	106–115	RQDILDLWIY	[Goulder1999]
B*0702 (B7)	Nef	128–137	TPGPGVRYPL	[Culmann-Penciolelli1994, Haas1996]
B*0801 (B8)			23 5 C	[Hill1992, Sutton1993, DiBrino1994a]
			K K L	
			R	
			PR	
			L	
B*0801 (B8)	p17	24–32	GGKKKYKLK	[Rowland-Jones1993, Goulder1997d]
B*0801 (B8)	p17	74–82	ELRSLYNTV	[Goulder1997d]
B*0801 (B8)	p24	128–135	EIYKRWII	[Sutton1993, Goulder1997d]
B*0801 (B8)	p24	197–205	DCKTILKAL	[Sutton1993]
B*0801 (B8)	RT	18–26	GPKVKQWPL	[Walker1989, Sutton1993]
B*0801 (B8)	gp160	2–10	RVKEKYQHL	[Sipsas1997]
B*0801 (B8)	gp160	586–593	YLKDQQLL	[Johnson1992, Shankar1996]
B*0801 (B8)	Nef	13–20	WPTVRERM	[Goulder1997d]
B*0801 (B8)	Nef	90–97	FLKEKGGL	[Culmann-Penciolelli1994, Price1997]
B*14 (B14)	p15	42–50	CRAPRKKGC	[Yu2002b]

Table 1 (cont.): Best Defined HIV CTL Epitopes

HLA	Protein	AA	Sequence	Reference
B*1402 (B14)			23 5 C <b>R R L K H</b> L  Y  F	[DiBrino1994b]
B*1402 (B14) B*1402 (B14)	p24 gp160	166–174 584–592	DRFYKTLRA ERYLKDQQL	[Harrer1996b] [Johnson1992]
B*1501 (B62)  B*1501 (B62)  B*1501 (B62)  B*1501 (B62)  B*1501 (B62)  B*1501 (B62)  B*1503 (B72)  B*1503 (B72)  B*1503 (B72)  B*1503 (B72)  B*1503 (B72)	p24 RT RT Nef Nef Integrase Tat Pol Nef	137–145 260–271 309–318 19–27 117–127 263–271 38–47 651–660 183–191	2 C Q Y L F M GLNKIVRMY LVGKLNWASQIY ILKEPVHGVY RMRRAEPAA TQGYFPDWQNY  RKAKIIRDY FQTKGLGISY VTDSQYALGI WRFDSRLAF	[Barber1997] [Barber1997] [Barber1997] [Johnson1991, Goulder1999] [Johnson1999] [Johnson1991, Johnson1999] [Cao2002] [Culmann1999]  [Cao2003] [Novitsky2001] [Sabbaj2003] [Cao2002]
B*1516 (B63)			2 9 T Y S I V	[Barber1997, Seeger1998]
B*1516 (B63)	gp160	375–383	SFNCGGEFF	[Wilson1997, Wilson1999a]
B*1801 (B18) B*1801 (B18) B*1801 (B18)	p24 Vif Nef	161–170 102–111 135–143	FRDYVDRFYK LADQLIHLHY YPLTFGWCY	[Ogg1998] [Altfeld2001a] [Culmann1991, Culmann-Penciolelli1994]
B*2703 (B27)	p24	131–140	RRWIQLGLQK	[Rowland-Jones1998, Rowland-Jones1999]

Table 1 (cont.): Best Defined HIV CTL Epitopes

HLA	Protein	AA	Seq	uence	Reference
B*2705 (B27)			12	С	[Jardetzky1991, Rammensee1995]
			R	L	
				F	
			K	K	
			R	R	
			G	I	
			A		
B*2705 (B27)	p17	19–27	IRLRP	GGKK	[McKinney1999, Lewinsohn1999a]
B*2705 (B27)	p24	131–140	KRWIIL	GLNK	[Nixon1988, Buseyne1993, Goulder1997c]
B*2705 (B27)	gp160	786–795	GRRGWE	ALKY	[Lieberman1992, Lieberman1999]
B*2705 (B27)	Nef	105–114	RRQDIL	DLWI	[Goulder1997a]
B*3501 (B35)			2	С	[Hill1992, Rammensee1999]
			P	Y	
			А	F	
			V	M	
			S	L	
				I	
B*3501 (B35)	p17	36–44	WASRE		[Goulder1997b]
B*3501 (B35)	p17	124–132	NSSKV		[Rowland-Jones1995]
B*3501 (B35)	p24	122–130	PPIPV		[Rowland-Jones1995]
B*3501 (B35)	p24	122–130	NPVPV		[Rowland-Jones1995]
B*3501 (B35)	RT	107–115	TVLDV		[Wilkes1999b, Wilson1999b]
B*3501 (B35)	RT	118–127	VPLDED		[Sipsas1997, Shiga1996]
B*3501 (B35)	RT	175–183	NPDIV		[Sipsas1997, Shiga1996]
B*3501 (B35)	RT	175–183	HPDIV		[Rowland-Jones1995]
B*3501 (B35)	gp160	42–52	VPVWKEA		[Wilkes1999b]
B*3501 (B35)	gp160	78–86	DPNPQ		[Shiga1996]
B*3501 (B35)	gp160	606–614	TAVPW		[Johnson1994a]
B*3501 (B35)	Nef	74–81	VPLR	PMTY	[Culmann1991, Culmann-Penciolelli1994]
B*3701 (B37)			2	С	[Falk1993]
			D	F	
			E	M	
				L	
				I	
B*3701 (B37)	Nef	120–128	YFPDW	QNYT	[Culmann1991, Culmann1999]

Table 1 (cont.): Best Defined HIV CTL Epitopes

HLA	Protein	AA	Sequence	Reference
B*3801 (B38)	gp160	104–112	MHEDIISLW	[Cao2002]
B*3901 (B39)			2 C	[Falk1995a]
			R L	
			H	
B*3901 (B39)	p24	61–69	GHQAAMQML	[Kurane1999]
B*4001 (B60)			2 C	[Falk1995b]
			E L	
B*4001 (B60)	p17	92–101	IEIKDTKEAL	[Altfeld2000b]
B*4001 (B60)	p24	44–52	SEGATPQDL	[Altfeld2000b]
B*4001 (B60)	p6	33–41	KELYPLTSL	[Yu2002b]
B*4001 (B60)	RT	202-210	IEELRQHLL	[Altfeld2000b]
B*4001 (B60)	gp160	805-814	QELKNSAVSL	[Altfeld2000b]
B*4001 (B60)	Nef	92–100	KEKGGLEGL	[Altfeld2000b]
B*4002 (B61)	p17	11–19	GELDRWEKI	[Sabbaj2003]
B*4002 (B61)	p24	70–78	KETINEEAA	[Sabbaj2003]
B*4002 (B61)	p24	78–86	AEWDRVHPV	[Sabbaj2003]
B*4002 (B61)	Nef	92-100	KEKGGLEGL	[Sabbaj2003, Altfeld2000b]
B*4002 (B61)	p15	64–71	TERQANFL	[Sabbaj2003]
B*42 (B42)	Integrase	260–268	VPRRKAKII	[Kiepiela2002]
B*4201 (B42)	p24	48–56	TPQDLNTML	[Goulder2000a]
B*4201 (B42)	RT	271-279	YPGIKVRQL	[Wilkes1999b]
B*4201 (B42)	Nef	128-137	TPGPGVRYPL	[Goulder1999]
B*4402 (B44)			2 C	[Rammensee1999]
			E F	
			Y	
B*4402 (B44)	p24	162-172	RDYVDRFYKTL	[Ogg1998]
B*4402 (B44)	p24	174–184	AEQASQDVKNW	[Lewinsohn1999a]
B*4402 (B44)	gp160	31–40	AENLWVTVYY	[Borrow1997]
B*4415 (B12)	p24	28–36	EEKAFSPEV	[Bird2002]
B*51 (B51)	Vpr	29–37	EAVRHFPRI	[Cao2003]

Table 1 (cont.): Best Defined HIV CTL Epitopes

HLA	Protein	AA	Sequence	Reference
B*5101 (B51)			2 C	[Falk1995a]
			A F	
			P I	
			G	
B*5101 (B51)	RT	42-50	EKEGKISKI	[Haas1998, Haas1999]
B*5101 (B51)	RT	128-135	TAFTIPSI	[Sipsas1997]
B*5101 (B51)	gp160	416–424	LPCRIKQII	[Tomiyama1999b]
B*5201 (B52)			2 C	[Rammensee1999]
			I	
			v	
			Q	
B*5201 (B52)	p24	143–150	RMYSPTSI	[Wilkes1999b, Wilson1997]
B*53 (B53)	Nef	135–143	YPLTFGWCF	[Kiepiela2002]
B*5301 (B53)			2 C	
D 2301 (B23)			P L	[Hill1992]
B*5301 (B53)	p24	48–56	TPYDINOML	[Gotch1993]
B*5301 (B53)	p24	176–184	QASQEVKNW	[Buseyne1996, Buseyne1997, Buseyne1999]
B*5301 (B53)	Tat	2–11	EPVDPRLEPW	[Addo2001]
B*5301 (B53)	Nef	135–143	YPLTFGWCY	[Sabbaj2003]
				[
B*5501 (B55)			2 C	[Barber1995]
` ,			P	-
			А	
B*5501 (B55)	gp160	42-51	VPVWKEATTT	[Shankar1996, Lieberman1999]

Table 1 (cont.): Best Defined HIV CTL Epitopes

HLA	Protein	AA	Sequence	Reference
B*5701 (B57)			12 C	[Barber1997]
			A F	
			T W	
			S	
			K Y	
B*5701 (B57)	p24	15–23	ISPRTLNAW	[Johnson1991, Goulder1996b]
B*5701 (B57)	p24	30–40	KAFSPEVIPMF	[Goulder1996b]
B*5701 (B57)	p24	108–118	TSTLQEQIGWF	[Goulder1996b]
B*5701 (B57)	p24	176–184	QASQEVKNW	[Goulder1996b]
B*5701 (B57)	RT	244–252	IVLPEKDSW	[van der Burg1997, Hay1999]
B*5701 (B57)	Integrase	173–181	KTAVQMAVF	[Goulder1996b, Hay1999]
B*5701 (B57)	Vpr	30–38	AVRHFPRIW	[Altfeld2001a]
B*5701 (B57)	Vif	31–39	ISKKAKGWF	[Altfeld2001a]
B*5701 (B57)	Rev	14–23	KAVRLIKFLY	[Addo2001]
B*5701 (B57)	Nef	116–125	HTQGYFPDWQ	[Culmann1991]
B*5701 (B57)	Nef	120–128	YFPDWQNYT	[Culmann1991]
B57 (B57)	Nef	116–124	HTQGYFPDW	[Draenert2002]
B*5703 (B57)	p24	30-37	KAFSPEVI	[Goulder2000b]
B*5703 (B57)	p24	30–40	KAFSPEVIPMF	[Goulder2000b]
B*5801 (B58)			12 C	[Barber1997, Falk1995b]
			A F	
			T W	
			S	
			K	
			V	
			I	
B*5801 (B58)	p24	108-117	TSTVEEQQIW	[Bertoletti1998]
B*5801 (B58)	p24	108-117	TSTLQEQIGW	[Goulder1996b]
B*5801 (B58)	RT	375-383	IAMESIVIW	[Kiepiela2002]
B*5801 (B58)	Rev	14–23	KAVRLIKFLY	[Addo2001]
B*81 (B81)	Pol	715–723	LFLDGIDKA	[Addo2002a]

Table 1 (cont.): Best Defined HIV CTL Epitopes

HLA	Protein	AA	Sequence	Reference
B*8101 (B81) B*8101 (B81)	p24 Vpr	48–56 34–42	TPQDLNTML FPRIWLHGL	[Goulder2000a] [Altfeld2001a]
Cw*0102 (Cw1)			23 C <b>A L</b> <b>L</b>	[Barber1997]
Cw*0102 (Cw1)	p24	36–43	VIPMFSAL	[Goulder1997b]
Cw*0304 (Cw10)	gp41	46–54	RAIEAQQHL	[Currier2002, Trocha2002]
Cw*0401 (Cw4)			2 6 C Y L P F V U	[Falk1994]
Cw*0401 (Cw4)	gp160	375–383	L SFNCGGEFF	[Wilson1997, Johnson1993]
Cw*0501 (Cw5)	Rev	67–75	SAEPVPLQL	[Addo2001]
Cw*07 (Cw7) Cw*07 (Cw7)	Nef Nef	105–115 105–115	KRQEILDLWVY RRQDILDLWIY	[Kiepiela2002] [Yu2002a]
Cw*0802 (Cw8) Cw*0802 (Cw8)	p24 Nef	48–56 83–91	TPQDLNTML AAVDLSHFL	[Goulder2000a] [Cao2003]
Cw*12 (Cw12)	Tat	30–37	CCFHCQVC	[Cao2003, Nixon1999]
Cw*15 (Cw15)	gp41	46–54	RAIEAQQHL	[Trocha2002]

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### Mutational Analyses and Natural Variability of the gp41 Ectodomain

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The HIV-1 envelope glycoproteins mediate viral attachment and release of the viral core in susceptible target cells. A single gp160 precursor protein is processed intracellularly to yield the native form of the envelope complex, consisting of three gp120 and three gp41 molecules associated through non-covalent interactions. Upon receptor and co-receptor binding to the surface subunit gp120, conformational changes within the envelope glycoprotein complex enable the insertion of the hydrophobic fusion peptide of the transmembrane subunit gp41 into the target membrane. Subsequent rearrangements within gp41 allow fusion of viral and cellular membranes. These late structural alterations are targeted by the entry inhibitor T-20 (for reviews see 13, 20, 21, 24, 46, 75).

A considerable body of mutagenesis data on structure-function relationships within the HIV-1 gp41 ectodomain (gp41e) has been published over the years. The value of this data-set has been increased considerably by the determination of the structure of the gp41e core, allowing some of the mutational effects to be interpreted and at least partially understood (9, 12, 38, 41, 68, 71). The native, pre-fusion structure of gp41e in the trimeric gp120-gp41 complex on the virion surface prior to receptor engagement is not known, however, and the various transitional structures of gp41 during the virus-cell fusion process are still ill-defined. Consequently, the structural and functional consequences of many amino acid substitutions in gp41e remain unclear.

Here, we have summarized the results of published mutagenesis studies on gp41e (see the accompanying table). The HXB2 reference strain has been used as a basis for numbering individual amino acid residues (Figure 1). This information should facilitate the research of those who study the HIV-1 envelope glycoproteins as fusogens or vaccine antigens. In general, we have tabulated only data for single mutants, but several publications contain information on the effects of multiple amino acid substitutions (25, 43, 44, 49, 56, 57, 62). The table does not include information on every naturally occurring gp41e sequence variant, as the variation is extensive. However, a summary of natural variability in clades B and C is presented in Figure 2. Also, the last two columns in the table present the entropy scores for gp41e positions that have a defined impact on Env function, for both the B clade and the C clade. Not surprisingly, positions identified through mutational analysis as those where substitutions can abrogate key functions, also tend to be highly conserved among the natural variants. The clearest example is provided by positions where substitutions essentially eliminate cell-cell fusion (i.e., where fusion efficiencies in syncytium assays or reporter gene assays have been reduced to less than 3% of the wild-type value). Sites at which substitutions can abrogate cell-cell fusion tended to be more invariant among 123 B clade sequences (26/44, 59%), compared to those sites where amino acid changes did not dramatically reduce fusion (11/39, 28%, Fisher's exact test p = 0.004). Some unusual gp41e variants found in neutralization-resistant isolates are also included in the table, as are variants that arise in response to selection pressure, both in vitro and in vivo, from the entry inhibitor T-20, which targets gp41e.

The precision with which the available data could be analyzed was sometimes limited because different viral clones, isolates and assays were used to obtain the experimental data. We have therefore chosen to summarize quantitative parameters using the grading system –, +, ++ and +++, as indicated in the footnotes. In some cases these grades had to be deduced from the primary reports, so readers are encouraged to consult the original papers for quantitative details; we regret any errors of interpretation we may have made during this estimation process. Not surprisingly, perhaps, different studies sometimes yielded conflicting results. We have recorded the conflicting data sets but shall leave it to the readers to judge which are the more plausible.

The natural variability of residues in clade B and C isolates was analyzed and mapped on the structure of gp41 (see Figures 2 and 3). A focus of variable residues in clade B sequences is located in the upper part of the C-terminal helix

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gp41 ectodomain gp41 ectodomain

centered around the highly variable leucine-glutamate-glutamine (LEQ) triplet, indicating that this region is under selective pressure. However, it is also possible that certain changes in residues in this region have little impact on Env function, particularly if there is some flexibility in Env structure(s) around this region. This relatively variable region also contains four glycosylation sites, which could be involved in immune evasion (30). Indeed, mutations that affect glycosylation in this region can modulate neutralization sensitivity (65). Of note is that no CTL or antibody epitopes have been mapped to this region despite the intense positive selection. One interpretation of this observation is that the selection pressure is exerted indirectly on distant antibody epitopes elsewhere in gp41e or even in gp120 (32). Another is that some neutralizing antibodies remain as yet undiscovered in this region of gp41e. In clade C viruses the variability is somewhat shifted towards the 2F5 epitope, compared to clade B. Furthermore, certain residues are significantly more variable in clade C viruses compared to clade B, and vice versa, suggesting that subtly different selection pressures may operate on viruses from the two clades.

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#### gp41 start, position 512 of HXB2 gp160 AVGIGALFL GFLGAAGSTM GAASMTLTVQ ARQLLSGIVQ 550 QQNNLLRAIE AQQHLLQLTV WGIKQLQARI LAVERYLKDQ QLLGIWGCSG 600 KLICTTAVPW NASWSNKSLE QIWNHTTWME WDREINNYTS LIHSLIEESQ 650 NQQEKNEQEL LELDKWASLW NWFNITNWLW YIKLFIMIVG GLVGLRIVFA 700 VLSIVNRVRQ GYSPLSFQTH LPTPRGPDRP EGIEEEGGER DRDRSIRLVN GSLALIWDDL RSLCLFSYHR LRDLLLIVTR IVELLGRRGW EALKYWWNLL 800 QYWSQELKNS AVSLLNATAI AVAEGTDRVI EVVQGACRAI RHIPRRIRQG 850 LERILL 856

Figure 1: The HXB2 reference strain and the numbering of positions in the gp41 sequence. Only information on the ectodomain (residue 512–684) is incorporated in subsequent analyses.

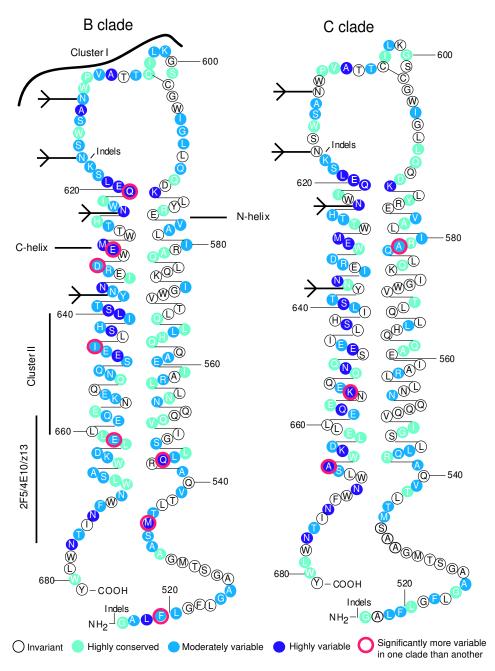


Figure 2: Variability of gp41e. The relative entropies of residues were mapped onto a 2D representation of the HXB2 gp41e (adapted from 29, 61). The variability of residues in clade B isolates (left panel) and clade C isolates (right panel) is indicated according to their entropy values. The entropy is a simple measure of variation in each position based on a sequence alignment (33). Not surprisingly, entropy values for each amino acid were highly correlated with the ratio of the nonsynonymous/synonymous substitution rates, a measure which is indicative of selective pressure, calculated using PAML (76) (Spearman's rank correlation tests gave  $z = 7.3, p = 2 \times 10^{-13}$  for the B clade, and  $z = 7.5, p = 5 \times 10^{-14}$ for the C clade). We used the entropy scores as our measure of variability here because they lent themselves to testing for differences in variability between the B clade and C clade (33). The color coding for the sites is as follows: white, invariant (entropy score of zero); light blue, very conserved (entropy score below the median, corresponding to only one observed substitution); medium blue, variable (entropy score above the median: 2 or more observed substitutions); dark blue, highly variable (highest 10% of entropy scores: > 0.8 for clade B and > 0.75 for clade C). Residues that are significantly more variable in clade B than in clade C or vice versa (p value < 0.03 after a Bonferroni correction for multiple tests, using a Monte Carlo scheme and randomizing the B and C clade data 10,000 times) are indicated by red circles. 123 clade B sequences and 48 clade C sequences were used for the analyses. The four glycans and the major antibody epitopes (non-neutralizing clusters I and II and the neutralizing 2F5/4E10/z13 cluster) are also indicated, as are regions labelled "indel" where insertions and deletions are frequently observed in natural variants.

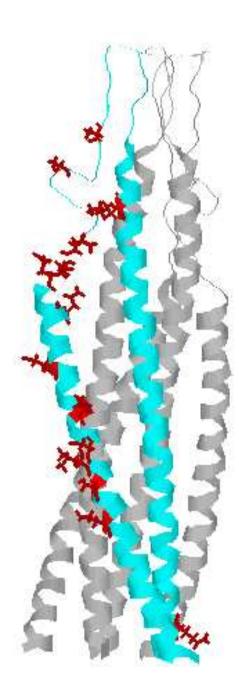


Figure 3: The residues with the highest 10% of entropy scores in clade B are indicated in red on the 3D structure model of Caffrey (pdb accession number 1IF3, (8)). These residues are only indicated in one monomer. The other two monomers are shown in grey for orientation purposes.

Residue <sup>1</sup>	Comments	Substitution	Isolate <sup>2</sup>	Reference	Expression (cell lysate) <sup>3</sup>	Expression (cell surface) <sup>4</sup>	gp160 processing <sup>5</sup>	gp120 association <sup>6</sup>	CD4-binding <sup>7</sup>	CD4-induced shedding <sup>8</sup>	Cell-cell fusion <sup>9</sup>	Virion incorporation $^{10}$	Virus entry <sup>11</sup>	Viral Replication <sup>12</sup>	Oligomerization $(gp160/gp140)^{13}$	Trimerization (SOS gp140) <sup>14</sup>	Thermal stability (gp41 core) <sup>15</sup>	B-clade entropy	C-clade entropy
WT A512		$V^{16}$	NL4-3	Freed90	++	++	++	++	++	++		++	++	++	++	+	++	0.126	0
A312		E	NL4-3 NL4-3	Freed90	++		++	++	++		+							0.136	U
V513		E E	NL4-3 NL4-3	Freed90	++ ++		++ ++	++ ++	++		+							0.326	0.44
V 313		E A	NL4-3 NL4-3	Buchschacher95	++		++	++	++		_							0.320	0.44
		G	NL4-3 NL4-3	Buchschacher93							++ ++								
		R	NL4-3 NL4-3		++		++				-								
G514		V	NL4-3 NL4-3	Delahunty96	++		++	++			++							0.628	0.594
G514 G516		V	NL4-3 NL4-3	Delahunty96	+++		++	++			++							0.028	0.101
A517		17	HXB2	Kowalski91	++	++	++	++	++		' '			++				0.115	0.101
11317		18	HXB2	Kowalski91	• •		• •							_				0.113	O
M518		$V^{19}$	ELI1	Kozak97					+++					++				0.985	0.658
F519		$L^{16}$	NL4-3	Freed90	++		++	++	++		+			• •				0.19	0.473
1317		V	NL4-3	Delahunty96	+++		++	++			++			++				0.17	0.175
L520		R	NL4-3	Freed90	++		++	++	++		_							0.13	0.101
G521		V	NL4-3	Delahunty96	+	++	++	++			_			_				0	0
F522		V	NL4-3	Delahunty96	+++		++	++			+							0	0.302
		G	BH8	Pritsker99	++		++				+								
G524		V	NL4-3	Delahunty96	+++	++	++	++			+			+				0.083	0.101
A525		$T^{20}$	LAI	Bahbouhi01	++		++					++		++				0.115	0.202
A526		E	NL4-3	Freed90	++		+	+	++		_							0	0
G527		V	NL4-3	Delahunty96	+++		++	_			_							0	0
S528		T	HXB2	Cao93		+	+	_		+	_		+					0	0
M530		S	HXB2	Cao93		++	_	_		+	_		_					0	0
G531		V	NL4-3	Delahunty96	+++		++	++			++							0	0
L537		R	NL4-3	Freed90	++		+	+	++		_							0	0
V539		E	NL4-3	Freed90	++		++	++	++		+							0.083	0.334
Q540		L	NL4-3	Freed90	++		+	+	++		_							0	0
R542	e in heptad-repeat	G	NL4-3	Freed90	++		++	++	++		+							0	0.101
Q543	f in heptad-repeat	Н	PI	Wei02, Kilby02										++				0.811	0.202
		R												++					
P543		$L^{28}$	MN	Park00										++					
L544	g in heptad-repeat	S <sup>22</sup>	PI	Fikkert02										++				0.094	0.234

F242 Residue	steemen OO a in heptad-repeat	uoinninsquo $S$ F <sup>21</sup> N <sup>21</sup> P <sup>21</sup> G <sup>21</sup>	Isolate lsolate lsolat	Reference Sanders02	Expression (cell lysate) <sup>3</sup>	‡ ‡ ‡ † Expression (cell surface) <sup>4</sup>	gp160 processing <sup>5</sup>	gp120 association <sup>6</sup>	${ m CD4-binding}^7$	CD4-induced shedding <sup>8</sup>	Cell-cell fusion <sup>9</sup>	Virion incorporation <sup>10</sup>	Virus entry <sup>11</sup>	Viral Replication <sup>12</sup>	Oligomerization (gp160/gp140) $^{13}$	+ + + + Trimerization + $(SOS gp140)^{14}$	Thermal stability (gp41 core) <sup>15</sup>	O.047	<ul> <li>C-clade entropy</li> </ul>
G547	c in heptad-repeat	$S^{22}$ $D^{22}$ $D^{22}$ $V^{22}$ $D^{22}$	NL4-3 NL4-3 PI PI PI	Rimsky98  Baldwin03 Poveda02 Wei02		TT								++ ++ ++ ++		т		0	0.101
I548	d in heptad-repeat	A T <sup>22</sup> K <sup>22</sup> V <sup>22</sup> V <sup>21</sup> L <sup>21</sup> H <sup>21</sup> S <sup>21</sup> G <sup>21</sup> R <sup>21</sup>	HXB2 NL4-3 PI PI JR-FL JR-FL JR-FL JR-FL JR-FL JR-FL	Cao93 Rimsky98 Baldwin03 Wei02, Kilby02 Sanders02	++	++	+	+++		++	+		++	++ ++ ++		+ + + + + + + +		0	0.101
V549	e in heptad-repeat	M <sup>22</sup> M <sup>22</sup> A <sup>22</sup> A <sup>22</sup> W <sup>22</sup> G <sup>22</sup> A	NL4-3 PI PI PI PI PI HXB2	Rimsky98 Wei02 Baldwin03		++	++	++			++			++ ++ ++ ++ ++			++	0.047	0
Q551 Q552 N554	g in heptad-repeat a in heptad-repeat c in heptad-repeat	A L K <sup>22</sup>	HXB2 HXB2 PI	Lu01, Follis02 Cao93 Fikkert02	++	++	++	++			++ -		++	++			++	0 0 0.047	0 0 0

Residue <sup>1</sup>	Comments	Substitution	Isolate <sup>2</sup>	Reference	Expression (cell lysate) <sup>3</sup>	Expression (cell surface) <sup>4</sup>	gp160 processing <sup>5</sup>	gp120 association <sup>6</sup>	CD4-binding <sup>7</sup>	CD4-induced shedding <sup>8</sup>	Cell-cell fusion <sup>9</sup>	Virion incorporation 10	Virus entry <sup>11</sup>	Viral Replication <sup>12</sup>	Oligomerization $(gp160/gp140)^{13}$	Trimerization (SOS gp140) <sup>14</sup>	Thermal stability (gp41 core) <sup>15</sup>	B-clade entropy	· C-clade entropy
L555	d in heptad-repeat	G	HXB2	Cao93	++		_	_			_							0	0
		A V <sup>21</sup>	BH8 JR-FL	Poumbourios97 Sanders02	++		_		++		_				++				
		$\mathbf{W}^{21}$	JR-FL	Sanuers02		_													
		$\mathbf{Y}^{21}$	JR-FL			_													
		$S^{21}$	JR-FL			_													
		$P^{21}$	JR-FL			_													
L556	e in heptad-repeat	P	HXB2	Chen94	++		+	_					_					0.047	0
		R	HXB2	Weng98	_						_		_						
		E A	HXB2 HXB2		+						_		_						
		D	HXB2	Weng00	++	_	++					++	_						
		G	HXB2	vvengoo	++		++					++	_						
		K	HXB2		_								_						
		N	HXB2		++		++					++	_						
		A	HXB2	Lu01, Follis02		++	+	++			_		+				++		
		$P^{21}$	JR-FL	Sanders02		++										+			
R557	f in heptad-repeat	$P^{21}$	JR-FL	Sanders02		++										+		0.237	0.334
A 550	. 1 . 1	M	PI	Wei02										++				0	0
A558	g in heptad-repeat	R E	HXB2 HXB2	Weng98	+								_					0	0
		C	HXB2	Weng00	++		++					++	_						
		G	HXB2		++		++					++	_						
		T	HXB2		++		++					++	+						
		$P^{21}$	JR-FL	Sanders02		++										+			

Residue <sup>1</sup>	Comments	d Substitution	Isolate <sup>2</sup>	Seference Chen93, Chen94	‡ Expression (cell lysate) <sup>3</sup>	Expression (cell surface) <sup>4</sup>	gp160 processing <sup>5</sup>	gp120 association <sup>6</sup>	. CD4-binding <sup>7</sup>	CD4-induced shedding <sup>8</sup>	Cell-cell fusion <sup>9</sup>	Virion incorporation $^{10}$	Virus entry <sup>11</sup>	Viral Replication <sup>12</sup>	Oligomerization (gp160/gp140) $^{13}$	Trimerization (SOS gp140) <sup>14</sup>	Thermal stability (gp41 core) <sup>15</sup>	B-clade entropy	<ul> <li>C-clade entropy</li> </ul>
1559	a in heptad-repeat	A	BH8	Poumbourios97	++	++	_	_	++ ++		_		_		++ ++			0.047	U
		$V^{21}$	JR-FL	Sanders02	TT	+	_		TT						77	+			
		$F^{21}$	JR-FL	Sunder 502		_										+++			
		$N^{21}$	JR-FL			_										+++			
		$P^{21}$	JR-FL			++	++									+++	_		
		$G^{21}$	JR-FL			+	++									+++	+		
		$R^{21}$	JR-FL	G 1 021		+										+++			
		P	LAI/ JR-FL	Sanders03b										_			_		
		G	JK-FL LAI/											_			+		
		J	JR-FL																
		L	LAI/											++			++		
			JR-FL																
E560	b in heptad-repeat	P <sup>21</sup>	JR-FL	Sanders02		+++										+		0.217	0
1.561		G <sup>19</sup> P <sup>21</sup>	ELI1	Kozak97							+							0.004	0.101
A561 S561	c in heptad-repeat	$A^{28}$	JR-FL MN	Sanders02 Park00		+++										+		0.094	0.101
Q562	d in heptad-repeat	L	HXB2	Cao93	++		+	_			_			++				0	0.101
Q302	a in neptad-repeat	A	BH8	Poumbourios97	++		++	+	++		_				++			O	0.101
		$P^{21}$	JR-FL	Sanders02	• •	+++		•								+			
Q563	e in heptad-repeat	A	HXB2	Weng00	++		++					++	++					0.047	0
		E	HXB2		++		++					++	_						
		M	HXB2		++		++					++	_						
		G	HXB2		++		++					++	++						
		R A	HXB2 HXB2	Lu01, Follis02	++	++	++	++				++	++				++		
		$P^{21}$	JR-FL	Sanders02		+++	TT	TT			++		TT			+	TT		
R564	f in heptad-repeat	$P^{21}$	JR-FL	Sanders02		+++										+		0.047	0
H564	1	$N^{28}$	MN	Park00										++					
		$C^{26}$	HXB2	Rabenstein95											++				
L565	g in heptad-repeat	P	HXB2	Chen94	++	++	+	++	++		_							0.402	0.584
		A - 21	HXB2	Lu01, Follis02		++	++	++			_		_				+		
		$P^{21}$	JR-FL	Sanders02		++										+			

P2997	st un mentad-repeat	uoinninsquo G P A V <sup>23</sup> V <sup>21</sup> I <sup>21</sup> V <sup>21</sup> T <sup>21</sup> P <sup>21</sup> K <sup>21</sup>	Colate NXB2 HXB2 BH8 BH8 JR-FL JR-FL JR-FL JR-FL	Cao93 Chen93, Chen94 Poumbourios97 Earl93 Sanders02	‡ ‡ Expression (cell lysate) <sup>3</sup>	++++ + # Expression (cell surface) <sup>4</sup>	+ + + gp160 processing <sup>5</sup>	+ + gp120 association <sup>6</sup>	$\ddagger \ddagger \ddagger CD4-binding^7$	CD4-induced shedding <sup>8</sup>	Cell-cell fusion <sup>9</sup>	Virion incorporation <sup>10</sup>	+ Virus entry <sup>11</sup>	Viral Replication <sup>12</sup>	$\ddagger \ddagger \ddagger$ Oligomerization $(gp160/gp140)^{13}$	$+ + \ddagger + \ddagger + \ddagger$ Trimerization <sub>14</sub> (SOS gp140) <sup>14</sup>	Thermal stability (gp41 core) <sup>15</sup>	B-clade entropy 0.047	O C-clade entropy
Q567	b in heptad-repeat	R	LAI	Sanders03a										++			++	0.177	0
L568	c in heptad-repeat	A	HXB2	Cao93	++	++	+	++	++	++	_		+					0	0
		P	HXB2 HXB2	Chen94 Ji00	++	++	+	+	++		_								
T569	d in heptad-repeat	A A	BH8	Poumbourios 97	++		_		++						++		+	0	0.101
1309	u iii iieptau-repeat	C	HXB2	Farzan98	TT		_		TT		_				TT			U	0.101
		$S^{21}$	JR-FL	Sanders02		+										+			
		$\mathbf{P}^{21}$	JR-FL	Sundersoz		+	++									++	+		
		$K^{21}$	JR-FL			+										++			
		$E^{21}$	JR-FL			_													
V570	e in heptad-repeat	R	HXB2	Weng98	++	++			++		_	++	_					0	0
		$E^{35}$	HXB2		++	++			++			++							
		A	HXB2	Weng00	++		++					++	_						
		D	HXB2		++		++					++	-						
		E	HXB2		++		++					++	_						
		G	HXB2		++		++					++	-						
		I	HXB2	I 01 E 11 02	++		++					++	++						
W571	fin hantad samaat	A	HXB2	Lu01, Follis02		++	++	++			_		_				+	0	0
W 3 / 1	f in heptad-repeat	R R	HXB2 HXB2	Cao93 Ji00	++	++	+	++	++	_	_		_				++	U	U
		$C^{26}$	HXB2	Rabenstein95											++		T' <b>T</b>		
G572	g in heptad-repeat	G	HXB2	Weng98	++	_			++		_	_	_					0	0
00.2	S nopula repout	A	HXB2	Lu01		++	++	++			_						+++	-	~

Residue <sup>1</sup>	Comments	Substitution	Isolate <sup>2</sup>	Reference	Expression (cell lysate) <sup>3</sup>	Expression (cell surface) <sup>4</sup>	gp160 processing <sup>5</sup>	gp120 association <sup>6</sup>	CD4-binding <sup>7</sup>	CD4-induced shedding <sup>8</sup>	Cell-cell fusion <sup>9</sup>	Virion incorporation $^{10}$	Virus entry <sup>11</sup>	Viral Replication <sup>12</sup>	Oligomerization (gp160/gp140) <sup>13</sup>	Trimerization (SOS gp140) <sup>14</sup>	Thermal stability (gp41 core) <sup>15</sup>	B-clade entropy	C-clade entropy
I573	a in heptad-repeat	L	HXB2	Dubay92	++		++	++			++	++		++	++			0.083	0
		V	HXB2		++	++	++	++			++	++		++	++				
		A	HXB2 HXB2		++		++	++			+	++		+	++				
		G E	HXB2		++	++	++	++			_	++		_	++				
		D D	HXB2		++	++	++	++			_	++		_	++ ++				
		S	HXB2		++		++	++			_	++		_	++				
		P <sup>24</sup>	HXB2	Bernstein95	TT		77	77				TT			_				
		$A^{24}$	HXB2	Bernstein/3											+				
		$D^{24}$	HXB2												_				
		$A^{25}$	HXB3	Shugars96											++				
		$S^{25}$	HXB3	Shagaraya											_				
		P	HXB2	Chen93, Chen94	++	+++	+	+	++		_		_		++				
		$P^{26}$	HXB2,	Wild94	++		++	+			_						_		
			LAI																
		$A^{26}$	HXB2,		++	++	++	++			+			+			_		
			LAI																
		$S^{26}$	HXB2,		++	++	++	++			_			_			_		
			LAI																
		$P^{26}$	HXB2	Rabenstein95											_				
		$D^{26}$	HXB2												_				
		$S^{26}$	HXB2												_				
		S	168P	Liu01													_		
		T	168P			++	++	++			++	++	++				+		
		V	LAI	Sanders03a										++			++		
		A	BH8	Poumbourios97	++		++	++	++		_				++				
		V	HXB2	Markosyan02													++		
		A	HXB2														+		
		S	HXB2 HXB2														+		
		$_{\mathrm{L}^{21}}^{\mathrm{P}}$	JR-FL	Sanders02													_		
		F <sup>21</sup>	JR-FL JR-FL	Saliucisuz		++										++			
		$Y^{21}$	JR-FL JR-FL			++													
		$Q^{21}$	JR-FL JR-FL			++										+			
		Ų	JK-FL			++										+			

Residue <sup>1</sup>	Comments	Substitution	Isolate <sup>2</sup>	Reference	Expression (cell lysate) <sup>3</sup>	Expression (cell surface) <sup>4</sup>	gp160 processing <sup>5</sup>	gp120 association <sup>6</sup>	CD4-binding <sup>7</sup>	CD4-induced shedding <sup>8</sup>	Cell-cell fusion <sup>9</sup>	Virion incorporation $^{10}$	Virus entry <sup>11</sup>	Viral Replication <sup>12</sup>	Oligomerization (gp160/gp140) <sup>13</sup>	Trimerization (SOS gp140) <sup>14</sup>	Thermal stability (gp41 core) <sup>15</sup>	B-clade entropy	C-clade entropy
I573 (cont)		$N^{21}$ $T^{21}$	JR-FL JR-FL			++ ++										+ +			
(00111)		$P^{21}$	JR-FL			++										+			
		$G^{21}$	JR-FL			++										+			
K574	h in hantad ranget	K <sup>21</sup> R	JR-FL BH8	MaInamay 00		++										+		0	0
L576	b in heptad-repeat d in heptad-repeat	R P	нхв2	McInerney98 Chen94	++ ++		++	++	++ ++	++	+							0	$0 \\ 0$
2370	a in neptace repeat	A	BH8	Poumbourios97	++		_		++		_				++			Ü	Ü
		$C^{27}$	HXB2	Farzan98	++	+	_								+++				
		$V^{21}$	JR-FL	Sanders02		_										+			
		$F^{21}$	JR-FL			_										+			
		$Y^{21}$	JR-FL			_										+			
		$Q^{21} N^{21}$	JR-FL			_										+			
		$G^{21}$	JR-FL JR-FL			_										+			
		K <sup>21</sup>	JR-FL JR-FL			_										+			
Q577	e in heptad-repeat	R	HXB2	Weng98	++	++			++			++	_			Т		0.047	0.173
<b>C</b>	F	E	HXB2		++	++			++		+	+	+						
		A	HXB2	Weng00	++		++					++	+						
		D	HXB2		++		++					++	++						
		E	HXB2		++		++					++	+						
		G	HXB2		++		++					++	++						
		M C <sup>27</sup>	HXB2 HXB2	Г 00	++		++					++	+						
		A	HXB2	Farzan98 Lu01	++	+ ++	- ++	++			++				+++		++		
A578	f in heptad-repeat	$G^{27}$	HXB2	Farzan98	++	+	_	TT			TT				+++		TT	0.047	0.483
R579	g in heptad-repeat	G	HXB2	Weng00	++	•	+					++	_					0	0.101
		A	HXB2	Lu01		++	+	++			_						++		

Residue <sup>1</sup>	O common of the contract of th	d Substitution	Isolate <sup>2</sup>	Reference Chen94	‡ Expression (cell lysate) <sup>3</sup>	‡ Expression (cell surface) <sup>4</sup>	+ gp160 processing <sup>5</sup>	gp120 association <sup>6</sup>	† CD4-binding <sup>7</sup>	CD4-induced shedding <sup>8</sup>	Cell-cell fusion <sup>9</sup>	Virion incorporation $^{10}$	Virus entry <sup>11</sup>	Viral Replication <sup>12</sup>	Oligomerization (gp160/gp140) <sup>13</sup>	Trimerization $(SOS gp140)^{14}$	Thermal stability (gp41 core) <sup>15</sup>	D-clade entropy 8-78	C-clade entropy
		A	BH8	Poumbourios97	++		++	++	++		_				++				*****
		$L^{21}$	JR-FL	Sanders02		++										+			
		$\frac{H^{21}}{T^{21}}$	JR-FL			++										+			
		P <sup>21</sup>	JR-FL JR-FL			++ ++										+ +			
		$G^{21}$	JR-FL			++										+			
L581	b in heptad-repeat	$Q^{28}$	MN	Park00										++				0	0
A582	c in heptad-repeat	$T^{28}$	PI	Reitz88										++				0.094	0.101
		$C^{26}$	HXB2	Rabenstein95											++				
V583	d in heptad-repeat	A	BH8	Poumbourios97	++		+	++	++		_				++			0.244	0.503
		C L <sup>21</sup>	HXB2	Farzan98			_												
		$Q^{21}$	JR-FL JR-FL	Sanders02		++										+			
		N <sup>21</sup>	JR-FL JR-FL			++ ++										+ +			
		$S^{21}$	JR-FL			++										+			
		$P^{21}$	JR-FL			++										+			
		$R^{21}$	JR-FL			++										+			
		$K^{21}$	JR-FL			++										+			
E584	e in heptad-repeat	A	HXB2	Cao93		++	_	-		+	_		_					0	0
		Q	BH8	Maerz01	++	++	++	+			+								
		D N	BH8 BH8		++ ++		++				+								
Y586	f in heptad repeat	R	HXB2	Weng98	++	+	TT		++		_	+	_					0	0.101
1000	r in neptua repeat	E	HXB2	,,eng,o	++	+			++			+	_					Ü	0.101
		$C^{29}$	HXB2	Farzan98			_												
L587	a in heptad-repeat	P	HXB2	Chen93, Chen94	++	++	++	_	++		_		_		++			0	0
		A	BH8	Poumbourios97	++		++	++	++		_				++				
		$C^{29}$	HXB2	Farzan98			_												
		$A^{21}$ $P^{21}$	JR-FL JR-FL	Sanders02		_										+			
		R <sup>21</sup>	JR-FL JR-FL			_										+ +			
		$D^{21}$	JR-FL			_										+			
		$E^{21}$	JR-FL			_										+			

Residue <sup>1</sup>	Comments	Substitution	Isolate <sup>2</sup>	Reference	Expression (cell lysate) <sup>3</sup>	Expression (cell surface) <sup>4</sup>	gp160 processing <sup>5</sup>	gp120 association <sup>6</sup>	CD4-binding <sup>7</sup>	CD4-induced shedding <sup>8</sup>	Cell-cell fusion <sup>9</sup>	Virion incorporation $^{10}$	Virus entry <sup>11</sup>	Viral Replication <sup>12</sup>	Oligomerization (gp160/gp140) <sup>13</sup>	Trimerization (SOS gp140) <sup>14</sup>	Thermal stability (gp41 core) <sup>15</sup>	B-clade entropy	C-clade entropy
K588		R	BH8	McInerney98	++		++	++	++	++	++							1.112	0.775
D589		L	HXB2	Cao93	++	++	+++	+	++	+	-		+					0	0.101
		$C^{30}$	JR-FL	Binley00		++													
		K	BH8	Maerz01	++	++	++	+			-								
Q591		A	BH8	Maerz01	++	++	++	++			++							0.083	0.101
		K	BH8		++		++				++								
		L	LAI	Sanders03c										+					
L592		V	BH8	Maerz01	++		++				++							0	0.101
		A	BH8		++		++				++								
L593		V	BH8	Maerz01	++		++				+		_					0.143	0
		A	BH8		++	++	++	_			+		-						
		Q	LAI	Sanders03c										+/-					
I595		$F^{31}$	PI	Moore93										++				0.162	0.555
W596		M	HXB2	Cao93, Cao94	++	++	++	+	++		-		++	++	++			0	0
		Y	LAI, NL4-3	Rovinski99			++					++							
		A	LAI,				_					+							
			NL4-3																
		$C^{30}$	JR-FL	Binley00		++													
		F	BH8	Maerz01	++	++	++	+			++		++						
		Н	BH8		++		++				+								
		L	BH8		++	++	++	+			+								
G597		P	BH8	Maerz01	++	++	++	_			_							0	0
		A	BH8		++	++	++	_			_								
		S	BH8		++	++	++	_			_								
C598		S	HXB2	Dedera92a	++		_				_							0	0
		$S^{23}$	BH8	Earl93		++	++		++						++				
		G	HXB2	Syu91	++		_							_					
		A	LAI	Van Anken03										_					
G600		A	LAI, NL4-3	Rovinski99			++					++						0	0.101

Residue <sup>1</sup>	Comments	N N Substitution	Solate <sup>2</sup> Isolate <sup>3</sup> LAI, NL4-3	McInerney98 Rovinski99	‡ Expression (cell lysate) <sup>3</sup>	Expression (cell surface) <sup>4</sup>	† † gp160 processing <sup>5</sup>	‡ gp120 association <sup>6</sup>	‡ CD4-binding <sup>7</sup>	† CD4-induced shedding <sup>8</sup>	‡ Cell-cell fusion <sup>9</sup>	† Virion incorporation <sup>10</sup>	Virus entry <sup>11</sup>	Viral Replication <sup>12</sup>	Oligomerization $(gp160/gp140)^{13}$	Trimerization (SOS gp140) <sup>14</sup>	Thermal stability (gp41 core) <sup>15</sup>	B-clade entropy	O C-clade entropy
		E	LAI, NL4-3				++					++							
		E	BH8	Merat99	++		+				++								
		E	BH8	Maerz01	++	++	++	+			++								
		H	BH8		++		++	+			++								
		Q	BH8		++		++	+			++								
C604		A S	BH8 HXB2	Dedera92a	++ ++		++				++							0.047	0
C00 <del>4</del>		$S^{23}$	BH8	Earl93	77	++	++		++		_				++			0.047	U
		G	HXB2	Syu91	++		_							_					
		A	LAI	Van Anken03										_					
T605		C <sup>30</sup>	JR-FL, HXB2, DH123, 89.6, GUN1-	Binley00		++	++	+++	++						+			0.177	0.173
		-	wt	G 1 02															
		C Y	LAI LAI	Sanders03c										++					
V608		S	HXB2	Cao93			_	_			_			TT				0.094	0.101
		$C^{30}$	JR-FL	Binley00		++													
P609		$C^{30}$	JR-FL	Binley00		++												0.047	0.101
W610		$C^{30}$	JR-FL	Binley00		++												0.047	0
		F	BH8	Maerz01	++	++	++	-			_								
N/C11	Cl	Н	BH8	D - 1 021-	++	++	++	-			-							0.141	0
N611	Glycosylation site	Q H	HXB2 HXB2	Dedera92b Lee92	++ ++		++ ++	++			+	++		++	++			0.141	0
		S	NL4-3	Dash94	++	++	++				++	77		т.					
		Q	SHIV- KB9	Johnson01	++		++							++					
S613	Glycosylation site N611	A	HXB2	Lee92	++		++							+				0.94	0.274

Nessidue <sup>1</sup>	Student of the state of the sta	uoitntious Q Q H S Q Q Q Q Q Q Q Q Q Q Q Q Q Q Q Q	HXB2 BH8 HXB2 NL4-3 BH10 SHIV- KB9	Dedera92b Earl93 Lee92 Dash94 Perrin98 Johnson01	+ + + + Expression (cell lysate) <sup>3</sup>	‡ ‡ Expression (cell surface) <sup>4</sup>	+ + + + + + gp160 processing <sup>5</sup>	gp120 association <sup>6</sup>	$\ddagger$ CD4-binding <sup>7</sup>	CD4-induced shedding <sup>8</sup>	+ $\ddagger$ + Cell-cell fusion <sup>9</sup>	† Virion incorporation <sup>10</sup>	Virus entry <sup>11</sup>	‡ ‡ Viral Replication <sup>12</sup>	Oligomerization $+$ $(gp160/gp140)^{13}$	Trimerization (SOS gp140) <sup>14</sup>	Thermal stability (gp41 core) <sup>15</sup>	B-clade entropy 0.237	O C-clade entropy
K617		R	BH8	McInerney98	++		++											0.348	0.658
S618	Glycosylation site N616	A	HXB2	Lee92	++		++	-	'''					-				0.495	0.483
N624	d in heptad-repeat Glycosylation site	Н	HXB2	Lee92	++		++					++		+				1.153	1.305
	(N625 in most	Q	BH10	Perrin98	++		++				++								
	isolates)	Q	SHIV- KB9	Johnson01	++		++							++					
N625	e in heptad-repeat Glycosylation site	$Q^{23}$	BH8	Earl93		++	++		++						++			0.047	0.274
T626	f in heptad-repeat Glycosylation site N624	M	HXB2	Cao93	++	_	-	_		_	_		-					0.244	0.444
		$M^{28}$	SHIV- HXBc2P	Si01										++					
W628	a in heptad-repeat	M	HXB2	Cao93			_	_		_	_							0	0
		A	HXB2	Weng00	++		_					++	_						
		F	HXB2	C	++		_					++	_						
		A	HXB2	Wang02		++	_	++			_						+		
W631	d in heptad-repeat	A	HXB2	Wang02		++	_	++			_						_	0	0.101
D632	e in heptad-repeat	$N^{32}$	BH10	Perrin98	++		++				_							0.591	0.287
R633	f in heptad-repeat	G	PI	Wei02										++				0.55	0.451
I635	a in heptad-repeat	A	HXB2	Wang02		++	_	++			_						+	0.047	0.173

Residue	c in heptad-repeat	uoinnissans K <sup>22</sup> Q Q <sup>23</sup> H S Q Q	PI HXB2 BH8 HXB2 NL4-3 BH10 SHIV- KB9	Baldwin03 Dedera92b Earl93 Lee92 Dash94 Perrin98 Johnson01	+ + + + + Expression (cell lysate) <sup>3</sup>	Expression (cell surface) <sup>4</sup>	+ + + + + gp160 processing <sup>5</sup>	gp120 association <sup>6</sup>	† CD4-binding <sup>7</sup>	CD4-induced shedding <sup>8</sup>	†   † Cell-cell fusion <sup>9</sup>	† Virion incorporation 10	Virus entry <sup>11</sup>	‡ † Viral Replication <sup>12</sup>	+ Oligomerization $(gp160/gp140)^{13}$	Trimerization (SOS gp140) <sup>14</sup>	Thermal stability (gp41 core) <sup>15</sup>	Declade entropy	O.101
Y638	d in heptad-repeat	A	HXB2	Wang02		++	++	++					++				++	0.13	0
T639	e in heptad-repeat	V	HXB2	Lee92	++		++							+				0.083	0.202
	Glycosylation site																		
	N637	A	HXB2	Cao93	++	_	_			_	_								
I642	a in heptad-repeat	A	HXB2	Wang02		++	_	++			_						++	0.094	0
		A	HXB2	Markosyan02													++		
11640		S Y <sup>20</sup>	HXB2	D 11 1101													++	0.115	0
H643	b in heptad-repeat		LAI	Bahbouhi01	++		++					++		++				0.115	0
T C 45	11 1 4 1 4	Y	LAI	Sanders03a										++				0	0
L645 E647	d in heptad-repeat	A L	H64333 HXB2	Wang02 Cao93		++	++	++					++				++	0 0.188	0 0.173
S649	f in heptad-repeat	L A	HXB2			++	+++	+			++		++					0.188	0.173
Q652	a in heptad-repeat d in heptad-repeat	A L	HXB2	Wang02 Cao93		++	++	++			++		++				++	0.401	0.101
Q032	u iii neptau-repeat	L L	HXB2	Shu00		++	++	+			++		++				++	0.047	0.101
		A	HXB2	Wang02		++	++	++					++				++		
K655	g in heptad-repeat	$R^{33}$	BH8	Poumbourios95	++		++	++			++						• • •	0.213	1.093
N656	a in heptad-repeat	L	HXB2	Cao93	++	++	+	++	++	++	_		+					0.213	0
L663	2F5 epitope	F	HXB2	Cao93		++	+++	++			++		++					0.047	0.101
K665	2F5 epitope	$R^{33}$	BH8	Poumbourios95	++		++	++			++							0.451	0.922
W666	2F5 epitope	P	HXB2	Cao93		++	++	++			++		++					0.047	0.101
		A	HXB2,	Salzwedel99	++		++	++			++								
			NL4-3																
S668	2F5 epitope	$N^{28}$	HXB2	Back93										++				0.497	0.573
L669		P	HXB2	Cao93		+++	++	+		+++	++		++					0.047	0
W670		Α	HXB2,	Salzwedel99	++		++	++			++							0.047	0
	474044 <b>a</b> :	-	NL4-3	a														0.5	0.0:-
N671	4E10/z13 epitope	P	HXB2	Cao93		++	++	++			++		++					0.713	0.945

Residue <sup>1</sup>	St me me of the state of the st	d S Substitution	HXB2 HXB2, NL4-3 HXB2, NL4-3	Salzwedel99	: ‡ ‡ Expression (cell lysate) <sup>3</sup>	‡ Expression (cell surface) <sup>4</sup>	:	$\div$ $\ddagger$ + gp120 association <sup>6</sup>	${ m CD4-binding}^7$	† CD4-induced shedding <sup>8</sup>	$\div$ $\ddagger$ $\ddagger$ Cell-cell fusion <sup>9</sup>	. Virion incorporation 10	. + ‡ Virus entry <sup>11</sup>	Viral Replication <sup>12</sup>	Oligomerization $(gp160/gp140)^{13}$	Trimerization (SOS gp140) <sup>14</sup>	Thermal stability (gp41 core) <sup>15</sup>	O B-clade entropy	• C-clade entropy
		F	HXB2, NL4-3		++		++	++			++	+	+						
F673	4E10/z13 epitope	P	HXB2	Cao93	++	++	++	+			++		++					0.94	0
		$S^{34}$	HXB2	Stern95							++			++					
N674	4E10/z13 epitope	Н	HXB2	Lee92	++		++					++		++				1.038	1.375
		S	NL4-3	Dash94	++	++	++				++								
		$D^{28}$	SHIV-	Si01										++					
1675	4E107.10	C	HXBc2F															0	0
I675	4E10/z13 epitope	S M <sup>28</sup>	HXB2	Cao93		++	++	+			++		++					0	0
N677		R	HXB2 HXB2	Back93 Cao93		++	++				++		++	++				1.237	0.769
W678		A	HXB2	Cao93		++	++	+			++		++					0	0.709
*******		A	HXB2,	Salzwedel99	++		++	++			++							O	U
		7.	NL4-3	Saizwedelyy			• • •												
W680		A	HXB2,	Salzwedel99	++		++	++			++							0.047	0.101
			NL4-3																
Y681		P	HXB2	Cao93			++	++			++		++					0	0
K683		R	BH8	McInerney98	++		++	++	++	++	++							0.375	0.325

#### **Table footnotes:**

<sup>&</sup>lt;sup>1</sup> Residue numbering is based on HXB2 gp160, although the amino-acids studied may be different in the isolate used. The one-letter code for amino acids is used <sup>2</sup>PI: primary isolate

<sup>&</sup>lt;sup>3</sup>As assessed by western blot or immunoprecipitation. –, minimal or no expression; +, reduced expression; ++, expression similar to WT; +++, increased expression <sup>4</sup>As assessed by surface biotinylation, iodination or FACS. When soluble gp140 constructs were used, the relative secretion levels (western blot or immunoprecipitation) are given. –, minimal or no expression; +, reduced expression; ++, expression similar to WT; +++, increased expression

<sup>&</sup>lt;sup>5</sup>As assessed by western blot or immunoprecipitation in combination with densitometric measurements. –, minimal or no processing; +, reduced processing; ++, processing similar to WT; +++, increased processing

- <sup>10</sup>As assessed by western blot or immunoprecipitation. –, minimal or no incorporation; +, reduced incorporation; ++, incorporation similar to WT
- <sup>11</sup>As assessed by various assays (replication complementation, use of reporter genes, p24 production). –, entry lower than 3% of WT; +, entry between 3 and 30% of WT; ++, entry greater that 30% of WT
- <sup>12</sup>–, no apparent replication; +, replication with a delay of more than 2 days compared to WT; ++ replication similar to WT
- <sup>13</sup>As assessed by sucrose gradient fractionation, immunoprecipitation, velocity sedimentation or FPLC, unless indicated otherwise. –, oligomerization below 25% of WT; +, oligomerization between 25% and 50% of WT; ++, oligomerization similar to WT. No distinction between dimerization, trimerization or tetramerization is made.
- <sup>14</sup>As assessed by Blue Native-PAGE. +, trimerization similar to WT SOS gp140 (occasional trimerization); ++, slightly more trimerization than in WT; +++, significantly more trimerization than in WT.
- $^{15}$ As analyzed using the N34(L6)C28 or N36(L6)C34 peptide model, unless indicated otherwise. –, melting temperature ( $T_m$ ) below 40°C; +,  $T_m$  between 40°C and 60°C; +++,  $T_m$  between 60°C and 80°C; +++,  $T_m$  over 80°C

<sup>&</sup>lt;sup>6</sup>As assessed by western blot or immunoprecipitation in combination with densitometric measurements. –, minimal or no association; +, reduced association; ++, association similar to WT; +++, increased association

<sup>&</sup>lt;sup>7</sup>As assessed by immunoprecipitation with CD4-based reagents. ++, similar to WT; +++, increased CD4 binding

<sup>&</sup>lt;sup>8</sup>As assessed by immunoprecipitation. –, no shedding; +, reduced shedding; ++, shedding similar to WT; +++, increased shedding. Note that CD4-induced shedding and to a lesser extent gp120 association (*i.e.*, the reverse of shedding), when measured in laboratory isolates, might be diminished in primary isolates that can retain gp120 more efficiently.

<sup>&</sup>lt;sup>9</sup>As assessed by syncytium formation or reporter gene assays. –, fusion lower than 3% of WT; +, fusion between 3 and 30% of WT; ++, fusion greater than 30% of WT

<sup>&</sup>lt;sup>16</sup>Analyzed in a double mutant, A512V + F519L

<sup>&</sup>lt;sup>17</sup>Four amino-acid insertion GIPA

<sup>&</sup>lt;sup>18</sup>Six amino-acid insertion IHRWIA

<sup>&</sup>lt;sup>19</sup>Involved in cell line adaptation

 $<sup>^{20}</sup>$ Identified in an isolate which is resistant to the furin inhibitor ( $\alpha$ 1-PDX)

<sup>&</sup>lt;sup>21</sup>Analyzed in soluble SOS gp140 constructs and so also contain the A501C and T605C substitutions

<sup>&</sup>lt;sup>22</sup>Involved in T-20 resistance

<sup>&</sup>lt;sup>23</sup>Analyzed in soluble gp140

<sup>&</sup>lt;sup>24</sup>Analyzed in an N-peptide/Protein A fusion protein

<sup>&</sup>lt;sup>25</sup>Analyzed in an N-peptide/maltose binding protein (MBP) fusion protein

<sup>&</sup>lt;sup>26</sup>Thermal stability (74) or oligomerization (53) of N-peptides analyzed in the absence of C-peptides

<sup>&</sup>lt;sup>27</sup>Analyzed in a triple mutant L576C + Q577C + A578G

<sup>&</sup>lt;sup>28</sup>Involved in neutralization resistance

<sup>&</sup>lt;sup>29</sup>Analyzed in a double mutant Y586C + L587C

<sup>&</sup>lt;sup>30</sup>Analyzed in combination with gp120 cysteine substitutions in the context of soluble gp140

<sup>&</sup>lt;sup>31</sup>Involved in resistance to soluble CD4

<sup>&</sup>lt;sup>32</sup>Generates a new glycosylation site

<sup>&</sup>lt;sup>33</sup>Analyzed in a double mutant K655R + K665R

<sup>&</sup>lt;sup>34</sup>Analyzed in a double mutant A582T + F673S

<sup>&</sup>lt;sup>35</sup>Data on this mutant were corrected in reference 73

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# **Web-based Tools for Vaccine Design**

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#### Introduction

Computational methods used in vaccine design have been changing drastically in recent years. In classical immunological research results could be recorded by pen and pencil or in a spreadsheet, but new experimental high-throughput methods such as sequencing, DNA arrays, and proteomics have generated a wealth of data that are not efficiently handled and mined by these approaches. This has fueled the rapid growth of the field of Immunological Bioinformatics (or Immunoinformatics) that addresses how to handle these large amounts of data in the field of immunology and vaccine design. Many of the methods have been made available on the Internet and can be used by experimental researchers without expert knowledge of bioinformatics. This review attempts to give an overview over the methods currently available and to point out the strengths and weaknesses of the different methods.

## Immunological processes described by prediction servers

Only a small fraction of the possible peptides that can be generated from proteins of pathogenic organisms actually generate an immune response. In order to be presented to CD8+ T cells a precursor peptide must be generated by the proteasome. This peptide may be trimmed at the N-terminal by other peptidases in the cytosol (Levy et al., 2002). It must then bind to the transporter associated with antigen processing (TAP) in order to be translocated to the endoplasmatic reticulum (ER). Here it can be trimmed N-terminally by the aminopeptidase associated

with antigen processing (ERAAP) while it binds to the major histocompatibility complex class I (MHC I) molecule (Serwold, 2002). Hereafter it is transported to the cell surface. Only half the peptides presented on the cell surface are immunogenic probably due to the limited size of the T cell receptor (TCR) repertoire. The most selective step is binding to the MHC I molecule, since only 1/200 binds with an affinity strong enough to generate an immune response (Yewdell, 1999). For comparison the selectivity of TAP binding is reported to be 1/7 (Uebel et al., 1997). This all happens in competition with other peptides so in order for a peptide to be immunogenic (immunodominant) it must go through the above described process more efficiently than other peptides produced in a given cell (Reviewed by Yewdell, 1999).

Whereas the MHC I molecule mainly samples peptides from the cytosol, the MHC II molecule presents peptides from endocytosed proteins. Unfolded polypeptides bind to MHC II in the endocytic organelles (Reviewed by Castllino, 1997). Both MHC I and MHC II are highly polymorphic, and the specificity of the alleles are often very different. Different individuals will thus typically react to a different set of peptides from a pathogen.

The specificity of some of the processes involved in antigen presentation can be predicted from the amino acid sequence. This can for example be used to select epitopes for use in a vaccine, and help to understand the role of the immune system in infectious diseases, autoimmune diseases and cancers. Below we describe a number of resources available on the web that can perform such predictions.

## **Databases of MHC binding peptides**

Several databases of MHC binding peptides now exist on the web (Table 1).

**SYFPEITHI**: The SYFPEITHI database contains information on peptide sequences, anchor positions, MHC specificity, source proteins, source organisms, and publication references. The database comprise approximately 3500 peptide sequences known to bind class I and class II MHC molecules and is based on previous publications on T-cell epitopes and MHC ligands from many species (Rammensee, 1999).

**MHCPEP**: The other major database of MHC binding peptides, MHCPEP, (Brusic, 1997) comprises over 13,000 peptide sequences known to bind MHC

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submissions of experimental data. Each entry contains the peptide sequence, its MHC specificity and, when available, experimental method, observed activity, binding affinity, source protein, anchor positions, and publication references. Unfortunately the database has since June 1998 been static. The database can be downloaded as an ASCII file.

JenPep: The JenPep database is a newer database that contains quantitative binding data of peptides to MHC and TAP, as well as T cell epitopes (Blythe, 2001). The database contains more than 8000 entries.

**FIMM**: The database by Schoenbach & Brusic is a functional database of molecular immunology. The database contains 571 antigens and 1591 peptides (Schonbach et al., 2002)

MHCBN: (Bhasin, 2002) is a database of MHC binding and non-binding peptides containing 14,816 binders, 1,782 non-binders and 5,456 T-cell epitope entries.

HLA Ligand/Motif database: This site's database can be searched by defining allele and specificity, amino acid pattern, ligand/motif in sequence of amino acids, author's last name, or advanced search with more criteria.

HIV Molecular Immunology database: The HIV Molecular Immunology Database is an annotated, searchable collection of HIV-1 cytotoxic and helper T-cell epitopes and antibody binding sites. The goal of the database is to provide a comprehensive listing of defined HIV epitopes (Korber et al., 2001).

**EPIMHC**: MHC ligand database that can be searched based on sequence, length, class, species, and on whether a ligand is an epitope or not.

NIH will over the next five to seven years fund an "Immune Epitope Database and Analysis Program" to design, develop, populate, and maintain a publicly accessible, comprehensive Immune Epitope Database containing linear and conformational antibody epitopes and T cell epitopes. This database may eventually incorporate most of the data from the above described databases.

## **Prediction of MHC binding**

Several peptide-MHC binding prediction servers exist on the web (Table 2). As indicated in the table some of the web based methods also allow prediction of binding to Class II molecules. Most methods available on the web for predicting

molecules. Entries were compiled from published reports as well as from direct MHC-peptide binding are matrix methods. Parameters are often derived from pool sequencing of ligands. Matrices or hidden Markov models may however also be derived from a set of ligand sequences. In these methods the amino acid on each position in the motif gives an independent contribution to the prediction score. Neural networks are able to make more accurate predictions if correlations between positions exist, and there are enough data to model them. This has the potential advantage that it can take correlations between different positions in the binding motif into account.

> **BIMAS**: The BIMAS method was developed by Parker et al., (1994). The method is based on coefficient tables deduced from the published literature. For HLA-A2, peptide binding data were combined together to generate a table containing 180 coefficients (20 amino acids x 9 positions), each of which represents the contribution of one particular amino acid residue at a specified position within the peptide (Parker et al., 1994).

> **SYFPEITHI**: The SYFPEITHI prediction is based on published motifs (pool sequencing, natural ligands) and takes into consideration the amino acids in the anchor and auxiliary anchor positions, as well as other frequent amino acids. The score is calculated according to the following rules: The amino acids of a certain peptide are given a specific value depending on whether they are anchor, auxiliary anchor or preferred residue. Ideal anchors will be given 10 points, unusual anchors 6-8 points, auxiliary anchors 4-6 and preferred residues 1-4 points. Amino acids that are regarded as having a negative effect on the binding ability are given values between -1 and -3 (Rammensee, 1997; 1999). On the SYFPEITHI web site predictions can be made for 5 different MHC II alleles in addition to a number of Class I alleles.

> **PREDEPP**: In this method the peptide structure in the MHC groove is used as a template upon which peptide candidates are threaded, and their compatibility to bind is evaluated by statistical pairwise potentials. This method has the advantage that it does not require experimental testing of peptide binding, and can thus be used for alleles where only limited data are available (Schueler-Furman et al., 2000).

> **Epipredict**: Method using synthetic combinatorial peptide libraries to describe peptide-HLA class II interaction in a quantitative way. The binding contribution of every amino acid side chain in a class II-ligand is described by allele-specific two-dimensional databases (Jung et al., 2001).

> **Predict**: The Predict method use neural networks to predict Class I, II and TAP binding (Yu et al., 2002).

<sup>1</sup>www.niaid.nih.gov/contract/archive/rfp0331.pdf

**Propred**: The Propred method (Singh, 2001) is based on the matrices published by Sturniolo (1999), and is an implementation and extension of the TEPITOPE program. (Hammer, 1995; Raddrizzani, 2000)). Besides differences that can be attributed to round off errors we have in our tests not seen any differences between the two implementations.

**MHCPred**: Prediction of binding to 11 different HLA class I alleles using a three-dimensional quantitative structure-activity relationship method (Doytchinova *et al.*, 2002).

**NetMHC**: Prediction of HLA-A2 binding using neural networks. This method predicts quantitatively the binding affinity, and is different from methods performing classification only (binding versus non-binding according to a threshold). The method has been trained using quantitative binding data generated by the same assay (Buus *et al.*, 2003), and some predicted binders have been tested for their ability to induce a CTL response in mice and be recognized by CD8+ T-cells from HLA-A2 HIV-1 positive patients (Corbet *et al.*, 2003). Two well-known prediction methods, TEPITOPE and EpiMatrix (Meister 1995; De Groot, 1997) that are not available through the web are listed in Table 3. TEPITOPE is popular since it allows prediction of peptides to many different Class II molecules.

#### Prediction of proteasomal cleavage sites

The C terminal of MHC class I ligands must most likely be cleaved by the proteasome. The proteasome usually generates precursors of MHC ligands with an extension at the N-termini. These precursors can be trimmed at the N-terminal in the ER. The existence of proteasome cleavage sites within epitopes need not abrogate the immune response for such epitopes. They may, however, reduce the availability, and thereby the immunogenecity of a given peptide (Yewdell, 1999). The proteasome thus plays an important role in selecting which peptides are presented to CD8+ T cells. In vertebrates stimulation with IFN- $\gamma$  leads to the replacement of three subunits of the constitutive proteasome to form the so-called immunoproteasome which has a different specificity (reviewed by Uebel, 1999). Different methods for predicting proteasomal cleavage sites exist on the web (Table 4).

**PAProC**: Prediction Algorithm for Proteasomal Cleavages is a prediction tool for cleavages by human and yeast proteasomes, based on experimental cleavage data. (Kuttler, 2000; Nussbaum, 2001). An updated version of the PAProC

program based on *in vitro* immunoproteasome cleavage data (Toes, 2001) is also in the making according to the PAProC homepage.

**FRAGPREDICT** comprises two different algorithms. One that aims at predicting potential proteasomal cleavage, based on a statistical analysis of cleavage-determining amino acid motifs present around the scissile bond (Holzhütter *et al.*, 1999, 2000). The second algorithm, which uses the results of the cleavage site analysis as an input, provides predictions of major proteolytic fragments.

**NetChop**: (Kesmir, 2002) is a method based on neural networks that have been trained on different data sets. C Kesmir suggests to use the C-term 2.0 network which was trained on C-terminal cleavage sites of 1,110 publicly available MHC class I ligands for predicting the boundaries of CTL. The specificity of this network may resemble the specificity of the immunoproteasome.

Margalit's group have also recently made their proteasomal cleavage site propensities (Altuvia and Margalit, 2000) available on the net (bioinfo.md.huji.ac.il/marg/cleavage/index.html).

## **Combined predictions**

A number of sites providing combined predictions have been developed recently. The MAPPP server (Table 2) allows the user to make an open reading frame (ORF) search combined with MHC binding and proteasomal cleavage site predictions, and Raghava have a prediction server<sup>2</sup> which implements matrices for 47 MHC Class-I alleles and proteasomal and immunoproteasomal models. The NetMHC server allows combination of HLA-A2 and NetChop predictions.

## **MHC** sequence databases

A number of databases containing sequences of proteins of immunological interest exist on the web (Table 5).

HIG: The HLA Sequence Database currently contains 1,596 allele sequences. To date (October 2002), some 263 HLA-A, 501 HLA-B, 125 HLA-C, 6 HLA-E, 1 HLA-F and 15 HLA-G class I alleles have been named. A total of 3 HLA-DRA, 397 HLA-DRB, 22 HLA-DQA1, 53 HLA-DQB1, 20 HLA-DPA1, 100 HLA-DPB1, 4 HLA-DMA, 6 HLA-DMB, 8 HLA-DOA and 8 HLA-DOB class II sequences have also been assigned. There are also 6 TAP1, 4 TAP2 and 54

<sup>2</sup>www.imtech.res.in/raghava/propred1/index.html

MICA sequences. The HLA Sequence Database also contains the comprehensive nomenclature for factors of the HLA system (listings for HLA class I and class II allele names) which is very helpful since the HLA nomenclature is very complicated and cumbersome.

IMGT: IMGT, the international ImMunoGeneTics project, is a collection of databases specializing in Immunoglobulins, T cell receptors and the Major Histocompatibility Complex (MHC) of all vertebrate species. The IMGT project was established in 1989 by the Université Montpellier II and the CNRS (Montpellier, France) and works in close collaboration with the EBI.

ASHI: The American Society for Histocompatibility and Immunogenetics (ASHI) Holzhutter HG, Kloetzel PM. A kinetic model of vertebrate 20S proteasome accounting for the genhosts databases of gene and allele frequencies (www.ashi-hla.org/).

MHCDB: "Registered users only" database of MHC sequences. This is an ACeDB-style database holding the Human Major Histocompatibility Database. It is largely superseded by 6ace which is ACeDB-style database of human chromosome 6 from the Sanger Centre.

#### Other sites

A number of other databases relevant to immunology and vaccine design are listed in Table 6. Table 7 contains a compilation of lists of links. As stated in Table 7 we will also make an HTML version of this article available on the net.

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Table 1: Databases of MHC binding peptides

Name	Principal Investigator	URL	Description
SYFPEITHI	Rammensee	syfpeithi.bmi-heidelberg.com/scripts/MHCServer.dll/home.htm	Database and prediction server for peptides that bind MHC molecules.
MHCPEP	Brusic, Harrison	wehih.wehi.edu.au/mhcpep	Database of MHC binding peptides
JenPep	Flower	www.jenner.ac.uk/JenPep	Database of MHC and TAP binding peptides
FIMM	Schoenbach & Brusic	sdmc.krdl.org.sg:8080/fimm	Database of functional molecular immunology/binding prediction
MHCBN	Raghava	www.imtech.res.in/raghava/mhcbn	Tools for subunit vaccine design
HLA Ligand/Motif Database	Hildebrand	hlaligand.ouhsc.edu	Ligand database/prediction
HIV Molecular Immunology	Korber	hiv-web.lanl.gov/content/immunology/	HIV CTL epitopes
ЕРІМНС	Reinherz	mif.dfci.harvard.edu/Tools/db_query_epimhc.html	Peptides that bind to MHC molecules

Table 2: HLA Peptide Binding Predictions

Name	URL	Description
BIMAS	bimas.dcrt.nih.gov/molbio/hla_bind	Prediction of MHC class I binding using matrices
SYFPEITHI	syfpeithi.bmi-heidelberg.com/Scripts/MHCServer.dll/EpPredict.htm	Prediction of Class I and II binding
PREDEPP	bioinfo.md.huji.ac.il/marg/Teppred/mhc-bind	MHC Class I epitope prediction
Epipredict	www.epipredict.de/index.html	Prediction of HLA class II restricted binding
Predict	http://sdmc.krdl.org.sg:8080/predict-demo	Prediction of Class I, II and TAP binding
Propred	www.imtech.res.in/raghava/propred	MHC class II prediction
MHCPred	www.jenner.ac.uk/MHCPred	HLA class I predictions
NetMHC	www.cbs.dtu.dk/services/NetMHC	Prediction of HLA-A2 binding using Neural networks
MAPPP	www.mpiib-berlin.mpg.de/MAPPP/expertquery.html	Combined ORF, MHC binding and proteasomal cleavage Registration needed for expert mode

Table 3: Non web MHC binding predictions

Name	URL	Description
ТЕРІТОРЕ	www.vaccinome.com	PC Program for Class II predictions can be downloaded
EpiMatrix	epivax.com/epimatrix.html	Commercial epitope prediction

Table 4: Prediction of proteasomal cleavage sites

Name	URL	Description
Paproc	paproc.de	A matrix based method for prediction of protasomal cleavage
FRAGPREDICT NetChop	www.mpiib-berlin.mpg.de/MAPPP/cleavage.html www.cbs.dtu.dk/services/NetChop	Proteolytic fragment predicter A neural network based method for prediction of proteasomal cleavage

## Table 5: MHC sequence databases

Name	URL	Description
HIG	www.anthonynolan.org.uk/HIG	HLA sequence database
IMGT	www.ebi.ac.uk/imgt	Sequences of MHC, TCR and immunoglobulin
		molecules
ASHI	www.ashi-hla.org	Sequences and Gene and Haplotype frequencies
MHCDB	www.hgmp.mrc.ac.uk/Registered/Option/mhcdb.html	Registered users only database of MHC
		sequences

#### Table 6: Other sites

Name	URL	Description
HIV Molecular	hiv-web.lanl.gov/content/immunology	HIV immunology
Immunology database		
School of Crystallogra	www.cryst.bbk.ac.uk/pps97/assignments/projects/coadwell/MHCSTFU1.HTM	Structure and Function of the Major
phy, Birkbeck College,		Histocompatibility Complex (MHC) Proteins
University of London		
MHC-Peptide	surya.bic.nus.edu.sg/mpid/	Structural information and characterization of
Interaction Database		MHC peptide interaction
(MPID)		
ELF	hiv-web.lanl.gov/content/hiv-db/ALABAMA/epitope_analyzer.html	Epitope Location Finder
ASHI	www.ashi-hla.org	The American Society for Histocompatibility and
		Immunogenetics

#### Table 7: Links to lists of links

•		
Name	URL	Description
Syfpeithi	http://syfpeithi.bmi-heidelberg.com/Scripts/MHCServer.dll/Info.htm	Rammensee's links
FIMM	http://sdmc.krdl.org.sg:8080/fimm	Brusic's links
CBS	www.cbs.dtu.dk/courses/27485.imm/links.html	Our links
HLA-RELATED LINKS	home.att.net/ dorak/hla/linkhla.html	Dorak's links
This article	www.cbs.dtu.dk/researchgroups/immunology/webreview.html	The present article in HTML format

# Part II HIV CTL Epitopes

# **II-A Summary**

Part II includes tables, maps, and associated references of HIV-specific CTL epitopes arranged sequentially according to the location of the proteins in the HIV-1 genome. We attempted to make this section as comprehensive as possible, requiring that the epitope be contained within a defined region of a maximum of 30 amino acids, but not that the optimal boundaries be defined. Studies that were based on the analysis of whole proteins are described at the end of each protein section. The same epitope can have multiple entries, and each entry represents a single publication in this section of the database. For more recent updates and useful searching capabilities, please see our web site: http://hiv-web.lanl.gov/immunology. For a concise listing of the best defined CTL epitopes, see the summary by Christian Brander and Philip Goulder on page 3 in Part I of this compendium. CTL protein reactions with no well-defined epitopes are listed at the end of each protein section.

Recent studies utilize multiple functions attributed to T cells to define responses, and the simple distinctions of cytotoxic T-cell and helper T-cells have become blurred as more is learned about the range of responses triggered in CD4 and CD8 positive T-cells responding to antigenic stimulus. When adding the most recent studies, we have tried to place T cell responses in a reasonable manner into our traditional helper T cell and CTL sections, and to specify the assay used to measure the response in each study.

## **II-A-1** CTL Epitope Tables

Each CTL reference has a six part basic entry:

HXB2 Location: The viral strain HXB2 (GenBank Accession Number K03455) is used as a reference strain throughout this publication. The position of the defined epitope location relative to the sequence of the HXB2 protein is indicated. The numbering in this table corresponds to the protein maps. Because of HIV-1 variation the epitope may not actually be present in HXB2, rather the position in HXB2 indicates the position aligned to the epitope. HXB2 was selected as the reference strain because so many studies use HXB2, and because crystal structures for HXB2-related proteins are often available. The precise positions of an epitope on the HXB2 reference strain can be readily obtained using the interactive position locator at

our web site: http://hiv-web.lanl.gov/content/hiv-db/ LOCATE\_SEQ/locate.html.

**Author Location:** The amino acid positions of the epitope boundaries and the reference sequence are listed as given in the primary publication. Frequently, these positions as published are imprecise, and do not truly correspond to the numbering of the sequence, but they provide a reasonable guide to the peptide's approximate location in the protein. Also, in many cases the reference sequence identification was not provided, and in such cases it is not possible to use these numbers to specify precise locations.

**Epitope Sequence:** The amino acid sequence of the epitope of interest as defined in the reference, based on the reference strain used in the study defining the epitope. On occasions when only the position numbers and not the actual peptide sequence was specified in the original publication, we tried to fill in the peptide sequence based on the position numbers and reference strain. If the sequences were numbered inaccurately by the primary authors, or if we made a mistake in this process, we may have misrepresented the binding site's amino acid sequence. Because of this uncertainty, epitopes that were not explicitly written in the primary publication, that we determined by looking up the reference strain and the numbered location, are followed by a question mark in the table.

**Immunogen:** The original stimulus of the CTL response. Often this is an HIV-1 infection. If a vaccine was used as the original antigenic stimulation, not a natural infection, this is noted on a separate line, and additional information about the vaccine antigen is provided as available.

**Species(HLA):** The species responding and HLA or MHC specificity of the epitope.

**Reference:** The primary reference (sometimes two or more directly related studies are included). Details for some of the earlier references are in Part V.

Following the entry for a given CTL epitope are brief comments explaining the context in which the epitope was studied and what was learned about the epitope in a given study.

#### **II-A-2 HIV Protein Epitope Maps**

All HIV CTL epitopes mapped to within a region of 21 amino acids or less are indicated on the HIV protein epitope maps. The location and HLA restriction elements of CTL epitopes are indicated on protein sequences of HXB2. These maps are meant to provide the relative location of defined epitopes on a given protein, but the HXB2 sequence may not actually carry the epitope of interest, as it may vary relative to the sequence for which the epitope was defined. Epitopes with identical boundaries and HLA fields are included in the maps only once. If one laboratory determines HLA presenting molecules at the serotype level (example: A2) and another at the genotype level (example: A\*0201) both will be included in the map. MHC specificities are indicative of the host species; when no MHC presenting molecule is defined, the host species is noted.

#### II-A-3 Alignments

To conserve space, no epitope alignments are provided in this book, but they can be generated using the CTL epitope search tool at http://hiv-web.lanl.gov/immunology. All epitopes are aligned to the HXB2 sequence, with the sequence used to define the epitope indicated directly above it. Sequences are sorted by their subtype and country of origin.

The master alignment files from which the epitope alignments were created are available at our web site (http://hiv-web.lanl.gov/ALIGN\_CURRENT/ALIGN-INDEX.html). The alignments were modified in some cases to optimize the alignment relative to the defined epitope and minimize insertions and deletions; epitope alignments are generated by anchoring on the C-terminal residue. A dash indicates identity to the consensus sequence, and a period indicates an insertion made to maintain the alignment. Stop codons are indicated with a \$, and frameshifts by a #, or ambiguous codons (nucleotide was r, y, or n) by an x; they are inserted to maintain the alignments. In consensus sequences an upper case letter indicates the amino acid was present in all sequences, a lower case letter indicates the amino acid was present in most sequences in a given position, and a question mark indicates two or more amino acids were represented with equal frequency.

# **II-B HIV CTL Epitope Tables**

All HIV CTL epitopes arranged by protein position. The table entries are sorted in a nested way—first by protein, then by HXB2 start location and finally by HLA. CTL reactions against proteins with undefined epitopes are listed at the end of the protein which stimulated the response.

# II-B-1 p17 CTL Epitopes

HXB2 Location	<b>Author's Location</b>	Sequence	Immunogen	Species (HLA)	References			
p17 (11–19)		GELDRWEKI	HIV-1 infection	human (B*4002)	Sabbaj2002b			
	<ul> <li>Epitope name: Gag-GI</li> </ul>							
			-1 infected minority women living in t					
	1 1		sed new restricting elements but were					
	<ul> <li>Serial peptide truncation</li> </ul>	ons were used to define o	ptimal epitopes for CTL cell lines isol	lated from 12 individuals, assaye	d by a Cr-release			
	<ul> <li>This epitope was newly</li> </ul>							
		Hispanic, on HAART, ar I, RT(128-135), HLA A	nd had a viral load of 21000 and CD4 *0217	count of 623 – she also recognize	ed KETINEEAA p24(70-78), HLA			
	• Among HIV+ individu	als who carried HLA B4	0, 2/5 (40%) recognized this epitope					
p17 (18–26)	p17 (18–26 IIIB)	KIRLRPGGK		human (A*0301)	Brander2001			
	C. Brander notes that the content of the conte	nis is an A*0301 epitope						
p17 (18–26)	p17 (18-26 SF2)	KIRLRPGGK	HIV-1 infection	human (A*0301)	Altfeld2001a			
	• HIV+ individual AC-0	6 was tested for reactive	overlapping peptides spanning all HIV	V-1 proteins in an ELISPOT and	was found to react with 12 peptides			
	from 7 proteins, sugges	sting that the breadth of	CTL responses are underestimated if a	accessory proteins are not include	ed in the study			
	• The reactive peptide p1	7 gag WEKIRLRPGGK	KKYK contained two A*0301-restric	cted epitopes, KIRLRPGGK and	RLRPGGKKK A*0301			
p17 (18–26)	p17 (18–26 IIIB)	KIRLRPGGK	HIV-1 infection	human (A3)	Wilson1996			
	• Epitope defined in the	context of the Pediatric A	AIDS Foundation ARIEL Project, a m	other-infant HIV transmission stu	ıdy			
	<ul> <li>KIRLRPGGR and RIR</li> </ul>	LRPGGR, naturally occ	urring variants, were found in mother,	, and are escape mutants				
p17 (18–26)	p17 (18–26)	KIRLRPGGK	in vitro stimulation	human (A3)	Zarling1999			
	• This study compares the ability of macrophages and dendritic cells to stimulate primary responses in CD8+ lymphocytes isolated from HLA-appropriate							
	HIV-uninfected donors using peptide-pulsed APC – the dendritic cells performed better as APC for the stimulation of primary responses							
	<ul> <li>Strong CTL responses</li> </ul>	were elicited by the epite	opes DRFYKTLRA and GEIYKRWII	I when presented by either immat	ture or mature dendritic cells -			
	macrophages were not	able to prime a CTL resp	oonse against DRFYKTLRA					
	<ul> <li>A weak response to KI</li> </ul>	TPLCVSL was stimulat	ed using macrophages as the APC					
	<ul> <li>No detectable response</li> </ul>	was observed for the fo	llowing previously-defined HIV epitor	pes: KIRLRPGGK, ILKEPVHG	V, IRLRPGGK, GPKVKQWPL			
p17 (18–26)	Gag (18–26)	KIRLRPGGK	HIV-1 infection	human (A3)	Brodie1999			
	• The ability of CTL effe	ector cells was studied by	expanding autologous HIV-1 Gag-sp	pecific CTL in vitro, and adoptive	transfer			

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References		
	The transferred CTLs is appropriate target sites		nodes and transiently reduced circulating effects	productively-infected CD4+ T	cells, showing that CTL move to		
p17 (18–26)			HIV-1 infection of neo-marked CD8 HIV-specific CTL	human (A3)	Brodie2000		
	<ul><li>adjacent to cells expres</li><li>The CTL clones expression viral replication, sugge</li></ul>	ssing HIV tat-fusion transsed CCR5 and localized string a possible homing	cific CTL homed to specific lymph node inscripts, indicative of viral replication ed among HIV-1 infected cells expressing mechanism ng and studying antigen specific CTL in	g MIP-1alpha and MIP-1beta, C			
p17 (18–26)	p17 (18–26 IIIB)	KIRLRPGGK	HIV-1 infection	SJL/J HLA transgenic mice (A3)	Wilson1999a		
	<ul><li>Detection of CTL esca infants</li><li>KIRLRPGGR and RIR</li></ul>	pe mutants in the moth RLRPGGR were escape gnized and many escape	in the context of mother-to-infant transner was associated with transmission, but mutants e mutants were detected in an HLA A3 transmission.	the CTL-susceptible forms of the			
p17 (18–26)			HIV-1 infection infected with the same batch of factor Verthat summarizes this study.	human (A3) VIII. One had a response to this of	Goulder1997e, Goulder1997a epitope, the other did not.		
p17 (18–26)	<ul><li>CD8+ T cell responses</li><li>Low risk individuals di</li></ul>	tended to be to the san id not have such CD8+ DTVLEDINL (3 indiv	iduals), SLYNVATL (4 individuals), LSF	HIV-specific CD8 gamma-IFN re than cervical CD8+ T cell respo	nses		
p17 (18–26)	p17 (SF2) KIRLRPGGK HIV-1 infection human (A3) Goulder2000a  • WEKIRLRPGGKKKYKLK was the target of the dominant response in Caucasoids (38%) more frequently than non-Caucasoids (12%) – 7/10 that had a dominant response to this epitope were A3, and 5/7 targeted RLRPGGKKK while 2/7 targeted KIRLRPGGK  • Three peptides GSEELRSLYNTVATL (p17 residues 71-85), SALSEGATPQDLNTMLNTVG (p24 41-60), and WEKIRLRPGGKKKYKLK(p17 16-30) contained the dominant Gag-specific epitope in 31 out of 44 B-clade infected individuals from Boston who showed Gag-CTL responses  • Five peptides RLRPGGKKHYMIKHLVW (p17 20-36), ELRSLYNTVATLYCV (p17Gag 74-88), SALSEGATPQDLNTMLNTVG (p24 41-60), FRDYVDRFFKTLRAEQA (p24 161-177), and SILDIKQGKEPFRDY (p24 149-164) contained dominant Gag-specific epitopes in 32 out of 37 C-clade infected subjects from South Africa						
p17 (18–26)		•	HIV-1 infection ing in 41 patients with combination theretigen-specific cells capable of differential		•		

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References			
p17 (18–26)	p17 (18–26 SF2) KIRLRPGGK HIV-1 infection human (A3) Altfeld2001b  • Therapy provided during acute infection resulted in a narrower CTL response, stronger T help response, and a less diverse viral population than was seen individuals treated during chronic infection  • The breadth and specificity of the response was determined using ELISPOT by studying 19 individuals with pre-seroconversion therapy (Group 1), 11 individuals with primary infection but post-seroconversion therapy (Group 2), and 10 individuals who responded to HAART given during chronic infection (Group 3), using 259 overlapping peptides spanning p17, p24, RT, gp41, gp120 and Nef  • Previously described and newly defined optimal epitopes were tested for CTL response  • Number of HLA-A3+ individuals that had a CTL response to this epitope broken down by group: 3/7 group 1, 0/4 group 2, and 2/2 group 3							
p17 (18–26)	<ul><li>p17 (18–26)</li><li>KIRLRPGGK is cross-</li><li>ELISPOT was used to HIV-1-infected female</li></ul>	study CTL responses to	HIV-1 infection, HIV-1 expos seronegative O clades o a panel of 54 predefined HIV-1 epitopes i		Kaul2001a tently seronegative (HEPS) and 87			
p17 (18–26)	<ul> <li>p17 (JRCSF) KIRLRPGGK HIV-1 infection human (A3) Severino2000</li> <li>Primary HLA-A3+ CD4+ and HLA-mismatched lymphocytes from uninfected donors were infected with JRCSF after isolation then cocultured with the A3-restricted CTL clone 11504/A7 specific for KIRLRPGGK, and viral inhibition was MHC-restricted</li> <li>Primary monocytes and monocyte-derived DC were generated from the same donors, replication of HIV-1 in these cell types was less efficient than in lymphocytes and could also be inhibited by MHC-restricted CTL</li> <li>DC-lymphocyte cluster cultures allowed vigorous viral replication and MHC-restricted CTL viral inhibition was blunted or lost depending on the ratio of DC to CD4+ lymphocyte in the culture</li> </ul>							
p17 (18–26)	<ul> <li>p17 (18–26) KIRLRPGGK HIV-1 infection human (A3) Day2001</li> <li>The CTL response to optimally defined CTL epitopes restricted by HLA class I A and B alleles in individuals who coexpressed HLA A2, A3, and B7 was studied in eight HIV-1-infected subjects, two with acute infection, five with chronic, and one long-term non-progressor (LTNP)</li> <li>2 to 17 epitopes were recognized in a given individual, A2-restricted CTL response tended to be narrow and never dominated the response, and 25/27 epitopes were targeted by at least one person</li> <li>All patients recognized at least 1 A3 epitope, up to 8 A3 epitopes, but none was clearly dominant</li> </ul>							
p17 (18–26)	<ul> <li>p17 KIRLRPGGK HIV-1 infection human (A3) Ostrowski2000</li> <li>The role of CD4+ T-cell help in expansion of virus-specific memory CTL was studied through co-culture <i>ex vivo</i></li> <li>Optimal expansion of HIV-1-specific memory CTL depended on CD4+ T cell help in 9 of 10 patients – CD40 ligand trimer (CD40LT) could enhance CTL in the absence of CD4+ T cell help to a variable degree in most of patients</li> <li>Those CTL that didn't respond to CD40LT could expand with IL2 present, and IL15 produced by dendritic cells also contributes</li> <li>The T-helper epitope used for CD4+ T cell stimulation was the universal tetanus helper epitope TET830-843 (QYIKANSKFIGITE)</li> </ul>							
p17 (18–26)	<ul> <li>One individual, AC-06</li> </ul>	cutely HIV-infected HL was homozygous at all had only two detectabl	HIV-1 infection  A-A3 (n=7) or -B7 (n=4) or both -A3 and three class I alleles (A3, B7, Cw7), was true CTL responses during acute infection, by HLA-Cw7.	reated during acute infection	and had supervised treatment			

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References			
	<ul> <li>8/14 HLA-A3 positive individuals had detectable A3-restricted responses during acute infection. Only 5/15 of HLA-A3 epitopes tested were targeted during acute infection. 7/8 individuals with acute responses had specific responses for this epitope.</li> <li>KIRLRPGGK and RLRPGGKKK were the most commonly recognized HLA-A3 epitopes during acute infection, after 1 year of treatment, and after STI. RLRPGGKKK was immunodominant.</li> </ul>							
p17 (18–26)	p17 (18–26) • One of the 51 HIV-1 ep HLA alleles	KIRLRPGGK pitopes selected by Ferra	HIV-1 infection ri et al. as good candidate CTL epitor	human (A3, A3.1, B2 pes for vaccines by virtue of being	7) Ferrari2000 g conserved and presented by common			
p17 (18–26)	<ul> <li>KIRLRPGGK HIV-1 infection human (B*0301) Wilson2000a</li> <li>Three individuals with highly focused HIV-specific CTL responses were studied during acute infection using tetramers – high frequencies of HIV-1-specific CD8+ T cells were found prior to seroconversion, and there was a close temporal relationship between the number of circulating HIV-specific T cells and viral load was also found</li> <li>All three patients were B*2705, with HLA alleles: A1, A30/31, B*2705, B35; A1, A*0301, B7, B2705; and A*0201, A*0301, B2705, B39</li> <li>ELISPOT was used to test a panel of CTL epitopes that had been defined earlier and were appropriate for the HLA haplotypes of the study subjects – 3/3 subjects showed a dominant response to the B*2705 epitope KRWIILGGLNK</li> <li>The subject with A*0201 had a moderatly strong response to SLYNTVATL</li> <li>Weak responses were observed to A*301-RLRPGGKKK, A*301-QVPLRPMTYK, and B7-TPGPGVRYPL in the subject who was HLA A1, A*0301, B7, B*2705</li> <li>No acute response was detected to the following epitopes: A*201-ILKEPVHGV, A*301-KIRLRPGGK, A*301-AIFQSSMTK, A*301-TVYYGVPVWK, B35-EPIVGAETF, B35-HPDIVIYQY, B35-PPIPVGEIY, B35-NSSKVSQNY, B35-VPLRPMTY, B35-DPNPQEVVL</li> </ul>							
p17 (18–27)	p17 (18–27 LAI)  • D. Lewinsohn, pers. co	KIRLRPGGKK omm.		human (B27)	Brander1996b			
p17 (18–27)	p17 (18–27) • A study of p17 variation pressure from CTLs	KIRLRPGGKK on considering known p1	HIV-1 infection 7 epitopes and individuals with know	human (B27) on HLA types revealed that p17 e	Birk1998b volution is influenced by immune			
p17 (18–31)	p17 (18–31) • A study of p17 variation pressure from CTLs	KIRLRPGGKKKYKI on considering known p1	HIV-1 infection 7 epitopes and individuals with know	human (A3) on HLA types revealed that p17 e	Birk1998b volution is influenced by immune			
p17 (18–31)	p17 (18–31) KIRLRPGGKKKYKL HIV-1 infection human (B62) Lubaki1997  • Eighty two HIV-1-specific CTL clones from 5 long-term non-progressors were isolated and analyzed for breadth of CTL response  • A sustained Gag, Env and Nef response was observed, and clones were restricted by multiple HLA epitopes, indicating a polyclonal response  • A subject who was HLA-B62+ had CTL that recognized this peptide, and p24 LGLNKIVRMYS, and one additional unknown epitope							
p17 (18–42)	p17 (18–42 IIIB)  • Epitope recognized by	ASRELE	KHIVW- HIV-1 infection	human (A3)	Jassoy1992			
p17 (18–42)	p17 (18–42 PV22)  • HIV-1 specific CTLs re	KIRLRPGGKKKYKI ASRELE	KHIVW- HIV-1 infection	human (A3)	Jassoy1993			

	Author's Location	Sequence	Immunogen	Species (HLA)	References
p17 (18–42)	p17 (18–42 BH10)	KIRLRPGGKKKYKLKHIVW- ASRELE	HIV-1 infection	human (Bw62)	Johnson1991
	• Gag CTL response was	studied in three individuals			
p17 (19–27)	p17 (19–27 JRCSF)  • Noted by Brander to be	IRLRPGGKK B*2705 (Pers. Comm. D. Lewins	HIV-1 infection sohn)	scid-hu mouse (B*2705)	Brander2001
p17 (19–27)	p17 (19–27 LAI)	IRLRPGGKK		human (B27)	Brander1996b
p17 (19–27)	<ul><li>eradicated and the HIV-</li><li>No escape mutants wer</li></ul>	-specific CTL rapidly disappeared e observed		scid-hu mouse (B27) t decreases in viral load were observ d loss of CTL was due to target inter	
p17 (19–27)	that were B27+ had a d • Three peptides GSEEL contained the dominant	ominant response to this epitope RSLYNTVATL (p17 residues 71-{ Gag-specific epitope in 31 out of	85), SALSEGATPQDLNTN 44 B-clade infected individ	human (B27) (38%) more frequently than non-Cau MLNTVG (p24 41-60), and WEKIR! tuals from Boston who showed Gag-	LRPGGKKKYKLK(p17 16-30) CTL responses
		EQA (p24 161-177), and SILDIK		7Gag 74-88), SALSEGATPQDLNT 4) contained dominant Gag-specific	
p17 (19–27)	FRDYVDRFFKTLRAI	EQA (p24 161-177), and SILDIK			
p17 (19–27) p17 (19–27)	FRDYVDRFFKTLRAI infected subjects from S p17 (19–27) p17 (19–27) • Epitope name: IK9	EQA (p24 161-177), and SILDIK South Africa	QGKEPFRDY (p24 149-16  HIV-1 infection  HIV-1 infection	4) contained dominant Gag-specific  human (B27)  human (B27)	epitopes in 32 out of 37 C-clade
	FRDYVDRFFKTLRAI infected subjects from S p17 (19–27) p17 (19–27) • Epitope name: IK9 • This B27 epitope is gen p17 (20–28) • Only 4/11 HLA-A2+ H • 95 optimally-defined pe • Three of the four indivi	EQA (p24 161-177), and SILDIKO South Africa  IRLRPGGKK  IRLRPGGKK  terally recognized only if there is a  RLRPGGKKK  IV+ individuals had CTL that reaceptides from this database were us	PATE TO SET THE PROPERTY (P24 149-16)  HIV-1 infection  HIV-1 infection  escape in the B27 dominant  HIV-1 infection  cted to SLYNTVATL, callinged to screen for INFγ responsed to the screen for INFγ responsed to the screen for INFγ responsed the	4) contained dominant Gag-specific  human (B27)  human (B27)  epitope, p24 KRWIILGLNK  human  g into question whether it is immunication.	Day2001 Goulder2001b  Betts2000 odominant
p17 (19–27)	FRDYVDRFFKTLRAI infected subjects from S p17 (19–27) p17 (19–27) • Epitope name: IK9 • This B27 epitope is gen p17 (20–28) • Only 4/11 HLA-A2+ H • 95 optimally-defined pe • Three of the four indivirecognized this epitope p17 (20–28) • Identical twin hemophi • One had a response to g	EQA (p24 161-177), and SILDIKO South Africa  IRLRPGGKK  IRLRPGGKK  terally recognized only if there is of RLRPGGKK  RLRPGGKKK  IIV+ individuals had CTL that reaceptides from this database were us duals that responded to SLYNTVA	GGKEPFRDY (p24 149-16  HIV-1 infection  HIV-1 infection  escape in the B27 dominant  HIV-1 infection  cted to SLYNTVATL, calling  ted to screen for INFγ responished to Screen for INFγ responished HIV epitop  B.1), as well as one other  HIV-1 infection  with the same batch of factories other non-responder carries	human (B27) human (B27) epitope, p24 KRWIILGLNK human g into question whether it is immuniness to other epitopes es, and one individual who was A*0 human (A*03) VIII	Day2001 Goulder2001b  Betts2000 odominant

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
p17 (20–28)	CD8+ T cells were for viral load was also for All three patients were ELISPOT was used to	und prior to seroconversiond e B*2705, with HLA alle test a panel of CTL epito	HIV-1 infection cific CTL responses were studied during on, and there was a close temporal relatives: A1, A30/31, B*2705, B35; A1, A* topes that had been defined earlier and v*2705 epitope KRWIILGGLNK	tionship between the number of *0301, B7, B2705; and A*0201,	circulating HIV-specific T cells and A*0301, B2705, B39
	<ul><li>Weak responses were B*2705</li><li>No acute response was</li></ul>	observed to A*301-RLR s detected to the following	ng response to SLYNTVATL PGGKKK, A*301-QVPLRPMTYK, at ng epitopes: A*201-ILKEPVHGV, A*3 PIPVGEIY, B35-NSSKVSQNY, B35-V	801-KIRLRPGGK, A*301-AIFQ	QSSMTK, A*301-TVYYGVPVWK,
p17 (20–28)	from 7 proteins, sugge	esting that the breadth of	HIV-1 infection overlapping peptides spanning all HIV CTL responses are underestimated if ac KKKYK contained two A*0301-restrict	ccessory proteins are not include	ed in the study
p17 (20–28)	responded to Gag, 8/1 CD8+ T-cells in one w Tetramer analysis of b CD3+/CD8+ cells in b The frequencies of res	1 responded to Pol, 7/11 woman, and another wom breast milk and peripheral preast milk, and 0.22% of sponses in the two compa	HIV-1 infection  FHIV-1 infected women from the US at women to Nef, and 2/5 women to Env an had cytolytic responses measured by a blood samples of one volunteer shower fCD3+/CD8+ cells in peripheral blood artments differed, and 2/4 women that reconses in peripheral blood cells.	peptide pools. These responses by Cr-release. ed responses to RLRPGGKKK is cells.	were shown to be primarily due to n both compartments, 0.65% of
p17 (20–28)	<ul><li>Epitope name: Gag-R</li><li>Among HIV+ individu</li></ul>		HIV-1 infection 03, 7/20 (35%) recognized this epitope	human (A03)	Sabbaj2002b
p17 (20–28)	amino acids long, one	ten	HIV-1 infection lonor 021-BMC (HLA A3/3001, B42/-, erlapping this region, KIRLRPGGK, wa	-	
p17 (20–28)	p17 (20–28) • A control CTL line the	RLRPGGKKK at reacts with this peptide	HIV-1 infection e was included in the study	human (A3)	Goulder1997f
p17 (20–28)		RLRPGGKKK e of A, B, and D clade vir e of C clade viruses is RI	HIV-1 infection ruses is RLRPGGKKK LRPGGKKH and is equally reactive	human (A3)	Cao1997a

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References		
p17 (20–28)	<ul> <li>dominant response to t</li> <li>Three peptides GSEEL contained the dominan</li> <li>Five peptides RLRPGO</li> </ul>	this epitope were A3, and LRSLYNTVATL (p17 res at Gag-specific epitope in GKKHYMIKHLVW (p1' LEQA (p24 161-177), and	HIV-1 infection the dominant response in Caucasoids ( 5/7 targeted RLRPGGKKK while 2/ idues 71-85), SALSEGATPQDLNTN 31 out of 44 B-clade infected individ 7 20-36), ELRSLYNTVATLYCV (p1/ I SILDIKQGKEPFRDY (p24 149-16-	7 targeted KIRLRPGGK MLNTVG (p24 41-60), and WE uals from Boston who showed (7Gag 74-88), SALSEGATPQDI	KIRLRPGGKKKYKLK(p17 16-30) Gag-CTL responses LNTMLNTVG (p24 41-60),		
p17 (20–28)	p17 (20–28 SF2) RLRPGGKKK HIV-1 infection human (A3) Altfeld2001b  • Therapy provided during acute infection resulted in a narrower CTL response, stronger T help response, and a less diverse viral population than wa individuals treated during chronic infection  • The breadth and specificity of the response was determined using ELISPOT by studying 19 individuals with pre-seroconversion therapy (Group 1), individuals with primary infection but post-seroconversion therapy (Group 2), and 10 individuals who responded to HAART given during chronic i (Group 3), using 259 overlapping peptides spanning p17, p24, RT, gp41, gp120 and Nef  • Previously described and newly defined optimal epitopes were tested for CTL response  • Number of HLA-A3+ individuals that had a CTL response to this epitope broken down by group: 5/7 group 1, 2/4 group 2, and 2/2 group 3						
p17 (20–28)	<ul><li>studied in eight HIV-1</li><li>2 to 17 epitopes were r epitopes were targeted</li></ul>	-infected subjects, two warecognized in a given induby at least one person	HIV-1 infection itopes restricted by HLA class I A an ith acute infection, five with chronic, ividual, A2-restricted CTL response to to 8 A3 epitopes, but none was clear	and one long-term non-progress ended to be narrow and never do			
p17 (20–28)		pe were observed in auto	-		Goulder2001b  fection  fection  fection were A3-negative		
p17 (20–28)	<ul> <li>One individual, AC-06 interruptions (STI). He restricted by HLA-A3,</li> <li>8/14 HLA-A3 positive during acute infection.</li> <li>KIRLRPGGK and RLI</li> </ul>	cutely HIV-infected HLAs was homozygous at all to had only two detectable, 11 by HLA-B7, and 1 by individuals had detectab 7/8 individuals with acu RPGGKKK were the mo	le A3-restricted responses during acute responses had specific responses fo	as treated during acute infection in, but after STI this broadened to the infection. Only 5/15 of HLA- or this epitope. itopes during acute infection, af	and had supervised treatment o 27 distinct epitopes including 15  A3 epitopes tested were targeted ter 1 year of treatment, and after STI.		

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
p17 (20–28)	<ul> <li>Vpr is capable of arrest the granzyme B molect</li> <li>Vpr expression in the the Chromium release asset</li> <li>In contrast, deletion of</li> </ul>	ting infected cells in the ular complex. target cell did not inhibit ay and a TUNEL assay.  Nef, which is thought to	HIV-1 infection t forms pore in the plasma membrane, G2 phase, and it was hypothesized that epitope specific lysis – neither perfori p protect primary HIV infected cells by tells to CTL mediated killing 2-fold us	at Vpr may inhibit CTL-mediated in or granzyme mediated events way down-regulating cell-surface ex	d apoptosis because it interacts with were inhibited, as measured by a
p17 (20–28)	responded to Gag, 8/1 CD8+ T-cells in one w T-cells in breast milk f epitope RLRPGGKKK The frequencies of res	I responded to Pol, 7/11 roman, and another wom from a volunteer who wa K.  ponses in the two compa	HIV-1 infection HIV-1 infected women from the US a women to Nef, and 2/5 women to Envan had cytolytic responses measured bs HLA A3, A11, B35, B51 induced IF rtments differed, and 2/4 women that posses in peripheral blood cells.	peptide pools. These responses y Cr-release. Ngamma after stimulation with a	were shown to be primarily due to a peptide that carries known A3
p17 (20–29)	p17 (20–29 LAI) • C. Brander notes this i	RLRPGGKKKY s an A*0301 epitope	HIV-1 infection	human (A*0301)	Brander2001
p17 (20–29)	amino acids long, one	ten	HIV-1 infection lonor 021-BMC (HLA A3/3001, B42/- erlapping this region, KIRLRPGGK, w		
p17 (20–29)	p17 (20–29) • Unpublished, C. Jasso	RLRPGGKKKY y and Beatrice Culman, 1	HIV-1 infection pers. comm.	human (A3.1)	Brander1995b
p17 (20–29)	p17 (20–29 LAI) • Pers. comm., B. Wilke	RLRPGGKKKY	HIV-1 infection	human (A3.1)	Wilkens1999
p17 (20–29)	<ul> <li>95 optimally-defined p</li> </ul>	peptides from this databa duals was A30, and one	HIV-1 infection TL that reacted to SLYNTVATL, callin se were used to screen for INFγ responses A3, and both responded to RLRPother A3.1 epitopes	nses to other epitopes	Betts2000 nunodominant
p17 (20–29)		urally occurring variant,	HIV-1 infection AIDS Foundation ARIEL Project, a m was found in non-transmitting mother		Wilson1996 udy

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
p17 (20–29)	p17 (20–29) • One of the 51 HIV-1 epHLA alleles	RLRPGGKKKY pitopes selected by Ferrari	HIV-1 infection et al. as good candidate CTL epitop	human (B42, Bw62) bes for vaccines by virtue of being	Ferrari2000 conserved and presented by commo
p17 (20–29)	<ul> <li>Adoptively transferred adjacent to cells expres</li> <li>The CTL clones expressiviral replication, suggestion</li> </ul>	gene-marked HIV-specific ssing HIV tat-fusion transc ssed CCR5 and localized a esting a possible homing m	eripts, indicative of viral replication among HIV-1 infected cells expression	ng MIP-1alpha and MIP-1beta, Co	Brodie2000 afollicular regions of the lymph nod C-chemokines produced at sites of
p17 (20–29)	p17 (20–29 LAI) • Review of HIV CTL e • Also P. Johnson, pers.			human (Bw62)	McMichael1994
p17 (20–30)	response in a Haitian in determined  Three peptides GSEEL contained the dominan Five peptides RLRPGO	mmigrant living in Boston  LRSLYNTVATL (p17 resident Gag-specific epitope in 3  GKKHYMIKHLVW (p17  LEQA (p24 161-177), and	HIV-1 infection e dominant response in Caucasoids ( who was HLA A24/29 B7/B44 Cw. dues 71-85), SALSEGATPQDLNTM 1 out of 44 B-clade infected individ 20-36), ELRSLYNTVATLYCV (p1' SILDIKQGKEPFRDY (p24 149-16-	6/7 was to this epitope, although to MLNTVG (p24 41-60), and WEKI duals from Boston who showed Ga 7Gag 74-88), SALSEGATPQDLN	he restricting element was not  RLRPGGKKKYKLK(p17 16-30) g-CTL responses ITMLNTVG (p24 41-60),
p17 (20–35)	<ul><li>Twelve subjects had C</li><li>One of these 12 had C</li></ul>	CLRPGGKKKYKLKHI ad CTL specific for more t TL that could recognize va TL response to this peptident to the transfer of the tra	han 1 HIV-1 protein accinia-expressed LAI gag	human	Lieberman1997a
p17 (21–35)	Gag • Peptide 703.3: Memor	LRPGGKKKYKLKHIV y CTL specific for HIV-1	HIV-1 infection may contribute to oligoclonal expans	human sions within the CD57+ CD28- Cl	Weekes1999a D8+ CTLp populations
p17 (21–35)	<ul><li>Twelve subjects had C</li><li>One of these 12 had C</li></ul>	LRPGGKKKYKLKHIV ad CTL specific for more t TL that could recognize va TL response to this peptide t was HLA-A1, A2, B50,	han 1 HIV-1 protein accinia-expressed LAI gag	human	Lieberman1997a
p17 (21–35)	contribution of CD8+C		8+ at birth, and the proportion of CI ry pools for CTL clones specific for		<u> </u>

HXB2 Location	<b>Author's Location</b>	Sequence	Immunogen	Species (HLA)	References
	<ul> <li>The clonal composition</li> </ul>		vere studied es was studied and was found to be this epitope were Vbeta13.1 and V		beta-chain sequence tending to
p17 (21–35)	p17 (21–35) • Two CTL epitopes defi	LRPGGKKKYKLKHIV ned (see also p24(191-205))		human (B8)	Nixon1991
p17 (21–35)	p17 (21–35) • Unknown HLA specific	LRPGGKKKYKLKHIV city, but not B8	HIV-1 infection	human (not B8)	vanBaalen1996
p17 (21–40)	<ul><li>in East Africa</li><li>This epitope was defined</li></ul>	individuals with non-clade	B infections were studied, 2 with  - the B clade variant (LRPGGKK		Dorrell1999  otype C – their infections all originated mutations relative to the A subtype
p17 (22–31)	A dominant B7 epitope	was defined using conventiegy, EpiMatrix, to identify 2	HIV-1 infection responses detected in a long-term ronal methods, and three additiona 078 possible epitopes in the autology.	l sub-dominant HLA B7 epitope	Jin2000b es were defined by first using a schor residue prediction to narrow the
p17 (24–31)	<ul><li>The predictions were e.</li><li>The anchors for HLA-I.</li><li>Structural data suggests.</li><li>Small hydrophobic resi</li></ul>	xperimentally confirmed 38 epitopes, as defined by p s that a positive charge at P5 dues at P2 may be favorable	-B8 was used to predict new epito eptide elution data, are P3 (K), P5 is essential, but that the constrain e for binding residues in the C-term anchor	(K/R), and P8 (L)	Goulder1997g tope variation
p17 (24–31)	p17 (24–31 SF2) • CTL from a patient info	GGKKKYKL ected with clade B virus did	HIV-1 infection not recognize Ugandan variants o	human (B8) of this epitope	McAdam1998
p17 (24–31)	<ul> <li>Crystal structures were</li> <li>3R has been detected in movement</li> <li>7Q and 7R alter the TC</li> <li>Reactivity of 5R depen</li> </ul>	obtained to study these pep n 3 patients, and it abolishes CR exposed surface, and reta ds on the T cell clone, this a	HIV-1 infection  , 5R: GGKKRYKL, and 3R: GGR tides in the context of HLA-B8, at recognition causing extensive cor in some recognition unino acid is embedded in the C p 3, 5, and 8 are the anchor residues	nd CTL binding and activity wer formational changes upon bindi- ocket of B8 when the peptide is	ng including MHC main chain
p17 (24–31)	•		HIV-1 infection served in an HLA-B8+ infected in owed that a variant at position 5, a		Price1997 ., was present

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
p17 (24–31)	<ul> <li>individuals treated dur</li> <li>The breadth and specifindividuals with prima (Group 3), using 259 c</li> <li>Previously described a</li> </ul>	ing chronic infection ficity of the response was ry infection but post-ser- overlapping peptides span and newly defined optima	HIV-1 infection ed in a narrower CTL response, stronger T help s determined using ELISPOT by studying 19 in occonversion therapy (Group 2), and 10 individenting p17, p24, RT, gp41, gp120 and Nef all epitopes were tested for CTL response GL response to this epitope broken down by gr	ndividuals with pre-sero uals who responded to	oconversion therapy (Group 1), 11 HAART given during chronic infectio
p17 (24–31)	p17 (24–31)  • ELISPOT was used to HIV-1-infected female	•	HIV-1 infection, HIV-1 exposed seronegative a panel of 54 predefined HIV-1 epitopes in 91	human (B8) HIV-1-exposed, persist	Kaul2001a tently seronegative (HEPS) and 87
p17 (24–31)	p17 (24–31) • B8-restricted CTL acc	GGKKKYKL ounted for about 1/3 of t	HIV-1 infection he total CTL response in one individual	human (B8)	Day2001
p17 (24–31)			HIV-1 infection The natural epitope interactions with the HLA ken from [Reid1996], as an example.	human (B8) class I presenting mole	McMichael2002 ecules and T-cell receptors are
p17 (24–32)	p17 (24–32 LAI) • C. Brander notes epito	GGKKKYKLK pe to be presented by B*	HIV-1 infection	human (B*0801)	Brander2001
p17 (24–32)	p17 (24–32 LAI) • Exploration of HLA-B	GGKKKYKLK 8 binding motif through	HIV-1 infection peptide elution	human (B8)	Sutton1993
p17 (24–32)	p17 (24–32 LAI) • Study of an individual	GGKKKYKLK with partially defective	HIV-1 infection antigen processing	human (B8)	Rowland-Jones1993
p17 (24–32)	p17 (24–32) • Naturally occurring va	GGKKKYKLK riants GGKKKYQLK a	HIV-1 infection nd GGKKRYRLK may act as antagonists	human (B8)	Klenerman1994
p17 (24–32)	p17 (24–32) • Naturally occurring an	GGKKKYKLK tagonist GGKKKYQLK	HIV-1 infection found in viral PBMC DNA and RNA	human (B8)	Klenerman1995
p17 (24–32)	p17 (24–32) • Longitudinal study of	GGKKKYKLK CTL response and immu	HIV-1 infection ne escape – the variant GGRKKYKLK binds	human (B8) to HLA-B8 but is not re	Nowak1995 eactive
p17 (24–32)	natural attenuated strai	in of HIV-1 which was N	HIV-1 infection 1.3 to 1.5 year period in members of the Sydne lef-defective els of CTL effector and memory cells despite l		Dyer1999 (SBBC) who had been infected with a
p17 (24–32)	p17 • CTL responses in sero deletion in CCR5	GGKKKYKLK negative highly HIV-exp	osed African female sex workers in Gambia a	human (B8) nd Nairobi were studied	Rowland-Jones1999 d – these women had no delta 32

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
	<ul><li> In Gambia there is exp seems to be protective</li><li> HIV-2 sequence: GGK</li></ul>			es in exposed, uninfected women	are cross-reactive, and the B35 allele
p17 (24–32)	p17 (24–32)  • Epitope name: GGK  • Patients who started th CD4 proliferative resp HAART had no HIV s undetectable  • This epitope was recog  • Patient SC12(HLA A1 immunodominant resp	GGKKKKYKLK  derapy at acute HIV-1 infections and were able to me pecific CD4 proliferative gnized by 1/7 study subject, B8/39, Cw0701/0702, It wonse to FLKEKGGL through	HIV-1 infection ection (three with sustained therapy, to aintain a CTL response even with unceresponses and lost their CTL response ets that were HLA-B8+DR2/3, DR51/52, DQ2/6) had sustain oughout and minor responses to GEI	detectable viral load – three patieses when HAART was eventually ed therapy started during acute in	given and their viral loads became
p17 (24–32)	p17 • CTL responses were st		HIV-1 infection g in 41 patients with combination the		Seth2001 ecline as the viral load drops in and new epitopes may be recognized
p17 (24–32)	period including therap	py with standard treatmer			Oxenius2002b I infected patients were studied over a rebound rates, plateau viral loads, or
p17 (24–35)	relative to B8 epitopes • [Goulder1997a] is a re	, which varied over time	HIV-1 infection eople with the appropriate HLA types that points out that there may be a prof		Goulder1997a, Phillips1991 n the immunodominant B27 epitope, 7, and that HLA-B8 individuals tend to
p17 (24–35)	p17 (25–35) • A study of p17 variation pressure from CTLs	GGKKKYKLKHIV on considering known p1'	HIV-1 infection 7 epitopes and individuals with know	human (B8) n HLA types revealed that p17 e	Birk1998b volution is influenced by immune
p17 (28–36)	<ul><li>sex workers eventually</li><li>The epidemiological faworking for a period o</li></ul>	v seroconverted, and for sactor associated with seron retire	HIV-1 infection posed, persistently seronegative individual of these HIV CTL reactive epitope occurrence was stopping sex work and worker controls (ML1573)	s had been defined while seroneg	gative
p17 (28–36)	p17 (28–36 LAI) • Ikeda-Moore(1998) an	KYKLKHIVW ad D. Lewinsohn, pers. co	omm.	human (A*2402)	Brander2001

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
	C. Brander notes that the	is is an A*2402 epitop	pe		
p17 (28–36)	<ul><li>HLA A24 is very comm</li><li>This epitope was detect</li></ul>	non in Japanese (70% ed by looking for pept	HIV-1 infection ted in 2/3 HIV-infected individuals who carry it) and is common globally ides with appropriate A24 anchor residuaturally processed epitope that elicits a st	es (Y at position 2, carb-term II	Ikeda-Moore1998 LF or W) – 16/17 such peptides bound
p17 (28–36)	p17 (28–36 LAI) • P. Goulder, pers. comm	KYKLKHIVW		human (A23)	Goulder1999b
p17 (28–36)	p17 (28–36 LAI)  • D. Lewinsohn, pers. co.	KYKLKHIVW mm.		human (A24)	Brander1996b
p17 (28–36)	<ul> <li>individuals treated durin</li> <li>The breadth and specification individuals with primar (Group 3), using 259 ox</li> <li>Previously described an</li> </ul>	ng chronic infection city of the response way y infection but post-se verlapping peptides spad d newly defined optim	HIV-1 infection ited in a narrower CTL response, stronge as determined using ELISPOT by studying roconversion therapy (Group 2), and 10 anning p17, p24, RT, gp41, gp120 and Nat pittopes were tested for CTL response CTL response to this epitope broken down	ng 19 individuals with pre-sero individuals who responded to E ef e	conversion therapy (Group 1), 11 IAART given during chronic infection
p17 (28–36)	epitopes in this group, a	although E clade version. Ws tested did not reco	HIV-1 infection  x workers (FSW) from Northern Thailan ons of previously defined B-clade A2 and gnized the E clade version of this epitop	d A24 epitopes were also tested	
p17 (28–36)	<ul> <li>HIV-1-infected female</li> <li>Responses in HEPS wo reduced risk of infection women</li> <li>43/91 HEPS women ha</li> <li>Among HLA-Cw4 women</li> </ul>	Nairobi sex workers men tended to be lowe n, and there was a shif d CD8+ responses and nen, 2/2 HEPS and 7/1	HIV-1 infection, HIV-1 exp seronegative o a panel of 54 predefined HIV-1 epitope er, and focused on different epitopes with it in the response in the HEPS women up I detection of HIV-1-specific CTL in HEI 1 HIV-1 infected women recognized this s to this epitope in both of the 2/2 HEPS	es in 91 HIV-1-exposed, persisted HLA presenting molecules that on late seroconversion to epitope PS women increased with the disceptione	t have previously been associated with bes recognized by the HIV-1 infected uration of viral exposure
p17 (28–36)	p17 (28–36)  • This epitope is newly de  • Combined tetramer and	•	HIV-1 infection staining was used to study the function of	human (Cw4) of circulating CD8+ T cells spe	Appay2000 cific for HIV and CMV

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
	CD27 expression on H	IV-specific cells, sugge	evels of perforin than CMV-specific CD esting impaired maturation activated virus-specific CD8+ T cells p		-
p17 (36–44)	<ul> <li>determined – this epito</li> <li>Three peptides GSEEL contained the dominan</li> <li>Five peptides RLRPGO</li> </ul>	pe fell outside the mos RSLYNTVATL (p17 r t Gag-specific epitope GKKHYMIKHLVW (p EQA (p24 161-177), a	HIV-1 infection an who was HLA A3/33 B35/B53 Cw4/ t recognized peptides in the study esidues 71-85), SALSEGATPQDLNTM in 31 out of 44 B-clade infected individ- 17 20-36), ELRSLYNTVATLYCV (p17 nd SILDIKQGKEPFRDY (p24 149-164	MLNTVG (p24 41-60), and WEK uals from Boston who showed G 7Gag 74-88), SALSEGATPQDL	CIRLRPGGKKKYKLK(p17 16-30) ag-CTL responses NTMLNTVG (p24 41-60),
p17 (36–44)	Dominant CTL response	se in an HIV+ asympto	HIV-1 infection 44), LKHIVWASRELERFA matic donor was to this epitope the previously-defined Tyr for B*3501	human (B*3501)  C-term anchors	Goulder1997d
p17 (36–44)	p17 (36–44 LAI) • C. Brander notes this is	WASRELERF s a B*3501 epitope		human (B*3501)	Brander2001, Goulder1997b
p17 (36–44)	p17 (36–44) • A study of p17 variation pressure from CTLs	WASRELERF n considering known p	HIV-1 infection p17 epitopes and individuals with known	human (B35) n HLA types revealed that p17 ev	Birk1998b volution is influenced by immune
p17 (36–44)	p17 (36–44) • One of the 51 HIV-1 ep HLA alleles	WASRELERF bitopes selected by Ferr	HIV-1 infection rari et al. as good candidate CTL epitop	human (B35) es for vaccines by virtue of being	Ferrari2000 g conserved and presented by common
p17 (36–44)	<ul> <li>individuals treated duri</li> <li>The breadth and specifindividuals with primare (Group 3), using 259 o</li> <li>Previously described as</li> </ul>	ng chronic infection icity of the response wary ry infection but post-se verlapping peptides spand and newly defined optim	HIV-1 infection leted in a narrower CTL response, strong as determined using ELISPOT by study proconversion therapy (Group 2), and 10 anning p17, p24, RT, gp41, gp120 and 10 hal epitopes were tested for CTL response to this epitope broken do	ing 19 individuals with pre-seroe individuals who responded to H Nef ise	conversion therapy (Group 1), 11 AART given during chronic infection
p17 (36–44)	• Epitope name: Gag-W	WASRELERF F9	HIV-1 infection 335, 1/21 (5%) recognized this epitope	human (B35)	Sabbaj2002b

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
p17 (69–93)	p17 (69–93 BH10)	QTGSEELRSLYNTVATLYC- VHQRIE	HIV-1 infection	human (A2)	Johnson1991
	Gag CTL response stud	ied in three individuals			
p17 (71–79)	p17 (71–79 LAI) • P. Goulder, pers. comm	GSEELRSLY		human (A1)	Brander1996b
p17 (71–79)	p17 (71–79) • A study of p17 variation pressure from CTLs	GSEELRSLY n considering known p17 epitopes	HIV-1 infection s and individuals with known HLA t	human (A1) ypes revealed that p17 evol	Birk1998b lution is influenced by immune
p17 (71–79)	CD4 proliferative respo HAART had no HIV sp undetectable	nses and were able to maintain a	HIV-1 infection  ree with sustained therapy, two with CTL response even with undetectables and lost their CTL responses when s that were HLA-A1	le viral load – three patient	s that had delayed initiation of
p17 (71–79)	<ul> <li>HIV-1-infected female I</li> <li>Responses in HEPS woreduced risk of infection women</li> <li>43/91 HEPS women had</li> </ul>	Nairobi sex workers men tended to be lower, and focus n, and there was a shift in the resp d CD8+ responses and detection of	HIV-1 infection, HIV-1 exposed seronegative 54 predefined HIV-1 epitopes in 91 sed on different epitopes with HLA ponse in the HEPS women upon late of HIV-1-specific CTL in HEPS worted women recognized this epitope,	presenting molecules that he seroconversion to epitopes onen increased with the dura	have previously been associated with recognized by the HIV-1 infected ation of viral exposure
p17 (71–79)	period including therapy	with standard treatment interrup			Oxenius2002b infected patients were studied over a bound rates, plateau viral loads, or
p17 (71–85)	<ul><li>Twelve subjects had CT</li><li>One of these 12 had CT</li></ul>	GSEELRSLYNTVATL  I CTL specific for more than 1 HI  L that could recognize vaccinia-e  L response to this peptide  was HLA-A1, A11, B8, B27		human	Lieberman 1997a

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
p17 (74–82)	p17 • Noted by Brander to be	ELRSLYNTV a B*0801 epitope		human (B*0801)	Brander2001
p17 (74–82)	p17 • Defined in a study of th	ELRSLYNTV e B8 binding motif		human (B8)	Goulder1997g
p17 (74–82)	p17 (74–82) • A study of p17 variation pressure from CTLs	ELRSLYNTV n considering known p	HIV-1 infection o17 epitopes and individuals with known	human (B8) HLA types revealed that p17 ev	Birk1998b solution is influenced by immune
p17 (74–82)	p17 (74–82) • One of the 51 HIV-1 ep HLA alleles	ELRSLYNTV itopes selected by Ferr	HIV-1 infection rari et al. as good candidate CTL epitopes	human (B8) s for vaccines by virtue of being	Ferrari2000 conserved and presented by common
p17 (74–82)	p17 (74–82) • B8-restricted CTL acco	ELRSLYNTV unted for about 1/3 of	HIV-1 infection the total CTL response in one individual	human (B8)	Day2001
p17 (76–86)	p17 (74–86 LAI) • C. Brander notes this is	RSLYNTVATLY an A*3002 epitope		human (A*3002)	Brander2001
p17 (76–86)	<ul><li>in the study</li><li>Three peptides GSEELI contained the dominant</li><li>Five peptides RLRPGG</li></ul>	RSLYNTVATL (p17 r Gag-specific epitope : KKHYMIKHLVW (p EQA (p24 161-177), a	HIV-1 infection this epitope in a single HIV+ individual f esidues 71-85), SALSEGATPQDLNTMI in 31 out of 44 B-clade infected individua olf 20-36), ELRSLYNTVATLYCV (p170 nd SILDIKQGKEPFRDY (p24 149-164)	LNTVG (p24 41-60), and WEK als from Boston who showed Gag 74-88), SALSEGATPQDL1	IRLRPGGKKKYKLK(p17 16-30) ag-CTL responses NTMLNTVG (p24 41-60),
p17 (76–86)	• Only 3 of 13 (23.1%) A	*3002-positive subjec	nses and full length HIV-1 genome sequents demonstrated moderate CTL responses		
p17 (76–86)	<ul> <li>characterized that are pi</li> <li>A rapid method was devivere defined – this method</li> <li>Two individuals were st African-Caribbean</li> <li>In both HLA-A*3002 in</li> </ul>	ommon in African popresented by this HLA is veloped combining EL hod was completed witudied: Subject 199 (Handividuals the respons	HIV-1 infection culations, 50% of Zimbabweans express I molecule LISPOT with intracellular IFN-γ staining ithin 48 to 72 hours of receipt of blood ILA A*0201/*3002 B*4402/51 Cw2/5), are to RSLYNTVATLY was dominant or frequency and chromium release, confin	of PBMCs to map optimal epitoral a Caucasian, and Subject 6007 (	opes, then HLA presenting molecules (HLA A*3002/ B53/*5801 Cw4/7) an

HXB2 Location	<b>Author's Location</b>	Sequence	Immunogen	Species (HLA)	References
	HLA-A*3001-positive t	argets do not present RS	LYNTVATLY		
p17 (76–86)	<ul> <li>24 epitopes were descri</li> <li>Serial peptide truncation</li> <li>Subject 00RCH33 was on B*5301; AETFYVDGA</li> </ul>	bitope responses in HIV- bed – 8 were novel, 8 use his were used to define op on HAART had a viral lo A, RT(437-445), HLA B	HIV-1 infection  1 infected minority women living in ed new restricting elements but were of timal epitopes for CTL cell lines iso and of 2900 and CD4 count of 727 are 4501; and HIGPGRAFY, gp160(310), 3/16 (19%) recognized this epitope	previously defined epitopes, and plated from 12 individuals, assaying also recognized the epitopes \$20-318), HLA A*3002	ed by a Cr-release
p17 (76–86)	<ul> <li>individuals treated durin</li> <li>The breadth and specific individuals with primary (Group 3), using 259 ov</li> <li>Previously described an</li> </ul>	ng chronic infection city of the response was y infection but post-serod erlapping peptides spand d newly defined optimal	determined using ELISPOT by study	ving 19 individuals with pre-sero O individuals who responded to F Nef nse	HAART given during chronic infection
p17 (76–86)	<ul> <li>CTL epitopes (http://hiv</li> <li>60 epitope responses we magnitude of the responses to the response of the response</li></ul>	nd lymph node (LN) CD r-web.lanl.gov/content/here detected in both PB at the LN. at the LN. at the the LN. at the PB be following HAART induction the PB, and the addition responses were shown for the PB, and the addition responses were shown for the PB.	-	for each person's class I HLA all and an additional 8 responses were cells in the LN is lower so the nuell response was decreased in both 6 in the LN.  In the LN.  In the LN is lower so the number of the latest testing the content of the latest testing testing the latest testing	lleles. e detected only in LN. The total lumber of HIV-specific cells per million oth LN and PB, but more dramatically the detection of 13 epitopes that had
p17 (77–85)	p17 • Review of the impact of inversely correlate with		HIV-1 infection and escape that notes that SLYNTV	human ATL-tetramer binding cells in ind	Sewell2000 dividuals that react to this epitope
p17 (77–85)	were unrelated to diseas	e progression.	HIV-1 infection  r strongest CD8+ T-cell response again three year study period and used six		

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
	<ul> <li>commonly SLYNTIAV</li> <li>In subject TX7, the observations of the subject TX7 in the observations.</li> <li>The BV17 T-cell clone</li> </ul>	L. These distinct form served mutations of SL recognized SL9 but no	be found initially, but three alternate forms bind A2, but have distinct abilities to support of selections of the selection of SLYNTIAVL, and BV17 became under the selection of the selection o	stimulate different T-cell clonoty ion, presumably because the six detectable at week 20 when SLY	T-cell clonotypes allowed a more
p17 (77–85)	peripheral blood cells. Three HLA-A*0201 cl either using PBMC spe	6/8 were studied using hildren were tested using ecimens, or PBMC whi children with therapy s	HIV-1 infection d viral suppression due to combination g a Chromium release assay and no respong SLYNTVATL or ILKEPVHGV HLA ich had been stimulated in vitro for a we uppressed HIV viral replication who wa 0.14% in the PBMC.	onse was detected using Gag exp. A*0201 tetramers and again no ceek.	pressed in vaccinia in the target cells. HIV-specific response was detected,
p17 (77–85)	<ul><li>Increases in gamma IF</li><li>4/8 A*02 subjects had</li></ul>	N producing cells were a positive response to the 27 individuals, the dom	HIV-1 infection d and highly specific, and found to work e observed in response to anti-retroviral this epitope indicating that it is a major inant response in gag measured by both upe	therapy using single cell IFN-ga epitope for CD8+ gamma IFN p	mma-production ELISPOT roduction
p17 (77–85)	responses in patients w	ith advanced HIV dise	HIV-1 infection erapy (IDV, 3TC and ZDV) sometimes ase, but there is a stable population of to below the level of detection		
p17 (77–85)	ILKEPVHGV  • 71% of the 28 HIV-1 in (SLYNTVATL) and 21  • There were no different	nfected HLA-A*02 pos children by the pol tet ces observed in childre	HIV-1 infection  LA A*02+ children by tetramer staining sitive children recognized both epitopes, ramer (ILKEPVHGV) en that had therapy versus those that did d CD28-, CD45RO+, CD45RA- HLAD	, with cells from 26 children stai	
p17 (77–85)	p17 (77–85 HXB2) • Epitope name: SL9 • Multiple natural variati	SLYNTVATL ions in the SL9 flanking	HIV-1 infection g regions of the immunodominant epitogesting that viral escape from the HLA	human (A*0201) pe SLYNTVATL were tested and	

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
		was an escape mutation still recognized by anoth	in that it interfered with CTL recognit ter CTL clone, 115.D4	tion by one CTL clone from an A	*0201 infected individual, clone
p17 (77–85)	into a patient – they we	ere well tolerated, but the	HIV-1 infection spanded CTL clones against the A*020 e SLYNTVATL clone was shown by te D4 and CD8 cell counts		
p17 (77–85)	<ul> <li>95 optimally-defined p</li> <li>Individuals that did not restricted by other class</li> </ul>	eptides from this databa respond to SLYNTVAT s I alleles	HIV-1 infection TL that reacted to SLYNTVATL, calling se were used to screen for INFγ respon L recognized other HIV epitopes, and a one individual that was HLA A*02	nses to other epitopes 1 2/4 SLYNTVATL responders ha	
p17 (77–85)	<ul><li>seven patients, and the</li><li>Levels of CTL effector</li></ul>	B*3501 epitope DPNPO s typically decline for 5-	HIV-1 infection  ARV therapy using HLA-tetramer co QEVVL in one additional patient -7 days and then rebound, fluctuating of exponential decay with a median half-l	during the first two weeks of ther	
p17 (77–85)	were prepared that can	stain CTL lines specific	HIV-1 infection  y which permits quantification of spec for ILKEPVHGV and SLYNTVATL, YNTVATL, one patient had the highes	and quantitate HIV-specific CD8	+ cell lines in freshly isolated PBMC
p17 (77–85)			HIV-1 infection nerapy (HAART) reduced CD8+ cell for replicating viral populations are neede		
p17 (77–85)	p17 (77–85 SF2) • Epitope name: SL9 • CTL from a patient inf	SLYNTVATL ected with clade B virus	HIV-1 infection  did not recognize the clade A analog	human (A*0201) of this epitope	McAdam1998
p17 (77–85)	<ul><li>cells was followed in v</li><li>Seven HIV+ people we</li><li>Three patients were followed</li></ul>	ivo ere studied, and all show lowed in detail, TCR VI	HIV-1 infection  Tusing MHC tetramers in combination  ed expansions of particular TCR BV of the expansions persisted for 2 to 3 years found to be BV8, and at its highest lev	clones, often several, relative to us, with occasional transient increa	ninfected controls

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References				
p17 (77–85)	p17 (77–85) • Epitope name: SL9	SLYNTVATL	HIV-1 infection	human (A*0201)	Ogg1998b				
	between HIV Gag and	<ul> <li>HLA-tetrameric complexes were used in a cross-sectional study of 14 untreated HLA A*0201 positive individuals, revealing an inverse relationship between HIV Gag and Pol specific CTL effector cells (CTLe) and viral load</li> <li>Inclusion of both the p17 SLYNTVATL and RT ILKEPVHGV epitopes gives a good representation of HLA A*0201-restricted activity</li> </ul>							
			and CD4 count or clearance rate of pr		restricted activity				
p17 (77–85)			in vitro stimulation ressed in E. coli were refolded in the peptide-specific CTL response in cel		Walter1997				
	Suggests that preforme	d HLA-peptide complexe	s could provide an alternate to intrace	ellular processing for immunoge	ens				
p17 (77–85)	stimulate a primary res	ponse, only secondary – p	HIV-1 infection imulation of CTLp using optimized p peptide-specific CTLp counts could be						
	This peptide was one o								
p17 (77–85)	<ul> <li>p17 (76–84)</li> <li>Epitope name: SL9</li> <li>Slow dissociation rate:</li> <li>CTL generated by in visual contents.</li> </ul>		in vitro stimulation ogenicity derived from uninfected individual	human (A*0201)	vanderBurg1996				
p17 (77–85)	<ul> <li>One had a response to</li> <li>Viral sequencing from</li> <li>71% of an additional se</li> <li>Those individuals with</li> </ul>	gag A2 epitope SLYNTV, the twin that had no respo et of 22 HIV-1 infected HI a pol ILKEPVHGV respo went from SLYNTVATL re	HIV-1 infection  fected with the same batch of factor of ATL, the other to pol A2 epitope ILK onse to SLYNTVATL indicated his virtual to the state of the state o	EPVHGV rus had the substituted form SLI tially responded to gag SLYNTV round SLYNTVATL	VATL .				
p17 (77–85)	Class I HLA-restricted • 17/18 asymptomatic pa	anti-HIV CD8+ T cells tients had a CTL respons	HIV-1 infection  NTVATL or ILKEPVHGV were used to one or both epitopes – 72% had a fic CTL were apparently memory cell	a CTL response to SLYNTVATL	Gray1999  HAART to determine the frequency of				
p17 (77–85)	<ul> <li>p17 (77–85 subtype A)</li> <li>Epitope name: SL9</li> <li>CTL responses in three in East Africa</li> </ul>		HIV-1 infection  de B infections were studied, 2 with s	human (A*0201) subtype A infections, 1 with sub	Dorrell1999 type C – their infections all originated				

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
			in B subtype, and CTL from the C sub and C clade form, SLFNTVATL	otype infection did not recognize	B clade gag or the 3Y form of the
p17 (77–85)	p17 (77–85) • Epitope name: SL9	SLYNTVATL	HIV-1 infection	human (A*0201)	Brander1998a
	<ul> <li>Of 17 infected HLA A<sup>3</sup> VIYQYMDDL, and the</li> <li>Only one subject had C</li> </ul>	ere was no correlation b TL against all three epi	CTL responses against the p17 SLYNT petween viral load and recognition of a itopes L response to this immunodominant ep	specific epitope	LKEPVHGV and five recognized
	immune pressure		e 17 who had a CTL response and 11 n Clinic Cohort, the ARIEL project and fi		luals was similar, suggesting a lack of
p17 (77–85)	p17 (77–85 HXB2) • Epitope name: SL9	SLYNTVATL	HIV-1 infection	human (A*0201)	Hay 1999b
	<ul> <li>CTL response to IPRR interestingly, no respon</li> <li>The individual showed</li> <li>Despite the initial narro</li> <li>No HIV-specific lymph</li> </ul>	as to commonly immura strong initial CTL resources to two epitosoproliferative response e was observed in vivo	nodominant response in a rapid progres modominant HLA A*0201 epitope SLY sponse at the time of the initial drop in opes, no other CTL responses developes were detected in this patient, and neu (-F—-V-), but this mutation is recognicific CTL	YNTVATL, although this individu viremia, but it was quickly lost, ed tralizing antibody response was	all was HLA A*0201 although memory cells persisted weak
p17 (77–85)	<ul><li>that by day 260 CTL ac</li><li>ERYLKDQQL was the</li><li>Sporadic breakthrough</li></ul>	ctivities were undetectal dominant response in in viremia resulted in t	HIV-1 infection IAART – reduced plasma HIV-1 RNA ble one of the individuals, SLYNTVATL so ransient increases in CTLp Gag, Vac-RT, Vac-Env, and Vac-Nef in	ubdominant	
p17 (77–85)	low CD4 counts, but C	D8 T cell mediated effe D8+ cells may be presen	HIV-1 infection negalovirus specific CTL were detected ector activity was not seen nt but may lack direct effector activity		
p17 (77–85)	• The highest CTL frequ	ency was directed at ep higher numbers of spo	HIV-1 infection sponse to the HIV-1 proteins Gag, Pol, itopes Pol t-forming T cells were directed against	-	

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
p17 (77–85)	<ul><li>individuals from Durb:</li><li>Three peptides GSEEI contained the dominan</li><li>Five peptides RLRPGO</li></ul>	an LRSLYNTVATL (p17 res at Gag-specific epitope in GKKHYMIKHLVW (p1 LEQA (p24 161-177), and	HIV-1 infection his epitope in 11/25 HLA A2 (A*0201 his epitope in	MLNTVG (p24 41-60), and WEK uals from Boston who showed G 7Gag 74-88), SALSEGATPQDLI	IRLRPGGKKKYKLK(p17 16-30) ag-CTL responses NTMLNTVG (p24 41-60),
p17 (77–85)	p17 (77–85 LAI) • C. Brander notes this i	SLYNTVATL s an A*0201 epitope		human (A*0201)	Brander2001
p17 (77–85)	<ul> <li>CTL responses to SL9</li> <li>Longitudinal studies o</li> <li>Low Gag expression le</li> <li>Autologous SL9 varian responses, sometimes</li> </ul>	and autologous SL9 var f two individuals (AC13 evels did not correlate wi nts SLYNTIAVL, SLYN strong, sometimes dimin	HIV-1 infection  O1, HIV+ adults, and the magnitude of iants were not detected in 11 HLA-A* and PI004) showed that the initial conth the delayed CTL response to this eproperty SLFNTVATL, SLFNTVATL, ished, and sometimes complete escapeoss-react with a particular variant was	0201 positive subjects during act trol of viremia was independent bitope and SLFNTVATL are each capal e relative to the than the wild type	of the SL9 CTL response ble of inducing a range of CTL
p17 (77–85)	criteria, and 30 of thes  Three additional previous	all peptides which carried e bound to HLA-A*0201 ously described HLA-A2 hat recognized at least on and maximum of 2) ed in 12/22 patients with		-A2 supertype alleles tested including p17 SL9, and 18/22 ch	ronically infected HLA-A2
p17 (77–85)	<ul> <li>The IFN-gamma ELIS pooled peptides gave to A correlation with resubigher number of cells IFN-gamma, some magnetic properties.</li> </ul>	POT assay was compare the highest number of spoults of the tetramer assay than could produce IFN by be undergoing apoptos	HIV-1 infection  different CTL assays, a SL9 tetramer dusing the single SL9, a pool of overlet forming cells, vaccinia gave high bawas found only for ELISPOT using the gamma in the ELISPOT assay – the ais, some may be producing other cytol LYNTVATL in most of the HLA-A*02	apping 20 mers, and recombinan ckground he Gag epitope as antigen, but the authors suggest not all tetramer-pakines	e tetramer assay detected a 10-fold ositive cells may produce

**HIV CTL Epitope Tables** 

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
p17 (77–85)	T-cells from HIV-1 inf	ected individuals at level	in vitro stimulation g HIV-1 sequences, upon infection of m s comparable to the response seen to H g HIV-1 sequences can also stimulate H	IV carried in vaccinia vectors	
p17 (77–85)	p17 (77–85 LAI)  • Epitope name: G3  • A panel of 16 epitopes tetramer staining or CI  • In general, during the specificities that were HIV-specific responses	SLYNTVATL s covering 15 class I allele D8+ cell IFNgamma proc first month of treatment v not previously detectable s diminished	HIV-1 infection  es was tested in 14 HIV+ patients from duction to measure responses viral load decreased and frequencies of I were newly detected, as were CMV spase: increases or decreases in pre-existing	human (A*0201)  an unselected Caucasian popula  HIV-specific CTL tripled and br  ecific CD8+ PBL – but with cor	Mollet2000  ation treated with HAART, using roadened – eight new HIV attinued viral suppression,
p17 (77–85)	High frequencies of ci	rculating CD8+ T-cells w	HIV-1 infection essors, no correlation between plasma vere HIV-1 specific, and the majority of e only 2 subjects (patient 3 and 19) teste	these responses were to gag-po	
p17 (77–85)	<ul> <li>for the A3 supertype)</li> <li>Progressors had memor</li> <li>A positive correlation observed, which may of Tetramer staining with HIV-specific sells in L</li> </ul>	while the effector cells of ory resting CD8+ T-cells to between effector CD8+ T contribute to the inability A2, beta2microglobuling	, and either SLYNTVATL, KLVGKLNV activated effector cells were the minori	far fewer epitopes LTNPs ve correlation between CD8+ ef WA, or LTFGWCFKL revealed	fector T-cells and CD4+ T-cells was
p17 (77–85)	by therapy, using a tetr	ramer assay	HIV-1 infection d in long term non-progressors (LTNP) low viral load, while HAART patients h	_	
p17 (77–85)	HIV-specific CD8+ T of CD27 expression on H	cells expressed lower leve IIV-specific cells, suggest	HIV-1 infection taining was used to study the function o els of perforin than CMV-specific CD8- ting impaired maturation ctivated virus-specific CD8+ T cells pro	+ T cells from the same donor, a	nd this was associated with persistent
p17 (77–85)		SLYNTVATL compared with three functimiting dilution assay [Ll	HIV-1 infection ctional assays in 42 people with chronic DA])	human (A*0201) HIV infection: ELISPOT, intra	Goulder2000b cellular cytokine staining, and

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
	HIV-specific tetramer s infection	staining CTLs appeared	to be active, and inert CTL were not for	und to play a significant role in	chronic pediatric or adult HIV
p17 (77–85)	<ul> <li>Optimal expansion of l</li> </ul>	HIV-1-specific memory	HIV-1 infection virus-specific memory CTL was studied CTL depended on CD4+ T cell help in le degree in most of patients		Ostrowski2000 trimer (CD40LT) could enhance CTL
			uld expand with IL2 present, and IL15 pmulation was the universal tetanus helpe		
p17 (77–85)	<ul><li>component: gp120, gp</li><li>Two vaccinees with Ga</li></ul>	41, Gag, Pol and Nef ep ag responses were HLA	Vaccine gp120 boost, canarypox prime with rgp1 pitope rich regions -A*0201+, but neither made SLYNTVA 0201 responses were observed to an En	TL responses to the Gag vaccin	
p17 (77–85)	threshold of infection v KAFSPEVIPMF, TST • CTL responses are bro	without therapy, and the LQEQIGW, and QASQ ader in B*5701+ indivi	HIV-1 infection including 10 LTNP with an over-expressir immune response tends to be focused EVKNW. duals with progressive viremia than thosonse was not as strong individuals that co	on peptides that contain B*570 se that control viremia.	
p17 (77–85)	immunodominance1 immunoproteasome. T  ILKEPVHGV was effi by the MB1 subunit of	74 cells were used that these genes could be adciently presented in TA the protease, and could	HIV-1 infection 60201 HIV epitopes was shown to use di lack TAP1 and TAP2 genes, as well as t ded back through transfection to study p P-1 and -2 transfected cells while VIYQ be expressed in the presence of the prored by lactacystin in a wild type cell line	he LMP2 and LMP7 genes that processing.  DYMDDL and SLYNTVATL we teasome inhibitor lactacystin, but	encode the beta-subunits of the ere not. VIYQYMDDL was destroyed
p17 (77–85)	<ul><li>monocyte-derived mac</li><li>HLA-A*0201 CTL res</li></ul>	crophages MDM in the l	were reconstituted with HLA-A*0201 pobasal ganglia to provide a mouse model y tetramer staining in the spleen in several contractions.	of HIV-1 encephalitis.	
p17 (77–85)	were used to identify H	HLA-A*0201 and HLA	computer prediction orks (ANN), hidden Markov models (H -B*3501 HIV T-cell epitope candidates 62 from SIV. Comparisons to known ep	from 533 Gag, Env and Pol sequ	uences of which 374 were derived

	Author's Location	Sequence	Immunogen	Species (HLA)	References
	variants would be recognized substitutions may be an	gnized, while BIMAS on tagonistic, including sl	scussion. SLYNTVATL, slFntvatl, slyntvaV only predicts SLYNTVATL and slFntvatl wor Fntvatl, and vaccines do not stimulate SLYN n of computational predictions of epitopes to	uld be recognized. Howeve NTVATL responses as well	r, [Sewell1997] suggested certain
p17 (77–85)	<ul> <li>C3H (H-2k) transgenic epidermal gene gun wi the proteasome.</li> <li>A single immunization</li> <li>Immunodominant epitoresponses and stimulatores The presence of multip</li> </ul>	mice carrying a fused left an ubiquitin expression with the UB-HIV-1 lib ppes SLYNTVATL (Gaged CTL that were functional left plasmids HLA-A*02	Vaccine HIV-1 divided into a 32 plasmids in a ubiq HLA-A*0201 alpha1 and alpha2 and H-2Dk on library of 32 plasmids that spanned the H rary vaccine induced potent, stable and mult g), ILKEPVHGV(Pol), RIQRGPGRAFVTIG ional in a Cr-release assay and against wild t 201-restricted CTL epitopes did not decrease based on mixtures of either 16 or 32 peptide	c alpha3 hybrid class I mole IIV-1 genome. Ubiquitin ta tivalent CTL responses agai GK(P18) and AFHHVARE type antigen. c CTL immunogenicity, and	rgets the expressed HIV-1 peptides to inst all library members. K (Nef) elicited strong CD8+/IFN-
p17 (77–85)	viremia but had progre- had much strong Th re- responses.	ssive CD4+ T-cell decli sponses, particularly to	HIV-1 infection 10 clinical non-progressors, and 3 immunolo ne) were analyzed for their T-helper cell res p24 peptides, and they tended to be balance	ponses to p24 and cytokine d between Th1, IL-2 produ	profile. Long term non-progressors cing and Th2, IL-4 producing
	all antigens and also a	shift from a Th1 to a Th ntient was also tested. It	essors became symptomatic during the cours n2 response. To find out if the CD8 response t to was found to shift, from IFNgamma to II	also shifted in cytokine pro	oduction, the CD8+ T-cell response to
p17 (77–85)	all antigens and also a s SLYNTVATL in this pa from IL-2 to IL-4 prod p17 (77–85)	shift from a Th1 to a Thatient was also tested. It uction.  SLYNTVATL	n2 response. To find out if the CD8 response	also shifted in cytokine pro	oduction, the CD8+ T-cell response to
p17 (77–85)  p17 (77–85)	all antigens and also a s SLYNTVATL in this pa from IL-2 to IL-4 prod p17 (77–85)  C. Brander notes that the p17 (SF2)  The CTL-dominant res individuals from Durba Three peptides GSEEL contained the dominant Five peptides RLRPGO	shift from a Th1 to a Thatient was also tested. It uction.  SLYNTVATL nis epitope can be prese SLYNTVATL ponse was focused on tan RSLYNTVATL (p17 reasons to the tangle of	n2 response. To find out if the CD8 response t to was found to shift, from IFNgamma to I	human (A*0202)  human (A*0202)  *0202) HIV+ individuals from Boston who showed C74-88), SALSEGATPQDL	Goulder2000a  Goulder2000a  Goulder2000a  Gom Boston and in 1/8 HLA A2 HIV+  KIRLRPGGKKKYKLK(p17 16-30)  Gag-CTL responses  NTMLNTVG (p24 41-60),
	all antigens and also a s SLYNTVATL in this pa from IL-2 to IL-4 prod p17 (77–85)  C. Brander notes that the p17 (SF2)  The CTL-dominant resindividuals from Durba Three peptides GSEEL contained the dominant Five peptides RLRPGOFRDYVDRFFKTLRA infected subjects from p17 (77–85 LAI)	shift from a Th1 to a Thatient was also tested. It uction.  SLYNTVATL nis epitope can be prese  SLYNTVATL ponse was focused on tun  RSLYNTVATL (p17 reat Gag-specific epitope in GKKHYMIKHLVW (p) EQA (p24 161-177), and South Africa  SLYNTVATL	n2 response. To find out if the CD8 response to was found to shift, from IFNgamma to II ented by A*0201 and A*0202  HIV-1 infection his epitope in 11/25 HLA A2 (A*0201 or A esidues 71-85), SALSEGATPQDLNTMLNT in 31 out of 44 B-clade infected individuals f 17 20-36), ELRSLYNTVATLYCV (p17Gag	human (A*0202)  human (A*0202)  *0202) HIV+ individuals from Boston who showed C74-88), SALSEGATPQDL	Goulder2000a  Goulder2000a  Goulder2000a  Gom Boston and in 1/8 HLA A2 HIV+  KIRLRPGGKKKYKLK(p17 16-30)  Gag-CTL responses  NTMLNTVG (p24 41-60),

CD8+ T cell responses tended to be to the same epitopes but at generally lower levels than cervical CD8+ T cell responses

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
	most commonly recogn	DTVLEDINL (3 indivinized by the HIV-resista	duals), SLYNVATL (4 individuals), LS	SPRTLNAW (3 individuals) and	d YPLTFGWCF (4 individuals) were
p17 (77–85)	<ul><li>Epitope name: Gag-SL</li><li>Among HIV+ individu</li></ul>		HIV-1 infection .02, 17/30 (57%) recognized this epitop	human (A02)	Sabbaj2002b
p17 (77–85)	<ul> <li>A polyepitope vaccine</li> <li>HHD mice have a transexpressed in the mice</li> <li>CTL responses to Gag observed in HIV polyte</li> <li>No CTL immune responses to Table 180-189 (VLEWR)</li> <li>Sixteen HLA A2+ patithe polytope – one indicates</li> </ul>	sgene of HLA A2 linke (77-85) SLYNTVATL, ope HHD-vaccinated m onses were generated ag (FDSRL) ents were tested for the ividual recognized all so re than one epitope, but	cinia construct that contiguously encoded to the transmembrane and cytotoxic of Pol (476-484) ILKEPVHGV, gp120 (1 ice, and these responses were enhanced anist HLA A2-restricted HIV epitopes in ability to make CTL responses by peeven of these epitopes; 7 patients had C they were not able to test all peptides:	domains of H-2D <sup>d</sup> – this transg 120-128) KLTPLCVTL, and No d with vaccinia boost 5 Nef 157-166 (PLTFGWCYKL optide restimulation in culture w CTL cultures able to recognize a	erene is the only MHC molecule of (190-198) AFHHVAREL were L), Pol 346-354 (VIYQYMDDL), and with the epitopes selected for inclusion in at least one of the epitopes, and 6 of
p17 (77–85)	<ul> <li>The vaccine used was a Gag, HIV-1 LAI protea</li> <li>CD4+ and CD8+ Gag</li> <li>CTL responses to epito</li> <li>The study explored wh process and present an</li> </ul>	a live recombinant cana ase) and Env specific CTL r opes SLYNTVATL and by vaccinees were non-r tigen	esponses were detected in only 1/5 vac TVYYGVPVWK from HIV+ control p esponsive – non-response was not due	nultiple HIV-1 genes (HIV-1 Mi cinated volunteers, and were no patients were used as positive c to inherent defects or difference	ontrols
p17 (77–85)	p17 (77–85) • Epitope name: SL9 • A study of p17 variation pressure from CTLs	SLYNTVATL on considering known p	HIV-1 infection 17 epitopes and individuals with know	human (A2) n HLA types revealed that p17	Birk1998b evolution is influenced by immune
p17 (77–85)	p17 (77–85) • Epitope name: SL9 • Included as a negative	SLYNTVATL control in a tetramer str	HIV-1 infection ady of A2-EBV CTL response	human (A2)	Callan1998
p17 (77–85)	p17 • Epitope name: SL9	SLYNTVATL	HIV-1 infection	human (A2)	Wagner1998a

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
			ow that the mediators of both the cytowere used as markers) anti-viral response		
p17 (77–85)	p17 (77–85 HXB2) • Epitope name: SL9	SLYNTVATL	HIV-1 infection	human (A2)	Collins1998
			t the NL4-3 form of the epitope SLYN hich inhibits CTL killing, and this down		ompensated for by adding excess
p17 (77–85)	p17 (77–85) • Epitope name: SL9	SLYNTVATL	HIV-1 infection	human (A2)	Durali1998
	<ul> <li>Cross-clade CTL response A subtype infection</li> <li>Pol reactivity: 8/8 had</li> <li>Gag reactivity: 7/8 reactivity: 7/8 reactivity: 3/8 reactivity</li></ul>	on from a person living in CTL to A subtype, and coted with A or B subtype, and coted with A subtype, and coted with A subtype, 1/8	rmining the CTL activity in seven pating France originally from Togo, to differ 7/8 to B subtype, and HIV-2 Pol was regag, 3/8 with HIV-2 Gag 5/8 with B subtype, none with HIV-2 with B subtype, none with HIV-2 Entity of response, and recognized Gag S	erent antigens expressed in vacci not tested  Nef	
p17 (77–85)	<ul> <li>monthly into six HIV-i</li> <li>1/6 showed increased on change – pulsed DO</li> <li>SLYNTVATL is a constitution</li> </ul>	infected patients env-specific CTL and inc Cs were well tolerated served HLA-A2 epitope	ereased lymphoproliferative responses included in this study – 3/6 patients h	, 2/6 showed increase only in prad this sequence as their HIV di	Kundu1998b ad HIV-1 epitope peptides, and infused oliferative responses, and 3/6 showed rect sequence, one had the form IVL or SLFSAVAAL and no detectable
p17 (77–85)	p17 (77–85 IIIB) • Epitope name: SL9 • HIV IIIB proteins wer • SLYNTVAVL, a varian • SLFNTVAVL, a varian	nt found in HIV-1 MANG		human (A2)  o workers accidentally infected v	Sipsas1997 with HIV-1 IIIB
p17 (77–85)		oss-reactivity could protosus is SLfNtvatL	HIV-1 infection  fected prostitutes from Nairobi using ect against both A and D and confer p		Rowland-Jones1998a  opes that tended to be conserved in A subtypes are circulating
p17 (77–85)	p17 • Epitope name: SL9 • Naturally occurring va	SLYNTVATL	HIV-1 infection aped killing and acted as antagonists	human (A2)	Sewell1997

p17 CTL Epitopes

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
	-L—, —I—, —I- • All variants bound to A	V-, -F-I—, -F-I-V-, -F A2 with at least half the observed at low concent	affinity of SLYNTVATL except the trip rations, abrogating lysis at an antagonis	le mutant: –F–I-V-	
p17 (77–85)	chain $\zeta$ , and transduce	d into CD8+ cells iversal-receptor-bearing in terms of kinetics and	•		_
p17 (77–85)	p17 (77–85) • Epitope name: SL9 • Keyhole limpit hemocy peptide-specific CTL	SLYNTVATL vanin or tetanus toxoid	in vitro stimulation  Th epitope co-expression with peptide C	human (A2) CTL epitopes on the same APC	Stuhler1997 was required for induction of
p17 (77–85)	<ul><li> Clones specific for RT</li><li> The distinction was the</li></ul>	lysed HIV-1 infected co ought to be due to lower	HIV-1 infection  re studied to determine their susceptibil ells at lower levels than Env or Gag spector expression of RT relative to Env and Gon, possibly prior to viral production	cific clones	Yang1996
p17 (77–85)		suppressive soluble fact	HIV-1 infection concentrations comparable to those four ors – MIP-1 $\alpha$ , MIP-1 $\beta$ , RANTES, afte $\gamma$ in HLA-matched cells		Yang1997a
p17 (77–85)	p17 (77–85 LAI) • Epitope name: SL9 • Examined in the context	SLYNTVATL	HIV-1 infection or HLA-A2 binding	human (A2)	Parker1992, Parker1994
p17 (77–85)	p17 (77–85 LAI) • Epitope name: SL9 • Review of HIV CTL ep	SLYNTVATL	HIV-1 infection	human (A2)	McMichael1994
p17 (77–85)	p17 (77–85) • Epitope name: SL9 • CTL clones recognize	SLYNTVATL naturally processed pep	HIV-1 infection	human (A2)	Tsomides1994
p17 (77–85)	p17 (77–85) • Epitope name: SL9	SLYNTVATL	in vitro stimulation	human (A2)	Stuhler1997

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
	A three cell-type cluster	consisting of APCs, Th	, and CTLs is the minimal regulatory	unit required for Th cell-depen	dent induction of CTLs
p17 (77–85)			HIV-1 infection s and some Cs have the sequence SLY have SLFNTVATL, a form that is cro		Cao1997a
p17 (77–85)	natural attenuated strain	of HIV-1 which was No	HIV-1 infection  3 to 1.5 year period in members of the ef-defective ls of CTL effector and memory cells d		Dyer1999 SBBC) who had been infected with a
p17 (77–85)	(SLYNTVATL)	ions were present in this	HIV-1 infection  long-term survivor, restricted by two of sindividual which did not affect viral rive of immune escape		
p17 (77–85)	<ul> <li>Individuals with long-te</li> <li>Vpr is a frequent target targeted proteins per unitargeted</li> </ul>	rm nonprogressive and pof HIV-1 specific CD8+ it length by CD8+ T-cel IIRLLQQL and p17 SLY		ed Vpr more frequently than in 5% of individuals tested and V	dividuals with treated acute infection for and p17 were the most preferentially
p17 (77–85)	<ul><li>epitope processing that</li><li>Dendritic cells treated w</li><li>without protein synthesis</li></ul>	may be important in the with AZT to inhibit protests, while macrophages d	in vitro stimulation  f epitopes by antigen presenting cells ( initial generation of viral specific CTI ein synthesis were able to elicit a stron emonstrated a decreased presentation ependent and required receptor-depen	L g specific CTL response in SL efficiency	-
p17 (77–85)	<ul><li>with viral load in patien</li><li>Most patients have high</li><li>In 15 of the patients, the</li></ul>	ts with high CD4, but in levels of HIV-specific To e proportion of IFN gam YNVATL response, no S	patients with CD4 T-cells below 400 F-cell expansions, but many of these cema producing tetramer cells correlated SLYNVATL mutations were found am	high tetramer frequencies were ells aren't functional I with AIDS-free survival	

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
p17 (77–85)	p17 (77–85) • One of the 51 HIV-1 e HLA alleles	SLYNTVATL epitopes selected by Ferra	HIV-1 infection ari et al. as good candidate CTL epitopes	human (A2) s for vaccines by virtue of beir	Ferrari2000 ng conserved and presented by common
p17 (77–85)	response to therapy, be 6/10 A*0201+ individ 4/10 A*0201+ individ	ut the overall level of ant luals had HIV-specific tet luals with chronic HIV-1 nean percentage of CD8+	HIV-1 infection  ng in 41 patients with combination thera igen-specific cells capable of differentiat ramer staining cells, and 5 of these decli infection recognized this epitope cells that recognized the immunodomin	ting into effectors stays consta ined upon successful therapy	ant and new epitopes may be recognized
p17 (77–85)	of samples collected 6 p175b recognizes the This epitope sequence Responses were stable	5-11 years post infection: A2 epitope SLYNTVATI a from clone p175b uses to be even through HAART v	HIV-1 infection  CTL clones from patient 115, with a chrocolone M21 and E15 recognize ERYLKI  The Vbeta5, CDR3 (FDS), Jbeta2.7 TCR with undetectable viral loads, but frequent to 3.78% for M21, with the relative free	DQQL,and clone D87 recogni beta gene ncies varied over time by 100-	zes variant ERYLQDQQL, and clone fold, ranging from 0.012% of the total
p17 (77–85)	<ul> <li>individuals treated dur</li> <li>The breadth and speci individuals with prima (Group 3), using 259 o</li> <li>Previously described a</li> </ul>	ring chronic infection ficity of the response was ary infection but post-ser overlapping peptides spa and newly defined optima	HIV-1 infection ed in a narrower CTL response, stronger s determined using ELISPOT by studyin oconversion therapy (Group 2), and 10 i nning p17, p24, RT, gp41, gp120 and Ne al epitopes were tested for CTL response TL response to this epitope broken dowr	ng 19 individuals with pre-sero ndividuals who responded to be ef	oconversion therapy (Group 1), 11 HAART given during chronic infection
p17 (77–85)	p17 (77–85)	SLFNTVATL	HIV-1 infection, HIV-1 exp seronegative	osed human (A2)	Kaul2001a

- Variants SL(F/Y)NTVATL are A/B clade specific
- ELISPOT was used to study CTL responses to a panel of 54 predefined HIV-1 epitopes in 91 HIV-1-exposed, persistently seronegative (HEPS) and 87 HIV-1-infected female Nairobi sex workers
- Responses in HEPS women tended to be lower, and focused on different epitopes with HLA presenting molecules that have previously been associated with
  reduced risk of infection, and there was a shift in the response in the HEPS women upon late seroconversion to epitopes recognized by the HIV-1 infected
  women
- 43/91 HEPS women had CD8+ responses and detection of HIV-1-specific CTL in HEPS women increased with the duration of viral exposure
- Among HLA-A2 women, 1/10 HEPS and 22/26 HIV-1 infected women recognized this epitope, likelihood ratio 18.3, p value < 0.003, and ILK(D/E)PVHGV tended to be more reactive in HEPS women, SL(F/Y)NTVATL in infected women
- The dominant response to this HLA allele was to this epitope in the 1/10 HEPS case and in 18 of the 22/26 HIV-1 infected women that responded
- Differences in epitope specificity were only seen for responses restricted by class I HLA alleles A2, A24, A\*6802, B14, and B18, previously shown to be associated with resistance to HIV-1 in this cohort

HXB2 Location	<b>Author's Location</b>	Sequence	Immunogen	Species (HLA)	References
	Subjects ML 1575 and I	ML 1592 had no response A2 response to ILK(D/	E)PVHGV prior to seroconversion, ve to SL(F/Y)NTVATL prior to seroco E)PVHGV prior to seroconversion, a	onversion, but made responses p	ost-seroconversion
p17 (77–85)	<ul> <li>HLA-A11 is very command CTL responses were</li> </ul>	non in this population, and found in 8/8 HIV+ cont	HIV-1 infection seronegative (HEPS) female sex work d was enriched among the HEPS sex trols, and 0/9 HIV- women that were subjects 125 and 144 who carried H	workers – weak CTL responses not exposed	Sriwanthana2001 nailand s were detected in 4/7 HEPS women,
p17 (77–85)	<ul><li>epitopes in this group, a</li><li>2/4 tested FSWs recogn:</li></ul>	Ithough E clade versions ized the E clade version of	HIV-1 infection  workers (FSW) from Northern Thaila of previously defined B-clade A2 ar of this epitope, SLYNTIATL, the B of subtypes B and D, and exact matches	nd A24 epitopes were also tested clade version is SLYNTVATL	•
p17 (77–85)	<ul> <li>studied in eight HIV-1-i</li> <li>2 to 17 epitopes were re epitopes were targeted b</li> </ul>	nfected subjects, two wit cognized in a given indiv by at least one person cominant A2 epitope reco 2 response only to SLYN	h acute infection, five with chronic, vidual, A2-restricted CTL response to gnized in patients with chronic infective actions.	and one long-term non-progress ended to be narrow and never do	ominated the response, and 25/27
p17 (77–85)	Eight transmitting moth	ers and 14 non-transmitte	HIV-1 infection  Insmitted both horizontally and verticers mothers were studied and variation ensus and vertical transmission was	on within the SL9 epitope was a	Goulder2001c ssociated carrying HLA-A2 (P=0.04),
p17 (77–85)	an HLA-B60 individual		HIV-1 infection y identifying new HLA-B60 epitopes but the HLA presenting molecule as		Altfeld2000b resented by another HLA molecule in ermined
p17 (77–85)	p17 (77–85 LAI) • Ritonavir (RTV) inhibits there is concern protease	SLYNTVATL s chymotryptic activity in e inhibitors may adversel	HIV-1 infection the 20S proteasome in vitro, as doe	human (A2) es Saquinavir (SQV) to a lesser of t this paper indicates that proces	Kelleher2001a extent; Indinavir (IDV) does not. Thus ssing is not inhibited at therapeutically

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
	(A2)).	e processing and assembly	ncentration of the two immunodoming of HLA-B35 or -A2, which are asso		
p17 (77–85)	<ul><li>T-cells, detected by int</li><li>Ghonorrhea caused the</li></ul>	racellular cytokine produc weaker HIV-1 specific C	HIV-1 infection a sex workers caused a functional delection and tetramer assays, while not a TL responses in 4 HIV-1 exposed pe TL in 2 HEPS subjects were shown	affecting the total number of epitersistently seronegative (HEPS) w	ope-specific CTLs.  vomen to become undetectable by
p17 (77–85)	than NL-43 with an int	act Nef. The effect was sl	HIV-1 infection and this study demonstrates directly hown to be specific for class I presen 23, specific for the class I A2 preser	tation of epitopes, and unlike Ne	f, deleting Vpr did not alter CTL
p17 (77–85)	sensitive to lysis by SL differences in processin  Incubation with a T1-c while ILKEPVHGV-pr  p17 was preferentially  In a competition experi  No difference in CTL a	YNTVATL-specific CTL ng. ell proteolytic extract sho recursors were far less frecleaved between Leu85 a ment, RSLYNTVATL bo avidity was detected in six	HIV-1 infection bitopes was compared, SLYNTVATL than by ILKEPVHGV-specific CTL wed that by four hours, 25% of a p1 quent (6.8%) even with four times m nd Tyr86, while appropriate Val484 and TAP 3.7-fold more efficiently the patients with HLA-A2-restricted re to p17 or RT epitopes was observed	7 peptide had a C-term Leu-85 are nore proteolytic extract after 30 he and Tyr485 cleavage was minor from RT peptides.	LYNTVATL-A2 resulting from and were SLYNTVATL-precursors, purs.
p17 (77–85)	<ul> <li>Transgenic mice expreprotein (vVK1).</li> <li>Compared to vVK1, vC</li> </ul>	ssing a HLA-A2/Kb chim  G/P-92 induced a significa	Vaccine of Adjuvant: IL-12 (IL-12p35 and I neric protein were vaccinated with eit ant increase in Gag and Pol induced by Elispot and 51Cr-release assays.	ther a p17-p24-p51 fusion protein	
p17 (77–85)	<ul><li>specific T-cell response</li><li>Nef epitope recognition</li></ul>	es by Elispot and Tetrame n was detected in all 4 sub	HIV-1 infection cessful anti-viral therapy but with on r staining, maintained for 2-4 years a bjects, gp120, Pol and Gag-specific is iate maturation phenotype characteri	after initiation of HAART. n 1 or 2 subjects.	
p17 (77–85)			HIV-1 exposed seronegating at the HIV-1 exposure is among the high	ese CTL may confer protection	Rowland-Jones1998b

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
	<ul><li>responses are frequentl</li><li>This epitope is conserv</li><li>The Clade A version of</li></ul>	y observed using A or I ed among B and D clad fithe epitope, SLFNTVA	obi, although clades C and D are also D clade versions of epitopes le viruses ATL, was preferentially recognized by exposed seronegative prostitutes		cross-reactive, however stronger
p17 (77–85)	<ul> <li>Epitope name: LR23</li> <li>The stability of peptide SLYNTVATL (p17), SI (GILGFVFTL), while in the four high-affinity part less than an hour.</li> <li>HLA-A2.1 transgenic in as adjuvants.</li> <li>All peptides except VI</li> </ul>	e binding to HLA-A2.1 LLNATDIAV (gp41) an RGPGRAFVTI and VI peptides formed stable of mice were immunized v	Vaccine Adjuvant: P30, incomplete Freund's was determined for six HLA-A2.1 pe id LLWKGEGAV (RT) all bound with YQYMDDL bound with a lower affin complexes with half-lives ranging bet with the six HIV-1 peptides and P30, a stong CTL response in Cr-release ass combination was used.	eptides included in this vaccine stuch high affinity comparable to a inflity (relative binding activity = 0.0 ween 8 and 32 hours, while the lowes as a universal T-helper epitope, with	dy – ILKEPVHGV (RT), uenza epitope reference 1). w affinity peptides had half lives of h IFA or Montanide or microspheres
p17 (77–85)	<ul> <li>Epitope name: LR23</li> <li>When HIV-1 peptides vigiven individually, but counteract immunodon</li> </ul>	were used to vaccinate I immunodominance lim ninance in BALB/c mic	Vaccine  Adjuvant: P30, incomplete Freund's  HLA-A2.1 transgenic A2-Kb mice, st ited the response to some of the pepti e, so it was given with the multiple ep of CTL responses. This was possibly a	rong responses to five peptides we des when they were given in comb pitope vaccination, and was instead	oination [Peter2001]. IL-12 can
p17 (77–85)	<ul> <li>CD8+ T cells were fou viral load was also four</li> <li>All three patients were</li> <li>ELISPOT was used to subjects showed a dom</li> <li>The subject with A*02</li> <li>Weak responses were compared to the subject with A*02</li> <li>No acute response was</li> </ul>	nd prior to seroconversiond  B*2705, with HLA alletest a panel of CTL epit inant response to the B'01 had a moderatly strophserved to A*301-RLR detected to the following	ion, and there was a close temporal receles: A1, A30/31, B*2705, B35; A1, copes that had been defined earlier and *2705 epitope KRWIILGGLNK ong response to SLYNTVATL	elationship between the number of A*0301, B7, B2705; and A*0201, d were appropriate for the HLA hat, and B7-TPGPGVRYPL in the sul*301-KIRLRPGGK, A*301-AIFQ	A*0301, B2705, B39 plotypes of the study subjects – 3/3 bject who was HLA A1, A*0301, B7, QSSMTK, A*301-TVYYGVPVWK,
p17 (77–85)	p17 (77–85) • Epitope name: SL9	SLYNTVATL	HIV-1 infection	human (B62)	Goulder1997a

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
	GLNKIVRMY  • As long as a strong CTI	L response to SLYNTV	VATL was evident, the epitope variants SL tide became undetectable, the CTL responted dominant form	LFNTVATL or SLYNTIATL do	ominated the viral population –
p17 (77–85)	Gag (77–85)  • This epitope served as a vaccine	SLYNTVATL a positive control in a s	study comparing peptide binding affinity t	human (HLA-A201) to HLA-A201 to CTL response	Sandberg2000 es upon vaccination with a nef DNA
p17 (82–91)	<ul><li>HLA-A11 is very command CTL responses wer</li><li>This epitope was weakl</li></ul>	non in this population, re found in 8/8 HIV+ c y reactive in the HEPS	HIV-1 infection, HIV-1 exposeronegative  ly seronegative (HEPS) female sex worker and was enriched among the HEPS sex wontrols, and 0/9 HIV- women that were not study subject 265 who was HLA A2/A1 udy subject 053 who carried HLA-A11	rs in Chiang Mai, northern The orkers – weak CTL responses ot exposed	
p17 (82–91)	Thailand, of whom mor 77 possible HLA-A11 e epitopes for CTL respon This epitope was predic that had been previously 3/8 tested FSWs recogn	re than half were HLA epitopes were first defi nses from 8 HLA-A11 eted by the EpiMatrix i y defined nized this epitope	HIV-1 infection  et al.) epitopes were identified that stimula-A11 positive ned using EpiMatrix, these were screened positive FSWs, six were novel, six were method to be likely to bind to A11, and it  epes, and exact matches were uncommon	I for binding to A11 finding an previously identified	d 26 bound, and 12 of these were
p17 (84–91)	cross-reactive and recog specific manner. Two of • TLYCVHQR was found is common in clade B) B clade infected Japane	gnized by clade E infecther HLA A*1101 claded to elicit clade-specificand clade E (tlWcvhqruse subjects, and tlWcvant peptides to HLA A	HIV-1 infection *1101 epitopes were generated for clade coted individuals. The clade E and B analogue B defined epitopes were found not to have coresponses in clade B (TLYCVHQR is most common). TLYCVHQR was not recognized by CTL from inferential to the comparable, but CTL that recognized in the comparable in the comp	gs to three more HLA A*1101 ave stimulated a response in cl nost common, and is also common recognized by any CTL, tlycvected Thai subjects, so this see	l epitopes was recognized in a clade lade E infected individuals. mon in clade A – the variant tlycvhqK rhqK was recognized by CTL from 1/5 ms to be a B clade exclusive epitope.
p17 (84–91)	p17 (83–91) • Two overlapping epitop (SLYNTVATL)	TLYCVHQR es were recognized in	HIV-1 infection a long-term survivor, restricted by two di	human (A11) fferent HLA molecules, HLA-	Harrer1998 A11(TLYCVHQR) and -A2

HXB2 Location	<b>Author's Location</b>	Sequence	Immunogen	Species (HLA)	References
	reduced recognition of	f the A11 epitope, indicative of esulted in a loss of the ability of	immune escape		L-recognition of the A2 epitope, but ive, and a R91Q substitution show a
p17 (84–92)	p17 (84–92) • C. Brander notes that	TLYCVHQRI this is an A*1101 epitope	HIV-1 infection	human (A*1101)	Brander2001
p17 (84–92)	p17 (84–92) • Epitope defined in the	TLYCVHQRI context of the Pediatric AIDS	HIV-1 infection Foundation ARIEL Project, a moth	human (A11) er-infant HIV transmission s	Brander1995b tudy
p17 (84–92)	p17 (84–92) • A study of p17 variati pressure from CTLs	TLYCVHQRI on considering known p17 epit	HIV-1 infection opes and individuals with known H	human (A11) LA types revealed that p17 e	Birk1998b evolution is influenced by immune
p17 (84–92)	p17 (84–92) • One of the 51 HIV-1 e HLA alleles	TLYCVHQRI pitopes selected by Ferrari et a	HIV-1 infection  l. as good candidate CTL epitopes f	human (A11) for vaccines by virtue of being	Ferrari2000 ag conserved and presented by commo
p17 (84–92)	<ul> <li>individuals treated dur</li> <li>The breadth and speci individuals with prima (Group 3), using 259</li> <li>Previously described a</li> </ul>	ring chronic infection ficity of the response was deter ary infection but post-seroconvoverlapping peptides spanning and newly defined optimal epite	mined using ELISPOT by studying	19 individuals with pre-sero dividuals who responded to I	HAART given during chronic infection
p17 (84–92)	p17 (84–92)  • ELISPOT was used to HIV-1-infected female		HIV-1 infection, HIV-1 expos seronegative el of 54 predefined HIV-1 epitopes i		Kaul2001a ently seronegative (HEPS) and 87
p17 (86–101)	an HLA-B60 individu	al	HIV-1 infection entifying new HLA-B60 epitopes, at the HLA presenting molecule and of		Altfeld2000b resented by another HLA molecule in ermined
p17 (86–101)	an HLA-B60 individu	al	HIV-1 infection entifying new HLA-B60 epitopes, at the HLA presenting molecule and of		Altfeld2000b resented by another HLA molecule in ermined
p17 (87–105)	p17 (91–105 SF2) • CTL expanded ex vivo	CRIDVKDTKEALEKIE  o were later infused into HIV-1	HIV-1 infection infected patients	human	Lieberman1997b

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
p17 (88–115)	p17 (88–115 ARV)	VHQRIEIKDTKEALDKIEE- EQNKSKKKA	HIV-1 infection	human (A2)	Achour1990
	• B cell epitope HGP-30	also serves as a CTL epitope			
p17 (88–115)	p17 (88–115 ARV)	VHQRIEIKDTKEALDKIEE- EQNKSKKKA	Vaccine	murine BALB/c (H-2 <sup>d</sup> )	Hamajima1997
	<ul><li>B cell epitope HGP-30</li><li>Vaccine combined HG</li></ul>	peptide <i>HIV component:</i> V3, HP also serves as a CTL epitope P-30, V3 loop peptide variants, and included with the vaccination e	d CD4 binding site peptide		
p17 (91–101)	<ul> <li>the most recognized pe</li> <li>Three peptides GSEEL contained the dominan</li> <li>Five peptides RLRPGO</li> </ul>	ptides in the study RSLYNTVATL (p17 residues 71-6 t Gag-specific epitope in 31 out of GKKHYMIKHLVW (p17 20-36), EQA (p24 161-177), and SILDIK	85), SALSEGATPQDLNTMLNT 44 B-clade infected individuals fi ELRSLYNTVATLYCV (p17Gag	VG (p24 41-60), and WEKIR rom Boston who showed Gag 74-88), SALSEGATPQDLN	-CTL responses TMLNTVG (p24 41-60),
p17 (91–105)	<ul><li>Twelve subjects had C</li><li>One of these 12 had C</li></ul>	RIDVKDTKEALEKIE ad CTL specific for more than 1 HI TL that could recognize vaccinia-e TL response to this peptide t was HLA-A3, A24, B8, B55		human	Lieberman1997a
p17 (92–101)	p17 (92–101) • C. Brander notes this is	IEIKDTKEAL s a B*4001 epitope	HIV-1 infection	human (B*4001)	Brander2001
p17 (92–101)		IEIKDTKEAL epitopes were used to show that the MIP-1 $\alpha$ and RANTES were used			
p17 (92–101)	<ul> <li>individuals treated duri</li> <li>The breadth and specified individuals with primare (Group 3), using 259 o</li> <li>Previously described and an arrangement of the primare of the previously described and previous</li></ul>	ing chronic infection icity of the response was determined	ed using ELISPOT by studying 19 on therapy (Group 2), and 10 indiv. p24, RT, gp41, gp120 and Nef were tested for CTL response	9 individuals with pre-serocor riduals who responded to HAA	ART given during chronic infection

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
p17 (92–101)	than NL-43 with an inta	act Nef. The effect was s	HIV-1 infection and this study demonstrates directly tha hown to be specific for class I presentati clone 161JD27, specific for the class I B	ion of epitopes, and unlike Nef,	deleting Vpr did not alter CTL
p17 (92–101)			HIV-1 infection ly identifying new HLA-B60 epitopes very common in Asian populations	human (B60(B*4001)	Altfeld2000b
p17 (92–101)			HIV-1 infection o five B61-restricted epitopes tested another subject, and the B60-restricted	human (B60/B61) responses together contributed	Day2001 over one-third of the total CTL
p17 (93–101)	<ul> <li>most recognized peptid</li> <li>Three peptides GSEEL contained the dominant</li> <li>Five peptides RLRPGO</li> </ul>	es in the study RSLYNTVATL (p17 res Gag-specific epitope in GKKHYMIKHLVW (p17 EQA (p24 161-177), and	HIV-1 infection is epitope in a HIV+ Caucasian from Boundaries idues 71-85), SALSEGATPQDLNTML1 31 out of 44 B-clade infected individual 7 20-36), ELRSLYNTVATLYCV (p17Gaustral) SILDIKQGKEPFRDY (p24 149-164) of	NTVG (p24 41-60), and WEKI s from Boston who showed Ga ag 74-88), SALSEGATPQDLN	RLRPGGKKKYKLK(p17 16-30) g-CTL responses ITMLNTVG (p24 41-60),
p17 (93–101)	p17 (93–101) • Examined in the contex	EIKDTKEAL at of motifs important for	Peptide-HLA interaction HLA-B8 binding, predicted epitope base	human (B8) sed on Achour et al.	DiBrino1994b
p17 (93–101)	p17 (93–101) • A study of p17 variatio pressure from CTLs	EIKDTKEAL n considering known p1	HIV-1 infection 7 epitopes and individuals with known H	human (B8) ILA types revealed that p17 evo	Birk1998b olution is influenced by immune
p17 (93–101)	p17 (93–101 LAI) • Pers. Comm. from A. 7	EIKDTKEAL  Frocha and S. Kalams to	C. Brander and B. Walker	human (B8, B60)	Brander1997
p17 (121–132)	p17 (121–132 HXB2R) • Clustering of Gag p24		HIV-1 infection I in 29 HIV-infected people	human (A33)	Buseyne1993b
p17 (121–132)	<ul> <li>Epitopes recognized in</li> </ul>	cytotoxic activity against five children were mapp	HIV-1 infection to 39% st at least one HIV protein was detected it ed using synthetic peptides and secondar sponse to two epitopes in Gag		Buseyne1993a
p17 (124–132)	p17 (124–132 LAI)  • Noted by Brander to be	NSSKVSQNY B*3501 epitope	HIV-1 or HIV-2 infection	human (B*3501)	Brander2001

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
p17 (124–132)	<ul><li>hydroxyl group of the l</li><li>Novel B53 epitopes (D B pocket of HLA-B35</li></ul>	P2 serine occupying a p TINEEAAEW and QA and B53 – while S, T,	HIV-1 infection HLA-B*3501 shows that a serine can fit in position almost identical to the P2 proline tarquever the provided in this study that P could all fit into the B pocket and for the high affinity of QATQEVKNM for B	that was previously considered that showed that A and T can a rm a hydrogen bond, A woul	ed the anchor motif also serve as P2 anchor residues for the
p17 (124–132)	p17 (124–132 LAI) • Review of HIV CTL ep	NSSKVSQNY pitopes	HIV-1 infection	human (B35)	McMichael1994
p17 (124–132)	<ul> <li>CD8+ T cells were fou viral load was also fou</li> <li>All three patients were</li> <li>ELISPOT was used to subjects showed a dom</li> <li>The subject with A*02</li> <li>Weak responses were of B*2705</li> <li>No acute response was</li> </ul>	nd prior to seroconversind B*2705, with HLA all test a panel of CTL epi inant response to the B 01 had a moderatly str observed to A*301-RLI detected to the following	HIV-1 infection secific CTL responses were studied during a scion, and there was a close temporal relation teles: A1, A30/31, B*2705, B35; A1, A*03 teles: A1, A30/31, B*2705, B35-VELWELT AND	anship between the number of 301, B7, B2705; and A*0201 are appropriate for the HLA has br-TPGPGVRYPL in the standard st	f circulating HIV-specific T cells and A*0301, B2705, B39 aplotypes of the study subjects – 3/3 abject who was HLA A1, A*0301, B7, QSSMTK, A*301-TVYYGVPVWK,
p17 (124–132)	p17 (124–132) • A study of p17 variation pressure from CTLs	NSSKVSQNY on considering known p	HIV-1 infection o17 epitopes and individuals with known H	human (B35) LA types revealed that p17 e	Birk1998b evolution is influenced by immune
p17 (124–132)	p17 (124–132 LAI) • Established by titration	NSSKVSQNY	HIV-1 or HIV-2 infection	human (B35)	Rowland-Jones1995b
p17 (124–132)	stimulate a primary res	ponse, only secondary f the B35 presented tes	in vitro stimulation estimulation of CTLp using optimized pep – peptide-specific CTLp counts could be of st peptides used in control experiments sho	obtained via staining with per	otide-Class I tetramers
p17 (124–132)	<ul><li>deletion in CCR5</li><li>In Gambia there is exp</li></ul>	osure to both HIV-1 an	posed African female sex workers in Gamb d HIV-2, CTL responses to B35 epitopes in l: PPSGKGGNY, but the CTLs are cross-re	n exposed, uninfected wome	n are cross-reactive

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
p17 (124–132)			HIV-1 infection ng in 41 patients with combination thera gen-specific cells capable of differentiat		
p17 (124–132)	<ul> <li>individuals treated duri</li> <li>The breadth and specification individuals with primare (Group 3), using 259 or</li> <li>Previously described and</li> </ul>	ng chronic infection leity of the response was ry infection but post-ser- verlapping peptides span and newly defined optima	HIV-1 infection ed in a narrower CTL response, stronger s determined using ELISPOT by studyin occonversion therapy (Group 2), and 10 in nning p17, p24, RT, gp41, gp120 and Ne all epitopes were tested for CTL response CTL response to this epitope broken dow	g 19 individuals with pre-sero ndividuals who responded to H	conversion therapy (Group 1), 11 IAART given during chronic infection
p17 (124–132)	<ul><li> Epitope name: Gag-NY</li><li> Among HIV+ individu</li></ul>		HIV-1 infection 35, 1/21 (5%) recognized this epitope	human (B35)	Sabbaj2002b

## II-B-2 p17-p24 CTL Epitopes

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References		
p17-p24 (127–3)	p17-p24 (127–135 subtype D)	QVSQNYPIV		human (A*6802)	Dong1998a		
	<ul> <li>Epitope starts in p17 and</li> </ul>	ends in p24					
	<ul> <li>Predicted on binding mo</li> </ul>	tif, no truncations analyzed					
p17-p24 (131-6)	p17-p24 (132-140 SF2)	NYPIVQNL	HIV-1 infection	human (A*2402)	Ikeda-Moore1997		
	• The epitope starts in p17	and ends in p24					
	• Defined using reverse immunogenetics – 59 HLA-A*2402 binding peptides were predicted by searching for A*2402 anchors in HIV proteins (Tyr at 2, and						
	Phe, Leu or Ile at the C term) – 53 of the 59 peptides bound A*2402						
	• This peptide induced CTL in 1/4 HIV-1+ people tested						
	• NYPIVQNL bound to A*2402 with medium strength, and the epitope can be processed in a vaccinia construct and presented – no CTL clone was obtained						

## II-B-3 p24 CTL Epitopes

<b>HXB2</b> Location	<b>Author's Location</b>	Sequence	Immunogen	Species (HLA)	References
p24 (8–17)	<ul> <li>95 optimally-defined pe</li> </ul>	ptides from this database we	HIV-1 infection at reacted to SLYNTVATL, calli re used to screen for INFγ resp B57 and responded to four B57		Betts2000 nunodominant
p24 (8–20)	p24 (140–152 IIIB) • Fine specificity of huma	GQMVHQAISPRTL on Cw3 restricted Gag CTL e	HIV-1 infection epitope	human (Cw3)	Littaua1991
p24 (8–27)	p24 (140–159) • CTL specific for this ep	GQMVHQAISPRTLNAWV itope were found in the perip	KVV HIV-1 infection wheral blood but not in the cervi	human (B14) cal mucosa of one donor	Musey1997
p24 (9–18)	for the A3 supertype) w • Progressors had memory • A positive correlation by observed, which may co	hile the effector cells of long y resting CD8+ T-cells that r etween effector CD8+ T-cells ontribute to the inability of L'	term nonprogressors recognized ecognized far fewer epitopes the s and plasma viremia and a neg	ed far fewer epitopes an LTNPs ative correlation between CD8+ ef	Propato2001 es tested, (18 for the A2 supertype, 16 effector T-cells and CD4+ T-cells was
p24 (10–18)	for the A3 supertype) w • Progressors had memory • A positive correlation by observed, which may co	hile the effector cells of long y resting CD8+ T-cells that r etween effector CD8+ T-cells ontribute to the inability of L'	term nonprogressors recognized ecognized far fewer epitopes the s and plasma viremia and a neg	ed far fewer epitopes an LTNPs ative correlation between CD8+ ef	Propato2001 st tested, (18 for the A2 supertype, 16 fector T-cells and CD4+ T-cells was
p24 (11–24)	<ul> <li>the most recognized pep</li> <li>Three peptides GSEELI contained the dominant</li> <li>Five peptides RLRPGG</li> </ul>	otides in the study RSLYNTVATL (p17 residues Gag-specific epitope in 31 o KKHYMIKHLVW (p17 20- EQA (p24 161-177), and SIL	s 71-85), SALSEGATPQDLNT ut of 44 B-clade infected indivi 36), ELRSLYNTVATLYCV (p	MLNTVG (p24 41-60), and WEK duals from Boston who showed G 17Gag 74-88), SALSEGATPQDL	
p24 (11–32)	p24 (143–164 BH10)  • Gag CTL response stud	VHQAISPRTLNAWVKVV KAF ied in three individuals	EE- HIV-1 infection	human (Bw57)	Johnson1991
p24 (12–20)	Gag (146–154)	HQAISPRTL	HIV-1 infection -term survival – among them ar		2) Balla-Jhagjhoorsingh1999b

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
	<ul> <li>CTL responses were streepitopes that are recogn</li> </ul>	udied in two HIV-1 infections in the color which presents this Pa	reported to be infected with HIV-1, only one heted chimpanzees that have strong CTL respondentext of HLA-B*27 and HLA-B*57 atr-B*02 epitope is HLA-B*5701 but the amin	nses, and they were four	
p24 (13–20)		•	HIV-1 infection, HIV-1 exposed seronegative a panel of 54 predefined HIV-1 epitopes in 91	human (Cw3) HIV-1-exposed, persist	Kaul2001a ently seronegative (HEPS) and 87
p24 (13–23)	<ul> <li>95 optimally-defined per</li> </ul>	QAISPRTLNAW IIV+ individuals had CT eptides from this databas	HIV-1 infection L that reacted to SLYNTVATL, calling into quese were used to screen for INFγ responses to α A1, B57 and responded to QAISPRTLNAW I	other epitopes	
p24 (13–23)	p24 (145–155 LAI)  • C. Brander notes that the	QAISPRTLNAW nis is an A*2501 epitope	,	human (A*2501)	Brander2001
p24 (13–23)	<ul> <li>individuals treated duri</li> <li>The breadth and specific individuals with primar (Group 3), using 259 or</li> <li>Previously described an</li> </ul>	ng chronic infection city of the response was by infection but post-sero verlapping peptides spar and newly defined optima	HIV-1 infection and in a narrower CTL response, stronger T help a determined using ELISPOT by studying 19 in a	ndividuals with pre-sero uals who responded to I	econversion therapy (Group 1), 11 HAART given during chronic infection
p24 (13–23)	p24 (145–155 LAI)	QAISPRTLNAW		human (A5)	Kurane1998
p24 (15–23)	<ul><li>sex workers eventually</li><li>The epidemiological fa working for a period or</li></ul>	seroconverted, and for sector associated with sero retire sistently recognized by 1	HIV-1 infection, HIV-1 exposed seronegative posed, persistently seronegative individuals, Hix of these HIV CTL reactive epitopes had beconversion was stopping sex work and HIV-syd22 HEPS sex worker controls (ML1250), and	en defined while serone pecific CTL activity dec	gative clines when HEPS sex workers stop
p24 (15–23)	p24 • Neisseria gonorrhea cer T-cells, detected by inti • Ghonorrhea caused the	LSPRTLNAW rvititis in 9 HIV+ Kenya acellular cytokine produ weaker HIV-1 specific (	HIV-1 infection in sex workers caused a functional deficiency in a sex workers caused a functional deficiency in a sex workers caused a function and tetramer assays, while not affecting CTL responses in 4 HIV-1 exposed persistently CTL in 2 HEPS subjects were shown to have	the total number of epi y seronegative (HEPS) v	tope-specific CTLs. women to become undetectable by

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
p24 (15–23)	p24 (147–155 IIIB) • C. Brander notes this is	ISPRTLNAW a B*5701 epitope	HIV-1 infection	human (B*5701)	Brander2001
p24 (15–23)		ane response that was hig	HIV-1 infection y in HIV-1 infected non-progressors, hly focused on four p24 epitopes that		
p24 (15–23)	threshold of infection w KAFSPEVIPMF, TSTI • CTL responses are broa	vithout therapy, and their LQEQIGW, and QASQEV ader in B*5701+ individu	HIV-1 infection cluding 10 LTNP with an over-expresimmune response tends to be focused VKNW.  Als with progressive viremia than tho se was not as strong individuals that of the second variable.	on peptides that contain B*570 se that control viremia.	
p24 (15–23)	Gag (147–155 LAI)  • B57 has been associate	ISPRTLNAW	HIV-1 infection	human (B*5701 B*5801)	Klein1998
			*5701 LTS were to RT and Gag		
p24 (15–23)	<ul> <li>95 optimally-defined per</li> </ul>	eptides from this database	HIV-1 infection  that reacted to SLYNTVATL, calling were used to screen for INFγ respon A1, B57 and responded to four B57 e	ises to other epitopes	
p24 (15–23)	• Three CTL responses, t	to epitopes TSTLQEQIG	HIV-1 infection esponse in patient PI004 during acute W, ISPRTLNAW, and KAFSPEVIPM were detectable at 5 months post-infe	IF, were evident early after infec	Goulder2001a esponse ction; CTL responses to SLYNTVATL
p24 (15–23)	CD4 proliferative responsible HAART had no HIV spundetectable	onses and were able to ma pecific CD4 proliferative i	HIV-1 infection  ction (three with sustained therapy, twintain a CTL response even with und responses and lost their CTL response ope but none were HLA B57+	letectable viral load – three patie	
p24 (15–23)	p24 (15–23) • One of the 51 HIV-1 ep HLA alleles	ISPRTLNAW itopes selected by Ferrari	HIV-1 infection et al. as good candidate CTL epitopo	human (B57) es for vaccines by virtue of being	Ferrari2000 g conserved and presented by commo
p24 (15–23)	p24 (147–155 SF2) • Therapy provided during individuals treated during the state of	_	HIV-1 infection I in a narrower CTL response, stronge	human (B57) er T help response, and a less di	Altfeld2001b werse viral population than was seen i

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
	individuals with prima (Group 3), using 259 co. • Previously described a	ry infection but post-se werlapping peptides spa nd newly defined optim	as determined using ELISPOT by studying roconversion therapy (Group 2), and 10 in anning p17, p24, RT, gp41, gp120 and Nefnal epitopes were tested for CTL response CTL response to this epitope broken down	dividuals who responded to F	IAART given during chronic infection
p24 (15–23)		als who carried HLA B	HIV-1 infection 357, 2/5 (40%) recognized this epitope 358, 0/4 (0%) recognized this epitope	human (B57)	Sabbaj2002b
p24 (15–23)	period including therap	y with standard treatm	HIV-1 infection 000, Oxenius2001a] in an IFNgamma Elispent interruptions (STI). bitopes, but there was no correlation between	•	-
p24 (15–23)			HIV-1 infection epitope, and in two it was the dominant reng motif, yet not cross-restricted except at		) Goulder1996b
p24 (15–23)	<ul><li>CD8+ T cell responses</li><li>Low risk individuals d</li><li>CD8+ T cell epitopes:</li></ul>	tended to be to the san id not have such CD8+	iduals), SLYNVATL (4 individuals), LSPR	an cervical CD8+ T cell response	onses
p24 (15–23)	<ul> <li>HIV-1-infected female</li> <li>Responses in HEPS we reduced risk of infection women</li> <li>43/91 HEPS women has</li> <li>Among HLA-B57/B58</li> </ul>	study CTL responses to Nairobi sex workers omen tended to be lowe on, and there was a shift ad CD8+ responses and 8 women, 4/6 HEPS and	HIV-1 infection, HIV-1 exposeronegative  A/B clades of a panel of 54 predefined HIV-1 epitopes or, and focused on different epitopes with Fit in the response in the HEPS women upor detection of HIV-1-specific CTL in HEPS detection of HIV-1 infected women recognized to this epitope in 2 of the 4/6 HEPS cases	in 91 HIV-1-exposed, persisted HLA presenting molecules that a late seroconversion to epitop S women increased with the distribution to be supported by the sepitope.	t have previously been associated with bees recognized by the HIV-1 infected uration of viral exposure
p24 (16–24)	p24 • 3/4 animals displayed	SPRTLNAWV HIV-1 Gag-specific CT o chimpanzees were abl	HIV-1 infection	chimpanzee	Santra1999

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References				
	• No chimpanzee CTL were detected to the following human HIV-1 specific Gag epitopes, although they were embedded within 20mer peptides that contained a reactive epitope: ISPRTLNAW, HLA-B57; KRWIILGLNK, HLA-B27; and DRFYKTLRA, HLA-B14								
p24 (16–24)	p24 (148–156)  C. Brander notes this is Optimal peptide mappe	1 1	mm. from D. Lewinsohn to C. Brande	human (B*0702)	Brander2001				
p24 (16–24)		als who carried HLA B	HIV-1 infection 07, 1/9 (11%) recognized this epitope 81, 1/6 (17%) recognized this epitope		Sabbaj2002b				
p24 (16–24)	p24 (148–156) • Optimal peptide mappe	SPRTLNAWV ed by titration, Pers. Co	mm. from D. Lewinsohn to C. Brande	human (B7) r and B. Walker	Brander1997				
p24 (16–24)	<ul> <li>Adoptively transferred adjacent to cells expres</li> <li>The CTL clones expres viral replication, sugge</li> </ul>	gene-marked HIV-spec sing HIV tat-fusion tran- sed CCR5 and localize sting a possible homing	nscripts, indicative of viral replication d among HIV-1 infected cells expressi	ng MIP-1alpha and MIP-1beta, (	Brodie2000 arafollicular regions of the lymph node CC-chemokines produced at sites of				
p24 (16–24)	<ul> <li>HIV-1-infected female</li> <li>Responses in HEPS we reduced risk of infectio women</li> <li>43/91 HEPS women ha</li> <li>Subject ML 1203 starte</li> </ul>	Nairobi sex workers omen tended to be lower n, and there was a shift d CD8+ responses and ed with CTL responses	HIV-1 infection, HIV-1 exseronegative of a panel of 54 predefined HIV-1 epitoper, and focused on different epitopes within the response in the HEPS women undetection of HIV-1-specific CTL in HI to A*6802 DTVLEDINL and to B7 FIYFILKL which became dominant, B7	pes in 91 HIV-1-exposed, persistenth HLA presenting molecules that apon late seroconversion to epitoperson to the control of t	at have previously been associated with pes recognized by the HIV-1 infected duration of viral exposure ersion, and upon seroconversion				
p24 (16–24)	studied in eight HIV-1- • 2 to 17 epitopes were repitopes were targeted • Subjects with chronic F • An acute seroconvertor • The other acute serocon	infected subjects, two vecognized in a given in by at least one person HIV-1 infection recognihomozygous for the Brayertor failed to recogni	HIV-1 infection rpitopes restricted by HLA class I A ar with acute infection, five with chronic, dividual, A2-restricted CTL response t zed between 2-8 out of 11 B7-restricte allele recognized five B7-restricted e ize any of the 11 B7-restricted epitope ariable and there was no clearly domin	and one long-term non-progress tended to be narrow and never do ed epitopes epitopes s tested	or (LTNP)				

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References				
p24 (16–24)	p24 (16–24) • Epitope name: B7-SV9		HIV-1 infection	human (B7)	Yu2002a				
	<ul> <li>CTL responses in 18 acutely HIV-infected HLA-A3 (n=7) or -B7 (n=4) or both -A3 and B7 (n=7) positive individuals were studied.</li> <li>One individual, AC-06, was homozygous at all three class I alleles (A3, B7, Cw7), was treated during acute infection and had supervised treatment interruptions (STI). He had only two detectable CTL responses during acute infection, but after STI this broadened to 27 distinct epitopes including 15 restricted by HLA-A3, 11 by HLA-B7, and 1 by HLA-Cw7.</li> <li>1/11 HLA-B7 positive individuals had detectable B7-restricted responses to this epitope during acute infection – 10/15 of HLA-B7 epitopes tested were targeted by at least one person during acute infection. 1/4 individuals had detectable responses to this epitope after STI.</li> </ul>								
p24 (16–24)	p24 (subtype B)  11/16 heavily HIV exp CD8+ T cell responses Low risk individuals d CD8+ T cell epitopes:	SPRTLNAWV osed but persistently ser tended to be to the same id not have such CD8+ c	HIV-1 exposed seronegative onegative sex-workers in Nairobi had HIV-spe e epitopes but at generally lower levels than coells luals), SLYNVATL (4 individuals), LSPRTLN	human (B7, B*8101) ecific CD8 gamma-IFN re- ervical CD8+ T cell respon	Kaul2000 sponses in the cervix – systemic ases				
p24 (16–24)	<ul><li>Seroprevalence in this</li><li>Most isolated HIV stra</li></ul>	cohort is 90-95% and the ins are clade A in Nairol y observed using A or D	HIV-1 exposed seronegative negative prostitutes from Nairobi – these CTL eir HIV-1 exposure is among the highest in the pi, although clades C and D are also found – Ho clade versions of epitopes lade viruses	e world	Rowland-Jones1998b cross-reactive, however stronger				
p24 (19–27)	<ul> <li>Increases in gamma in</li> </ul>	terferon producing cells	HIV-1 infection and highly specific, and found to work well e were observed in response to anti-retroviral the dominant epitope was against HLA B*27 Gag	nerapy using single cell IFI	N-gamma-production ELISPOT				
p24 (19–27)	responses in patients w	rith advanced HIV diseas	HIV-1 infection rapy (IDV, 3TC and ZDV) sometimes showed se, but there is a stable population of tetramer slow the level of detection						
p24 (19–27)	p24 (151–159) • Study of sequence mot	TLNAWVKVV ifs preferred for peptide	HIV-1 infection binding to class I HLA-A2	human (A2)	Parker1992, Parker1994				
p24 (19–27)	p24 (19–27) • One of the 51 HIV-1 epHLA alleles	TLNAWVKVV pitopes selected by Ferra	HIV-1 infection ri et al. as good candidate CTL epitopes for vi	human (A2) accines by virtue of being	Ferrari2000 conserved and presented by common				
p24 (19–27)	p24 (150–159)	TLNAWVKVI	HIV-1 infection, HIV-1 exposed seronegative	human (A2)	Kaul2001a				
	• Variants TLNAWVKV(I/V) are A/B clade specific								

HXB2 Location	<b>Author's Location</b>	Sequence	Immunogen	Species (HLA)	References			
	ELISPOT was used to s     HIV-1-infected female !		el of 54 predefined HIV-1 epitope	es in 91 HIV-1-exposed, persister	tly seronegative (HEPS) and 87			
p24 (19–27)	<ul> <li>Seroprevalence in this c</li> <li>Most isolated HIV strain responses are frequently</li> </ul>	ohort is 90-95% and their HI	e versions of epitopes	se CTL may confer protection	Rowland-Jones1998b cross-reactive, however stronger			
p24 (21–40)			1 HIV-1 protein	human	Lieberman1997a			
p24 (21–40)	<ul> <li>A VLP is a non-infection V3+CD4 linear domains neutralizing response of intervenous challenge w</li> </ul>	us virus-like particle self-ass s Gag and Env specific CTL courred only with whole gp12 oith SHIV chimeric challenge	conent: gag, gp120, V3, CD4BS sembled from HIV Pr55 gag – mawere stimulated in each case, and 20, not V3+CD4 – despite the CT	Rhesus macaque acaques were immunized with VL d Ab response to gag and gp120 v TL and Ab response, immunized r	vas elicited, but the gp120			
p24 (21–40)	• The transferred CTLs m	igrated to the lymph nodes a	anding autologous HIV-1 Gag-sp and transiently reduced circulating	human (B57) secific CTL in vitro, and adoptivel g productively infected CD4+ T c				
p24 (21–40)	<ul> <li>Adoptively transferred gadjacent to cells express</li> <li>The CTL clones express viral replication, sugges</li> </ul>	appropriate target sites and mediate anti-viral effects  p24 (153–172) NAWVKVVEEKAFSPEVIPMF HIV-1 infection human (B57) Brodie2000  • Study tracks and quantifies <i>in vivo</i> migration of neo-marked CD8 HIV-specific CTL  • Adoptively transferred gene-marked HIV-specific CTL homed to specific lymph node sites, colocalizing within the parafollicular regions of the lymph adjacent to cells expressing HIV tat-fusion transcripts, indicative of viral replication  • The CTL clones expressed CCR5 and localized among HIV-1 infected cells expressing MIP-1alpha and MIP-1beta, CC-chemokines produced at sites viral replication, suggesting a possible homing mechanism  • This study provides a methodology for tracking and studying antigen specific CTL <i>in vivo</i>						
p24 (21–42)	p24 (153–174 BH10)  • Gag CTL response stud	NAWVKVVEEKAFSPEVI FSA ied in three individuals	PM- HIV-1 infection	human (Bw57)	Johnson1991			
p24 (28–36)	p24 • 5/233, (4 HIV-1 positive	EEKAFSPEV e, 1 HEPS) (2.1%) Kenyan fe	HIV-1 infection emale sex workers carried the nov e identical to HLA B*4001, B*44		Bird2002 eferred E, an acidic residue, at the P2			

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References				
	<ul> <li>The amino acid residues forming the F pocket of allele B*4415 were not correlated with other known HLA molecules, but analogy suggests a binding preference for small, neutral amino acids.</li> <li>Based on the binding motif x[DE]xxxxxx[VILA], 19 potential B*4415 epitopes were identified, and 1/19 was reactive in an Elispot, EEKAFSPEV.</li> </ul>								
p24 (28–47)	p24 (160–179) • Cervical and peripheral	EEKAFSPEVIPMFSALSEGA blood derived CTL clones from a	HIV-1 infection an HIV-infected woman recognized t	human (B27) his epitope	Musey1997				
p24 (29–48)	<ul><li>each HIV protein.</li><li>Nef and p24 had the hig</li></ul>	hest percentage of reactive peption	HIV-1 infection  n 105 HIV-1 positive Botswanans; El  des, and p24 had the highest magnitu ptides from among over 350 tested sp	ide of HIV-1 responses.	Novitsky2002 om between 55 and 64 subjects for				
p24 (30–37)	p24 (162–170 LAI) • C. Brander notes this is	KAFSPEVI a B*5703 epitope	HIV-1 infection	human (B*5703)	Brander2001				
p24 (30–37)	<ul> <li>p24 (30–37) KAFSPEVI HIV-1 infection human (B57) Goulder2000c</li> <li>Two strong clonal CTL responses were generated in donor 026-BMC (HLA A3/-, B42/B57, Cw7/17) against different optimal versions of this epitope, one 8 amino acids long, one 11</li> <li>Improved stabilization of the B57-peptide complex was demonstrated by the 11 mer which fits the B57 binding motif, relative to the 8 mer, which does not</li> <li>B57 tolerates marked difference in optimal peptide length – and B57 is associated with non-progressive infection</li> </ul>								
p24 (30–37)	<ul><li> Epitope name: Gag-KI8</li><li> Among HIV+ individual</li></ul>		HIV-1 infection 0/5 (0%) recognized this epitope.	human (B57)	Sabbaj2002b				
p24 (30–40)	<ul> <li>sex workers eventually s</li> <li>The epidemiological fac working for a period or r</li> </ul>	eroconverted, and for six of thes tor associated with seroconversion	HIV-1 infection, HIV-1 exposed seronegative rsistently seronegative individuals, He HIV CTL reactive epitopes had been was stopping sex work and HIV-syontrols, ML1250	en defined while seronegat	ive				
p24 (30–40)	<ul> <li>CTLp (precursors) were were measured by ELIS</li> <li>CTL against B*57-KAF</li> </ul>	measured by stimulating in culti POT SPEVIPMF was a de novo responses initially increased in child	HIV-1 infection therapy (HAART) on HIV-1 plasma are and assaying using 51Cr release, onse observed in one of the children where with complete viral suppression,	against vaccina expressed when viral load increased a	IIIB Env, Gag, Pol, Nef, and CTLe as a result of stopping therapy				
p24 (30–40)		KAFSPEVIPMF ized by CTL from five slow prog asis of B*5801 binding motif, ye	HIV-1 infection gressors et not cross-restricted except at high o	human (B*5701)	Goulder1996b				

HXB2 Location	<b>Author's Location</b>	Sequence	Immunogen	Species (HLA)	References
	This epitope is highly co	onserved			
p24 (30–40)	p24 (162–172 LAI) • C. Brander notes this is	KAFSPEVIPMF a B*5701 epitope	HIV-1 infection	human (B*5701)	Brander2001
p24 (30–40)	tended to have an immu TSTLQEQIGW, and Qa • Attempts to make all for of CD8+ T cells staining KAFSPEVIPMF was hi	ne response that was high ASQEVKNW.  r HLA B*5701-epitope to g with this HLA B*57 gains gally correlated (r = 0.84)	HIV-1 infection y in HIV-1 infected non-progressors, hly focused on four p24 epitopes tha etramers were made, but only the HL ag tetramer and the fraction of CD69- (P = 0.005). The percent of CD8+ T e focus of the immune response on t	t were presented by B*5701, ISPI A B*5701-KAFSPEVIPMF tetra +IFN-+ cells responding to autolo cells that stain with the A*2 gag	RTLNAW, KAFSPEVIPMF, uner folded properly. The percentagogous B cells pulsed with
p24 (30–40)	threshold of infection w KAFSPEVIPMF, TSTL • CTL responses are broa	ithout therapy, and their QEQIGW, and QASQEV der in B*5701+ individu	HIV-1 infection cluding 10 LTNP with an over-expresimmune response tends to be focused VKNW.  Als with progressive viremia than the see was not as strong in individuals the	d on peptides that contain B*5701 ose that control viremia.	
p24 (30–40)	slow progression.  This epitope is located by strong reactions in B*57.  Broad heterogeneous cripatients, measured by II kGfNpevipmf (clades A kaLspevipmf KNFSPEV)	petween the structurally of individuals.  Find production Elispot as AC); kaLspevipmf (clack/IPMF A/G). Not all var	HIV-1 infection  From Nairobi Kenya or Oxford, UK vectors alpha-helix 1 and alpha-helix 1 and alpha-helix alpha-helix 2 and alpha-helix 3 and alpha-helix 3 and alpha-helix 4 and alpha-helix 4 and alpha-helix 4 and alpha-helix 5 and 5	elix 2 (H1-H2) region of the p24 c equence were observed in one B* the clade variants were: KAFSPEV elipmf (group O); kafspelipmf (A tients, for example kafsQevipmf w	apsid protein, and tends to elicit 5701 and 5 B*5703 HLA-restricted IPMF (clades A and B), /C); kafsQevipmf (A/C); and
p24 (30–40)	p24 (162–172 LAI) • C. Brander notes this is	KAFSPEVIPMF a B*5703 epitope	HIV-1 infection	human (B*5703)	Brander2001
p24 (30–40)	<ul><li>24 epitopes were descril</li><li>Serial peptide truncation</li><li>Subject 00RCH59 was a</li></ul>	oitope responses in HIV- bed – 8 were novel, 8 use as were used to define op African American, on HA	HIV-1 infection  I infected minority women living in the deal new restricting elements but were stimal epitopes for CTL cell lines iso AART, viral load 170, CD4 count 47', 6/6 (100%) recognized this epitope	previously defined epitopes, and lated from 12 individuals, assayed 7	

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
p24 (30–40)	<ul><li>8 amino acids long, one</li><li>Improved stabilization of</li></ul>	11 of the B57-peptide complex		which fits the B57 binding motif,	Goulder2000c t optimal versions of this epitope, one relative to the 8 mer, which does not
p24 (30–40)	<ul> <li>95 optimally-defined pe</li> </ul>	ptides from this database v	HIV-1 infection hat reacted to SLYNTVATL, callin were used to screen for INFγ respo , B57 and responded to four B57 of	nses to other epitopes	Betts2000 nunodominant
p24 (30–40)	<ul><li>the study</li><li>Three peptides GSEELI contained the dominant</li><li>Five peptides RLRPGG</li></ul>	RSLYNTVATL (p17 residu Gag-specific epitope in 31 KKHYMIKHLVW (p17 20 EQA (p24 161-177), and SI	tes 71-85), SALSEGATPQDLNTM out of 44 B-clade infected individ 0-36), ELRSLYNTVATLYCV (p1	MLNTVG (p24 41-60), and WEK uals from Boston who showed G7Gag 74-88), SALSEGATPQDL	
p24 (30–40)			HIV-1 infection  TSTLQEQIGW, ISPRTLNAW, ard FLKEKGGL were detectable at 2		Goulder2001a t early after infection; CTL responses
p24 (30–40)	CD4 proliferative respo HAART had no HIV sp undetectable	nses and were able to main ecific CD4 proliferative res	tain a CTL response even with und	detectable viral load – three patie	Oxenius2000  Ply infection) had strong HIV specific ents that had delayed initiation of given and their viral loads became
p24 (30–40)	<ul><li>with viral load in patien</li><li>Most patients have high</li></ul>	ts with high CD4, but in pales. Ievels of HIV-specific T-co	HIV-1 infection HLA-A2, B8 and B57 CTL in 54 patients with CD4 T-cells below 400 ell expansions, but many of these caproducing tetramer cells correlated	high tetramer frequencies were cells aren't functional	Kostense2001 positive cells were inversely correlated found despite high viral load
p24 (30–40)	<ul><li>individuals treated during</li><li>The breadth and specific individuals with primary</li></ul>	ng chronic infection city of the response was de y infection but post-serocor	termined using ELISPOT by study	ring 19 individuals with pre-seroo individuals who responded to H	Altfeld2001b verse viral population than was seen in conversion therapy (Group 1), 11 [AART given during chronic infection

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References					
		<ul> <li>Previously described and newly defined optimal epitopes were tested for CTL response</li> <li>Number of HLA-B57+ individuals that had a CTL response to this epitope broken down by group: 0/0 group 1, 0/0 group 2, and 2/2 group 3</li> </ul>								
p24 (30–40)	<ul> <li>HIV-specific CD8+ T CD27 expression on H</li> </ul>	cells expressed lower levels of IIV-specific cells, suggesting i	perforin than CMV-specific CD mpaired maturation	human (B57) in of circulating CD8+ T cells spends+ T cells from the same donor, produced IFN- $\gamma$ and MIP-1 $\beta$ with	and this was associated with persistent					
p24 (30–40)	Among HIV+ individu	KAFSPEVIPMF alls who carried HLA B57, 1/2	HIV-1 infection 5 (20%) recognized this epitope	human (B57)	Sabbaj2002b					
p24 (30–40)	period including thera	py with standard treatment int	erruptions (STI).		Oxenius2002b  1 infected patients were studied over a rebound rates, plateau viral loads, or					
p24 (30–40)	<ul> <li>HIV-1-infected female</li> <li>Responses in HEPS wreduced risk of infection women</li> <li>43/91 HEPS women h</li> <li>Among HLA-B57/B58</li> </ul>	Nairobi sex workers omen tended to be lower, and on, and there was a shift in the ad CD8+ responses and detect B women, 4/6 HEPS and 12/17	focused on different epitopes with response in the HEPS women untion of HIV-1-specific CTL in HIV-1 infected women recogni	pes in 91 HIV-1-exposed, persistenth HLA presenting molecules that apon late seroconversion to epitope EPS women increased with the d						
p24 (30–40)	<ul><li>T-cells, detected by int</li><li>Ghonorrhea caused the</li></ul>	racellular cytokine production weaker HIV-1 specific CTL	n and tetramer assays, while not a responses in 4 HIV-1 exposed pe	affecting the total number of epit ersistently seronegative (HEPS) v	Kaul2002 on in HIV-1 epitope-specific CD8+ ope-specific CTLs. vomen to become undetectable by egard to IFN-gamma production.					
p24 (30–40)	p24 (30–40) • One of the 51 HIV-1 e HLA alleles	KAFSPEVIPMF pitopes selected by Ferrari et a	HIV-1 infection al. as good candidate CTL epitop	human (B58) bes for vaccines by virtue of being	Ferrari2000 g conserved and presented by common					
p24 (31–50)	p24 (163–182) • HIV-specific CTL line	AFSPEVIPMFSALSEGA s developed by ex vivo stimul		human	Lieberman1995					
p24 (31–50)	p24 (163–182 SF2) • Of 25 patients, most h	AFSPEVIPMFSALSEGA ad CTL specific for more than	~	human	Lieberman1997a					

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
	<ul> <li>Twelve subjects had CTI</li> <li>One of these 12 had CTI</li> <li>The responding subject v</li> </ul>		xpressed LAI gag		
p24 (31–50)	p24 (163–182 SF2) • CTL expanded ex vivo w	AFSPEVIPMFSALSEGATPQ vere later infused into HIV-1 infe		human	Lieberman1997b
p24 (31–50)	an HLA-B60 individual		HIV-1 infection  ving new HLA-B60 epitopes, and wa  HLA presenting molecule and optimates.		•
p24 (35–43)	<ul><li>Relatively conserved epi</li><li>Suspected binding motif</li></ul>	EVIPMFSAL tope within Gag sequence AFSPF tope within B clade and in other for HLA-A26 includes T or V ars is an A*2601 epitope in the 199	clades achor at position 2, negative charge a	human (A*2601)  t position 1	Goulder1996a
p24 (35–43)	p24 (167–175 LAI) • C. Brander notes that this	EVIPMFSAL s is an A*2601		human (A*2601)	Brander2001
p24 (35–43)	<ul> <li>95 optimally-defined per</li> </ul>	otides from this database were use	HIV-1 infection  cted to SLYNTVATL, calling into qued to screen for INFγ responses to ote  VATL reacted with seven other epitors.	her epitopes	Betts2000 odominant
p24 (36–43)	p24 (168–175 LAI) • C. Brander notes this is a	VIPMFSAL a C*0102(Cw1) epitope		human (C*0102(Cw1))	Brander2001
p24 (36–43)	p24 (168–175 LAI)	VIPMFSAL		human (Cw*0102, Cw1)	Goulder1997b
p24 (36–43)	<ul> <li>95 optimally-defined per</li> </ul>	otides from this database were use	HIV-1 infection  cted to SLYNTVATL, calling into qued to screen for INFγ responses to ote  CVATL reacted with seven other epitors.	her epitopes	Betts2000 odominant
p24 (37–52)	<ul><li>Primary assays showed c</li><li>Epitopes recognized in fi</li></ul>	IPMFSALSEGATPQDL HIV ranges from 13% to 39% cytotoxic activity against at least of the children were mapped using sA+C+D2) had a CTL response to		human (B12) 6 of infected children	Buseyne1993a
p24 (37–52)	p24 (169–184 LAI) • Clustering of Gag p24 C	IPMFSALSEGATPQDL TL epitopes recognized in 29 HI	HIV-1 infection V-infected people	human (B12(44))	Buseyne1993b

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
p24 (37–52)	p24 (37–52) • One of the 51 HIV-1 ep HLA alleles	IPMFSALSEGATPDQL itopes selected by Ferrari et al. as	HIV-1 infection good candidate CTL epito	human (B44) opes for vaccines by virtue of being	Ferrari2000 g conserved and presented by common
p24 (39–58)	<ul><li>each HIV protein.</li><li>Nef and p24 had the high</li></ul>	ghest percentage of reactive peption	des, and p24 had the higher	human vanans; Elispot data was obtained is st magnitude of HIV-1 responses. tested spanning all HIV proteins.	Novitsky2002 from between 55 and 64 subjects for
p24 (41–60)	<ul><li>Twelve subjects had C</li><li>Three of these 12 had C</li></ul>	SALSEGATPQDLNTMLNTVG d CTL specific for more than 1 H L that could recognize vaccinia-out the response to this peptide s were HLA-A3, A32, B7, B14; a	IV-1 protein expressed LAI gag	human 4	Lieberman1997a
p24 (41–60)	p24 (173–192 SF2) • CTL expanded ex vivo	SALSEGATPQDLNTMLNTVG were later infused into HIV-1 info		human	Lieberman1997b
p24 (41–60)	an HLA-B60 individua	1	ying new HLA-B60 epitop	human es, and was one of the epitopes pro and optimal epitope were not dete	Altfeld2000b esented by another HLA molecule in rmined
p24 (41–60)	<ul><li>in East Africa</li><li>This CTL epitope is proand the epitope has yet</li></ul>	esented by B*8101 in one of the p to be mapped precisely	ections were studied, 2 with		Dorrell1999  type C – their infections all originated overed HLA allele found in Africans,  TPQDLNTMLNTVG
p24 (41–62)	p24 (173–194 BH10)  • Gag CTL response stud	SALSEGATPQDLNTMLNTV- GGH lied in three individuals	HIV-1 infection	human (B14)	Johnson1991
p24 (43–52)	cross-reactive CTL resp and D • Proteins corresponding was extensive inter-sub	conses in Ugandans to A, D, and I to the subtype of the infecting str type cross-reactivity with B clade	B clade recombinant vaccing ains tended to trigger high proteins and the co-circular in t	nia viruses expressing Gag, Env, Po er levels of CTL response measure ating subtype	Cao2000 s study addresses relative levels of ol, RT or Nef from HIV-1 clades A, B, ad by percent specific lysis, but there 11), is cross-reactive with subtypes A,

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
p24 (44–52)	p24 (176–184) • C. Brander notes this is	SEGATPQDL a B*4001, B60 epitope (Pers.	Comm. A. Trocha and S. Kalams)	human (B*4001)	Brander2001
p24 (44–52)		SEGATPQDL d by ELISPOT in a study iden % of the Caucasoid and very co	HIV-1 infection htifying new HLA-B60 epitopes common in Asian populations	human (B60(B*4001)	Altfeld2000b
p24 (44–52)	• All five B60-restricted e		HIV-1 infection B61-restricted epitopes tested er subject, the strongest CTL respon e-third of the total CTL response	human (B60/B61) se directed against the B60-ep	Day2001 pitope p24 SEGATPQDL, and the
p24 (46–59)	<ul> <li>epitope fell within the m</li> <li>Three peptides GSEELF contained the dominant</li> <li>Five peptides RLRPGGI</li> </ul>	nost recognized peptides in the RSLYNTVATL (p17 residues 7 Gag-specific epitope in 31 out KKHYMIKHLVW (p17 20-36 QA (p24 161-177), and SILD	HIV-1 infection  ppe in a HIV+ African American livit e study 71-85), SALSEGATPQDLNTMLNT of 44 B-clade infected individuals f 6), ELRSLYNTVATLYCV (p17Gag IKQGKEPFRDY (p24 149-164) cor	"VG (p24 41-60), and WEKII from Boston who showed Gag 74-88), SALSEGATPQDLN"	RLRPGGKKKYKLK(p17 16-30) g-CTL responses TMLNTVG (p24 41-60),
p24 (47–55)	p24 (47–55) • One of the 51 HIV-1 epi HLA alleles	ATPQDLNTM topes selected by Ferrari et al.	HIV-1 infection as good candidate CTL epitopes for	human (B7) vaccines by virtue of being c	Ferrari2000 conserved and presented by common
p24 (47–56)	CD8+ T cell responses t  Low risk individuals did CD8+ T cell epitopes:	ended to be to the same epitop not have such CD8+ cells	HIV-1 exposed seronegative we sex-workers in Nairobi had HIV-ses but at generally lower levels than SLYNVATL (4 individuals), LSPRTI en	cervical CD8+ T cell respon	ses
p24 (47–58)	p24 (181–192) • HIV-2 epitope defined fi	CTPYDINQMLNC com an infection in Gambia, B	HIV-2 infection ertoletti, Pers. Comm.	human (B58)	Bertoletti1998a
p24 (48–56)	Gag (96ZM651.8)  • Epitope name: G180-TL	TPQDLNTML		human (A*4201, B*8101)	Novitsky2001
	<ul> <li>This study is provides a</li> <li>19 of 46 (41.3%) had CTEKAFSPEVIPMFTALS</li> <li>1,447) SFC/10<sup>6</sup> PBMC</li> <li>7 of 11 HLA-A*4201+ s</li> </ul>	survey of CTL responses and IL responses to one or more p EGAT, and MFTALSEGATPO	full length HIV-1 genome sequences eptides within the first immunodomi QDLNTMLNT), with magnitudes of eptide MFTALSEGATPQDLNTML KVIEEKAFSPEVIP	nant region of Gag (peptides response with ELISPOT resu	TLNAWVKVIEEKAFSPEVIP,

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
p24 (48–56)	p24 (180–188 IIIB) • C. Brander notes this is	TPQDLNTML a B*0702 epitope	HIV-1 infection	human (B*0702)	Brander2001
p24 (48–56)	p24 (179–187 LAI) • C. Brander notes this is	TPQDLNTML a B*4201 epitope		human (B*4201)	Brander2001
p24 (48–56)	Gag (173–181 HIV-2) • C. Brander notes this is	TPYDINQML a B*5301 epitope	HIV-2 infection	human (B*5301)	Brander2001
p24 (48–56)	p24 (180–188 LAI) • C. Brander notes this is	TPQDLNTML a B*8101 epitope	HIV-1 infection	human (B*8101)	Brander2001
p24 (48–56)	• Epitope name: Gag-TL	TPQDLNTML	HIV-1 infection	human (B*8101, B*5301, B07)	Sabbaj2002b
	<ul> <li>Subjects 00RCH86 and</li> <li>Subject 00RCH86 was a</li> <li>Subject 03RCH59 was a</li> <li>Among HIV+ individua</li> <li>Among HIV+ individua</li> </ul>	03RCH59 both recog African American, not African American, ma Is who carried HLA E Is who carried HLA E	optimal epitopes for CTL cell lines isol nized this epitope, both restricted by HL ton HAART, viral load 51000, CD4 coule, on HAART, viral load 22000, CD4 c 807, 2/9 (22%) recognized this epitope 3*5301, 3/15 (20%) recognized this epitope 13*5301, 3/15 (20%) recognized this epitope 13*5301, 3/15 (20%) recognized this epitope 13*5301, 3/15 (20%) recognized this epitope 14/16 (67%) recognized this epitope	A B*8101 nt 520 ount 769	ed by a Cr-release
p24 (48–56)	<ul> <li>B42 and or B81 are expresponse was to TPQDI</li> <li>Three peptides GSEELI contained the dominant</li> <li>Five peptides RLRPGG</li> </ul>	ressed in 40-45% of Z NTML RSLYNTVATL (p17 ro Gag-specific epitope i KKHYMIKHLVW (p	HIV-1 infection resent this epitope to B42-positive effect Zulu and Xhosa infected individuals in S esidues 71-85), SALSEGATPQDLNTM in 31 out of 44 B-clade infected individuals 17 20-36), ELRSLYNTVATLYCV (p17 and SILDIKQGKEPFRDY (p24 149-164)	outh Africa, and in 14/18 B42 of LNTVG (p24 41-60), and WEK tals from Boston who showed G Gag 74-88), SALSEGATPQDL	r B81+ individuals, the dominant gag XIRLRPGGKKKYKLK(p17 16-30) fag-CTL responses NTMLNTVG (p24 41-60),
p24 (48–56)	precursor frequency (lin	niting dilution assay []	HIV-1 infection nctional assays in 42 people with chroni LDA]) I to be active, and inert CTL were not fo		
p24 (48–56)	p24 • CTL responses in seron deletion in CCR5	TPQDLNQML egative highly HIV-ex	posed African female sex workers in Ga	human (B53) ambia and Nairobi were studied	Rowland-Jones1999  – these women had no delta 32

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References				
	<ul> <li>In Gambia there is exposure to both HIV-1 and HIV-2, CTL responses to B35 epitopes in exposed, uninfected women are cross-reactive, and the B35 allele seems to be protective</li> <li>HIV-2 sequence: TPYDINQML, no cross-reactivity, [Gotch1993]</li> </ul>								
p24 (48–56)	Gag (173–181 HIV-2)	TPYDINQML	HIV-2 infection	human (B53)	Gotch1993				
p24 (48–56)			HIV-1 infection, in vitro stimulation opes from infected individuals is poss	human (B53)	Dorrell2001  odified vaccinia virus Ankara (MVA)				
p24 (48–56)	<ul> <li>This optimal epitope was that corresponds to it, as</li> <li>TPQDLNMML was reco</li> <li>TPQDLNMML was A su more efficiently to B53 – significantly alter the pos</li> </ul>	TPQDLNMML  bians, three HLA-B53 epitopes identified within the 20 mer re: B53 is part of the B7 superfami gnized in 6/7 HLA-B53 subject abtype-specific with no cross-re position 7 show great positional ition of the peptide in the binding	HIV-1 infection  were defined in Gag p24 using ELIS active peptide that carried it by homoly, and by the proline in the anchor at sand was immunodominant in most cognition of the subtype B, C, and D al variation in crystal structures of two groove and thus affect TCR interase with the HIV-2 and Mamu-A*01 variation.	ology with a B53 epitope fit the position 2 subjects variant, TPQDLNTML, a to HLA-B53 complexes, su actions	rom HIV-2, a B subtype B7 peptide although the B/C/D variant bound aggesting variation here might				
p24 (48–56)	• Detection of CTL escape infants	mutants in the mother was asso	HIV-1 infection text of mother-to-infant transmission ociated with transmission, but the CT ting mother that had a CTL response	L-susceptible forms of the	Wilson1999a virus tended to be found in infected				
p24 (48–56)	<ul> <li>Three additional sub-dom highlighted 2078 possible</li> </ul>	ninant HLA B7 epitopes were d	HIV-1 infection ponse defined using a conventional aperined using EpiMatrix, a non-ancho V-1 derived from the study subject— we as functional CTL epitopes	or based strategy for defining	ng potential epitopes, which				
p24 (48–56)	p24 (SF2) • Epitope name: TL9 • Recognized by patient 93	TPQDLNTML	HIV-1 infection ed as a positive control in a study of	human (B7) the SLYNTVATL epitope	Goulder2001a				
p24 (48–56)	<ul><li>studied in eight HIV-1-in</li><li>2 to 17 epitopes were recepitopes were targeted by</li></ul>	fected subjects, two with acute ognized in a given individual, A at least one person	HIV-1 infection stricted by HLA class I A and B allel infection, five with chronic, and one A2-restricted CTL response tended to en 2-8 out of 11 B7-restricted epitop	long-term non-progressor be narrow and never domi	(LTNP)				

HXB2 Location	<b>Author's Location</b>	Sequence	Immunogen	Species (HLA)	References
	• The other acute serocon	vertor failed to recognize	allele recognized five B7-restricted epe e any of the 11 B7-restricted epitopes able and there was no clearly domina	s tested	
p24 (48–56)	<ul> <li>One individual, AC-06, interruptions (STI). He restricted by HLA-A3,</li> <li>1/11 HLA-B7 individual</li> </ul>	was homozygous at all thad only two detectable 11 by HLA-B7, and 1 by lls had detectable B7-res		ras treated during acute infection n, but after STI this broadened to ng acute infection – 10/15 of HLA	and had supervised treatment
p24 (48–56)	<ul> <li>CTL epitopes (http://hiv</li> <li>60 epitope responses we magnitude of the responses to the compact of the response of the compact of the response of the compact of the compact</li></ul>	nd lymph node (LN) CD y-web.lanl.gov/content/hi- ere detected in both PB and asse was similar in LN and in the LN. atment in five patients state e responses in the PB be following HAART induct the PB, and the addition	udied, the magnitude of the CD8 T-cc came undetectable, in contrast to 5/20 ed resulted in increased viremia acco of 9 novel epitope responses. or 4 individuals. Patient A displayed	for each person's class I HLA all d an additional 8 responses were cells in the LN is lower so the nu ell response was decreased in bot 6 in the LN.  ompanied by the restoration of the	eles. detected only in LN. The total mber of HIV-specific cells per millior h LN and PB, but more dramatically e detection of 13 epitopes that had
p24 (48–56)	p24 (180–188 LAI) • C. Brander notes this is	TPQDLNTML a C*0802(Cw8) epitope	HIV-1 infection	human (C*0802(Cw8)	)) Brander2001
p24 (48–57)	<ul> <li>A subset of the potential epitopes were identified</li> <li>TPQDLNMMLN was n</li> <li>TPQDLNMMLN was s</li> </ul>	l epitopes was identified that could stimulate IFN newly defined as an HLA hown to stimulate an EL	with the program Conservatrix to identify that could bind to the appropriate HI γ production in an ELISPOT assay -B7 epitope in this study, athough it ISPOT response, but could not be she had previously been identified as a H	LA-allele, and 15 predicted B7 su was previously published as a B* own to bind to HLA-B7	sperfamily (HLA B7, B8, and B58) 8101 epitope
p24 (49–57)	<ul><li>A sustained Gag, Env at</li><li>Despite this being a well RAEQASQEV</li></ul>	nd Nef response was obs Il defined conserved epite	HIV-1 infection ong-term non-progressors were isolat erved, and clones were restricted by ope, none of the 11 gag-specific clone a linkage disequilibrium, and that this	multiple HLA epitopes, indicatin es from a B-14 positive subject co	g a polyclonal response

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
p24 (51–59)	p24 • 3/4 animals displayed	DLNTMLNTV HIV-1 Gag-specific CTL	HIV-1 infection activity	chimpanzee	Santra1999
	Effector cells from two and DLNTMLNTV, H	chimpanzees were able LA-B14)	to recognize two epitopes also recogn		
			wing human HIV-1 specific Gag epito <sub>l</sub> A-B57; KRWIILGLNK, HLA-B27; a		ed within 20mer peptides that
p24 (51–59)	<ul><li>CD8+ T cell responses</li><li>Low risk individuals d</li><li>CD8+ T cell epitopes:</li></ul>	s tended to be to the same id not have such CD8+ co	uals), SLYNVATL (4 individuals), LS	HIV-specific CD8 gamma-IFN than cervical CD8+ T cell resp	onses
p24 (51–59)	<ul><li>sex workers eventually</li><li>The epidemiological f working for a period of</li></ul>	y seroconverted, and for s actor associated with sero r retire	HIV-1 infection posed, persistently seronegative individual in the posed of these HIV CTL reactive epitopes aconversion was stopping sex work and worker controls, ML1792	had been defined while serone	gative
p24 (51–59)	CD8+ cell IFNgamma • In general, during the specificities that were HIV-specific response	production to measure refirst month of treatment v not previously detectable s diminished	HIV-1 infection es was tested in 14 HIV+ patients from esponses iral load decreased and frequencies of were newly detected, as were CMV see: increases or decreases in pre-exist	HIV-specific CTL tripled and be pecific CD8+ PBL – but with co	oroadened – eight new HIV ontinued viral suppression,
p24 (51–59)	p24 (183–191)	DLNMMLNIV	HIV-1 infection, HIV-1 ex- seronegative	posed human (B14)	Kaul2001a

- Variants DLNMMLNIV/DLNTMLNVV are specific for clades A/B
- ELISPOT was used to study CTL responses to a panel of 54 predefined HIV-1 epitopes in 91 HIV-1-exposed, persistently seronegative (HEPS) and 87 HIV-1-infected female Nairobi sex workers
- Responses in HEPS women tended to be lower, and focused on different epitopes with HLA presenting molecules that have previously been associated with reduced risk of infection, and there was a shift in the response in the HEPS women upon late seroconversion to epitopes recognized by the HIV-1 infected women
- 43/91 HEPS women had CD8+ responses and detection of HIV-1-specific CTL in HEPS women increased with the duration of viral exposure
- Among HLA-B14 women, 4/4 HEPS and 3/7 HIV-1 infected women recognized this epitope, likelihood ratio 4.8, p value 0.1, and HEPS women tended to respond to DLNMMLNIV/DLNTMLNVV, while infected women tended to respond to DRF(F/W)KTLRA
- The dominant response to this HLA allele was to this epitope for all 4/4 HEPS cases and in only one of the 3/7 HIV-1 infected women
- Differences in epitope specificity were only seen for responses restricted by class I HLA alleles A2, A24, A\*6802, B14, and B18, previously shown to be associated with resistance to HIV-1 in this cohort

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
		proteins: A2 ILK(D/E)	epitopes", as they were preferentially rea PVHGV in RT, A*6802 DTVLEDINL i		
p24 (51–59)	<ul><li>T-cells, detected by int</li><li>Ghonorrhea caused the</li></ul>	racellular cytokine prod weaker HIV-1 specific	HIV-1 infection an sex workers caused a functional defici- uction and tetramer assays, while not aff CTL responses in 4 HIV-1 exposed persi CTL in 2 HEPS subjects were shown to	ecting the total number of epitostently seronegative (HEPS) w	ope-specific CTLs. omen to become undetectable by
p24 (51–59)	p24 (183–191 LAI)  • Recent evidence indica Goulder, personal com	1 1	HIV-1 infection e; B14 and Cw8 are in linkage disequilib	human (B14, Cw8) brium and the HLA presenting r	Johnson1992, Nixon1988 molecule is hard to distinguish (P.
p24 (51–59)	<ul> <li>and D clades – such cro</li> <li>The A subtype consens</li> <li>The D subtype consens</li> </ul>	oss-reactivity could protous is identical to the Bous is dLNmMLNiV tes this is a Cw8 epitopo	HIV-1 exposed seronegative infected prostitutes from Nairobi using project against both A and D and confer proclade epitope  e;B14 and Cw8 are in linkage disequilibiting the conference in the	reviously-defined B clade epitor tection in Nairobi where both s	ubtypes are circulating
p24 (51–59)	p24 (183–191 LAI) • C. Brander notes this is	DLNTMLNTV s a C*0802 epitope	HIV-1 infection	human (C*0802)	Brander2001
p24 (51–59)		tes this is a Cw8 epitope	HIV-1 infection 4 motif found within a larger peptide e;B14 and Cw8 are in linkage disequilibiter	human (Cw8) rium and the HLA presenting n	McMichael1994 nolecule is hard to distinguish (P.
p24 (51–59)	<ul> <li>Seroprevalence in this e</li> <li>Most isolated HIV stra responses are frequentl</li> <li>This epitope is conserv</li> <li>The Clade A version of</li> </ul>	cohort is 90-95% and the ins are clade A in Nairo y observed using A or I ed among B and D clads the epitope, DLNNML tes this is a Cw8 epitope.	HIV-1 exposed seronegative negative prostitutes from Nairobi – these eir HIV-1 exposure is among the highest bi, although clades C and D are also four Clade versions of epitopes e viruses  NIV, was preferentially recognized by Ce;B14 and Cw8 are in linkage disequilibrit	CTL may confer protection in the world and – B clade epitopes are often	cross-reactive, however stronger
p24 (51–70)	p24 (183–202 SF2)  Of 25 patients, most ha Twelve subjects had C  One of these 12 had C  The responding subject	d CTL specific for more ΓL that could recognize ΓL response to this pept	vaccinia-expressed LAI gag ide	human	Lieberman1997a

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
p24 (51–82)	Gag (183–214 LAI)	DLNTMLNTVGGHQAAMQML- KETINEEAAEWDR	- Vaccine	human	Gahery-Segard2000
	<ul> <li>Anti-HIV lipopeptide va administered in a phase</li> <li>A CD4+ T cell prolifera</li> <li>9/12 tested mounted a C</li> </ul>	I trial tive response to at least one of the	no acid peptides derived from Ne he six peptides was observed in 9/ he six peptides; each of the six pep	/10 vaccinees – 2/10 reacted	
p24 (61–69)	p24 (193–201 LAI) • C. Brander notes this is	GHQAAMQML a B*3901 epitope		human (B*3901)	Brander2001
p24 (61–69)	p24 (193–201 LAI) • Optimal peptide defined	GHQAAMQML by titration		human (B39)	Kurane1998
p24 (61–71)	p24 (193–203 BRU) • One of 4 epitopes first p	GHQAAMQMLKE redicted, then shown to stimulat	HIV-1 infection e HLA-A2 restricted CTL line	human (A2)	Claverie1988
p24 (61–80)				human	Lieberman1997a
p24 (61–82)	p24 (193–214 BH10)  • Gag CTL response studi	GHQAAMQMLKETINEEAAE- WDR ed in three individuals	- HIV-1 infection	human (Bw52)	Johnson1991
p24 (62–70)	p24 (194–202 LAI) • P. Goulder, pers. comm.	HQAAMQMLK		human (B52)	Brander1996b
p24 (65–73)	<ul> <li>Different expression vec</li> <li>Stable Gag expression vec</li> <li>which promote RNA de</li> <li>Silent mutations were mexpression</li> </ul>	vas achieved in murine p815 cell gradation ore effective than introduction of	expression in cell lines and create ls, using a Gag gene that had muta of the D retrovirus cis-acting postt	ranscriptional control element	t disrupt inhibitory RNA sequences
p24 (65–73)	p24 (199–207 SF2)  Vaccine Vector/Type: pr (LT) from E. coli  Epitope name: p7g	AMQMLKETI rotein, vaccinia Strain: SF2	Vaccine HIV component: soluble Gag, or C	murine (H-2 <sup>d</sup> ) GagPol expressing vaccinia	Neidleman2000  Adjuvant: heat-labile enterotoxin

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
	<ul><li>as adjuvants was tested</li><li>Intranasal and intramucimmunization response</li></ul>	cosal immunization of p5 s of LTR72, with residual	ce with soluble gag p55 with LT Al 55 gag protein with LTK63 or LTK ADP-ribosyltransferase activity, in	72 adjuvant induced a CTL respons	•
p24 (65–73)	<ul> <li>BALB/c mice were injugilycoprotein (VSV-G).</li> <li>class II pathways, while</li> <li>Vaccination with DNA</li> </ul>	ected with plasmids expr The combination encode e exogenous Gag alone of	Vaccine Gag Adjuvant: vesicular stomatit ressing HIV-1 Gag with or without res VSV-G pseudotyped Gag particl ran only be taken into the class II pr dotyped Gag particles rather than ju ponse.	coinjection of a plasmid expressing es that can be taken up by cells for athway.	presentation in either the class I or
p24 (65–73)	<ul> <li>Epitope name: p7G</li> <li>Intramuscular or intrap studied in conjunction emulsions and PLG-mi</li> </ul>	eritoneal immunization of with the adjuvant CpG. C croparticle antigen.		ea-solubilized, emulsified, or PLG- y when combined with urea solubil	microparticle associated p55 Gag was lized p55, but did when combined with
p24 (65–73)	* 1		Vaccine  nt: Gag, Pol peptide observed after immunization	murine $(H-2K^d)$ on with vaccine VVgagpol	Doe1997
p24 (65–73)	<ul> <li>BALB/c mice were important D-alanine, and that exportant Parenteral immunization lasting memory CTL results of Oral immunization gave examined</li> <li>L. monocytogenes is a</li> </ul>	oresses HIV-1 HXB2 Gag on provided protection ag esponse against Gag in sp e protection only against	tenuated recombinant Listeria mong grainst systemic and mucosal challer pleen, mesenteric lymph nodes, and the mucosal virus challenge and was a mat enters the macrophage on phago	nges with a recombinant vaccinia val Peyer's patches directed against the associated with a transient CTL res	irus expressing HIV-1 gag, and a long
p24 (65–73)	Gag (197–205 SF2) Vaccine Vector/Type: I	AMQMLKETI Listeria monocytogenes	Vaccine  Strain: HXB2 HIV component: nt Listeria monocytogenes (Lm-Ga		Mata1998

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References		
	<ul><li>are processed and pres</li><li>This is the immunodor</li><li>AMQMLKETI does n</li></ul>	sented by both class I ar minant CTL epitope in ot contain established I		sine or phenylalanine, thus devia	ting from the typical Kd anchoring		
p24 (65–73)	<ul> <li>Gag (HXB2) AMQMLKETI Vaccine murine (H-2K<sup>d</sup>) Haglund2002a</li> <li>Vaccine Vector/Type: vesicular stomatitis virus (VSV), vaccinia Strain: Env, IIIB; Gag HXB2 HIV component: Gag, Env</li> <li>BALB/c mice were vaccinated with rec vesicular stomatitis virus (rVSV) expressing either HIV-1 Gag, Env, or both, and compared to using rec Env Gag in vaccinia virus (rVVs). The primary response was determined by cell lysis, cytokine production and tetramer staining.</li> <li>Primary CTL responses to the immunodominant Gag (AMQMLKETI) epitope peaked in 7 days for GAG-rVSV, 3% of the cells were tetramer posit this response was 8-fold higher than for Gag-rVV.</li> <li>Vaccinating with GagEnv-rVSV carrying both Gag and Env allowed recognition of both HIV-1 proteins, but at reduced levels compared to either Gag-rVSV or Env-rVSV alone.</li> <li>Intranasal immunization with Env-rVSV yielded CTL responses that were strong but reduced compared to an intraperitoneal route.</li> </ul>						
p24 (65–73)	<ul> <li>BALB/c mice were variand recall responses w</li> <li>Seven months after varimemory phenotype, C</li> <li>Env in rec vaccinia vir (expressing CD62L-Lo</li> <li>A prime with Env-rVS splenocytes being Env</li> <li>A Gag-rVSV or EnvG the fraction of IFN-gan</li> </ul>	ccinated with rec vesice rere studied by tetramer ccination with Env-rVS D44-Hi positive. rus (Env-rVV) elicited a co), and capable of IFN-SV and heterologous bo specific memory cells ag-rVSV prime and with mma producing cells were restricted.	Vaccine us (VSV), vaccinia Strain: Env, IIIB; of the control of the CD8+ cells were tetramer a strong recall response, with up to 45% gamma production. ost of Env-rVV gave remarkably high left 150 days after the boost. the a heterologous Gag-rVV or EnvGag-ras only about 25%. Still the heterologous a more potent combination than a vector.	positive for the immunodominar to the CD8+ T-cell population to evels of memory cells, with approxive boost combination gave 40% as vector prime-boost combination	at Env epitope; these cells had a etramer positive and activated eximately 1/3 of the CD8+  the tetramer positive CD8+ cells, but on showed a profound benefit.		
p24 (69–86)	<ul> <li>Epitopes recognized in</li> </ul>	d cytotoxic activity again five children were maj			Buseyne1993a		
p24 (70–78)	<ul><li>24 epitopes were descr</li><li>Serial peptide truncation</li><li>This epitope was newl</li><li>Patient 01RCH46 was</li></ul>	epitope responses in HI ribed – 8 were novel, 8 ons were used to define y defined in this study	HIV-1 infection  V-1 infected minority women living in to used new restricting elements but were optimal epitopes for CTL cell lines isoland had a viral load of 21000 and CD4 A*0217	previously defined epitopes, and lated from 12 individuals, assaye	d by a Cr-release		

women

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
	Among HIV+ individu	als who carried HLA B4	0, 3/5 (60%) recognized this epitope		
p24 (71–80)		ion, ETINEEAAEW is fo	HIV-1 infection ion of PBMC with 20-mer peptides ound in most B, D, and E subtype isolates ype sequences	human (A*2501)	Klenerman1996
p24 (71–80)	p24 (203–212) • C. Brander notes this is	ETINEEAAEW s an A*2501 epitope	HIV-1 infection	human (A*2501)	Brander2001
p24 (71–80)		recognizing the index p		human (A*2501) G, and H and a peptide	vanBaalen1996 of HIV-2ROD over this region were
p24 (71–80)	deletion in CCR5	osure to both HIV-1 and	osed African female sex workers in Gambia a HIV-2, CTL responses to B35 epitopes in exp tivity [vanBaalen1996]		
p24 (71–80)	<ul> <li>individuals treated duri</li> <li>The breadth and specifindividuals with primare (Group 3), using 259 o</li> <li>Previously described as</li> </ul>	ing chronic infection acity of the response was ry infection but post-sero verlapping peptides span and newly defined optima	HIV-1 infection d in a narrower CTL response, stronger T hel determined using ELISPOT by studying 19 is conversion therapy (Group 2), and 10 individ ning p17, p24, RT, gp41, gp120 and Nef l epitopes were tested for CTL response TL response to this epitope broken down by g	ndividuals with pre-seroc uals who responded to H	conversion therapy (Group 1), 11 [AART given during chronic infection
p24 (71–80)	<ul><li>Epitope name: Gag-DV</li><li>Among HIV+ individu</li></ul>		HIV-1 infection 5301, 2/15 (13%) recognized this epitope	human (B*5301)	Sabbaj2002b
p24 (71–80)	<ul><li>Epitope name: Gag-EV</li><li>Among HIV+ individu</li></ul>		HIV-1 infection 5301, 2/15 (13%) recognized this epitope	human (B*5301)	Sabbaj2002b
p24 (71–80)	<ul><li>HIV-1-infected female</li><li>Responses in HEPS wo</li></ul>	Nairobi sex workers omen tended to be lower,	HIV-1 infection, HIV-1 exposed seronegative a panel of 54 predefined HIV-1 epitopes in 91 and focused on different epitopes with HLA in the response in the HEPS women upon late	presenting molecules tha	t have previously been associated with

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
	<ul> <li>Among HLA-B53 wome</li> </ul>	n, 0/2 HEPS and 7/9 HIV-1 infe	of HIV-1-specific CTL in HEPS wor ected women recognized this epitope itope in 4 of the 7/9 responsive HIV-		tion of viral exposure
p24 (71–80)	<ul> <li>Two of the new epitopes anchor residue motif for</li> <li>Two overlapping 20 mer</li> <li>DTINEEAAEW was rec</li> <li>DTINEEAAEW was not</li> </ul>	bians, three HLA-B53 epitopes lacked the predicted by P2 anch B53 and the related B35 peptides carry this complete epiognized in only 2/7 HLA-B53 st A subtype specific and there was	HIV-1 infection  were defined in Gag p24 using ELIS nors, DTINEEAAEW and QATQEV  itope, but only one stimulates recognubjects as cross-recognition although diminification of the epitope, EI	KNM, and bound to B53 wintion, which could be due to shed, of the subtype B, C, a	th high affinity, thus extending the o different peptide processing
p24 (71–90)	p24 (203–222 SF2)  • Of 25 patients, most had	ETINEEAAEWDRVHPVVHA—GP CTL specific for more than 1 H that could recognize vaccinia-control response to this peptide	HIV-1 infection IV-1 protein	human	Lieberman1997a
p24 (78–86)	<ul> <li>24 epitopes were describ</li> <li>Serial peptide truncation</li> <li>This epitope was newly of</li> <li>Patient 01RCH59 was High</li> <li>HLA-B*4002, and KEK6</li> </ul>	itope responses in HIV-1 infecte ed – 8 were novel, 8 used new ress s were used to define optimal ep defined in this study		sly defined epitopes, and 8 vm 12 individuals, assayed b	y a Cr-release
p24 (83–92)	<ul><li>LHPVHAGPVA, a varian</li><li>LHPVHAGPIA, a varian</li><li>LHPVHAGPIT, a varian</li></ul>	nt found in HIV-1 PH136, was a nt found in HIV-1 RF, was also r t found in HIV-1 MN, was also n	ecognized	·	Sipsas1997 HIV-1 IIIB
p24 (84–92)	• One individual, AC-06, v interruptions (STI). He h	was homozygous at all three class	HIV-1 infection  7) or -B7 (n=4) or both -A3 and B7 (ss I alleles (A3, B7, Cw7), was treated ponses during acute infection, but after the state of t	ed during acute infection an	d had supervised treatment

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
			eted responses to this epitope duri viduals had detectable responses t		A-B7 epitopes tested were targeted by
p24 (87–101)	<ul><li>Primary assays showed</li><li>Epitopes recognized in</li></ul>		t least one HIV protein was detec using synthetic peptides and seco		Buseyne1993a
p24 (87–101)	p24 (219–233 BRU) • One of 4 epitopes predi	HAGPIAPGQMREPRG	HIV-1 infection e HLA-A2 restricted CTL line	human (A2)	Claverie1988
p24 (91–110)	<ul><li>Twelve subjects had CT</li><li>One of these 12 had CT</li></ul>	IAPGQMREPRGSDIAG d CTL specific for more that L that could recognize vacuur that could response to this peptide was HLA-A2, A24, B13, E	n 1 HIV-1 protein cinia-expressed LAI gag	human	Lieberman1997a
p24 (101–120)	<ul><li>Twelve subjects had CT</li><li>One of these 12 had CT</li></ul>	GSDIAGTTSTLQEQIG d CTL specific for more that L that could recognize vacc L response to this peptide was HLA-A26, A30, B38	n 1 HIV-1 protein	human	Lieberman1997a
p24 (107–115)	<ul><li>BALB/c mice were imr</li><li>L. monocytogenes is a</li></ul>	nunized with recombinant I		expressing HIV-1 HXB2 Gag	Mata1998  – secreted L. monocytogenes antigens
p24 (108–117)	<ul><li>sex workers eventually</li><li>The epidemiological fa working for a period or</li></ul>	seroconverted, and for six of ctor associated with serocon	of these HIV CTL reactive epitope eversion was stopping sex work a	es had been defined while serones	Kaul2001c roconverted – 11/114 HEPS Nairobi gative lines when HEPS sex workers stop
p24 (108–117)		ine response that was highly		human (B*5701) s, 11/13 (85%) versus 19/200 (9.5 at were presented by B*5701, ISI	Migueles2001 5%) of progressors. Non-progressors PRTLNAW, KAFSPEVIPMF,
p24 (108–117)	threshold of infection w		mune response tends to be focus	human (B*5701) ression of HLA B*5701 – these in ed on peptides that contain B*570	Migueles2001 ndividuals have viral loads below the 01 epitopes ISPRTLNAW,

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
			als with progressive viremia than the se was not as strong individuals that		
p24 (108–117)	p24 (241–250 LAI) • C. Brander notes this is	TSTVEEQQIW a B*5801 epitope	HIV-2 infection	human (B*5801)	Brander2001
p24 (108–117)	p24 (240–249 LAI) • C. Brander notes this is	TSTLQEQIGW a B*5801 epitope	HIV-1 infection	human (B*5801)	Brander2001
p24 (108–117)	<ul><li>immunologically norma</li><li>No direct CTL were fou</li><li>Epitope sequences were</li></ul>	al HIV-infected (INHI) ca and in any of the six INH deduced from larger rea	HIV-1 infection  r HIV-infected people who were infected people who were infected people who were infected asses occur at a frequency between 0.1 Its, but above background CTLp activative peptides based on HLA binding ther B57 long-term non-progressors	and 1% in the infected populativity was founded in 3/6 INHIs	
p24 (108–117)	<ul> <li>1-2 months post serocor against epitope SL9, SL</li> <li>Three CTL responses, to</li> </ul>	nversion, subject PI004 d YNTVATL and other ep to epitopes TSTLQEQIG		V10 peptide recognition, followed  AF, were evident early after infections.	Goulder2001a  d by an increased CTL response  tion; CTL responses to SLYNTVATL,
p24 (108–117)	CD4 proliferative respo HAART had no HIV sp undetectable	nses and were able to ma ecific CD4 proliferative	HIV-1 infection  ction (three with sustained therapy, twaintain a CTL response even with uncorresponses and lost their CTL responses tope but none were HLA B57+	letectable viral load – three patie	•
p24 (108–117)	p24 (108–117) • One of the 51 HIV-1 ep HLA alleles	TSTLQEQIGW itopes selected by Ferrar	HIV-1 infection i et al. as good candidate CTL epitop	human (B57) es for vaccines by virtue of being	Ferrari2000 g conserved and presented by common
p24 (108–117)	<ul><li>T-cells, detected by intr</li><li>Ghonorrhea caused the</li></ul>	acellular cytokine produc weaker HIV-1 specific C	HIV-1 infection a sex workers caused a functional defiction and tetramer assays, while not a TL responses in 4 HIV-1 exposed per TL in 2 HEPS subjects were shown	affecting the total number of epitorsistently seronegative (HEPS) w	ope-specific CTLs.  romen to become undetectable by
p24 (108–117)	<ul><li>p24</li><li>Epitope name: TST</li><li>Using previously define period including therapy</li></ul>			human (B57) lispot assay, 13 chronically HIV-	Oxenius2002b  1 infected patients were studied over a

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References	
	STIs induced increased clearance rates.	recognition of CTL epit	copes, but there was no correlation between C	TL responses with viral	rebound rates, plateau viral loads, or	
p24 (108–117)	p24 (235–243)	TSTLQEQIGW	HIV-1 infection, HIV-1 exposed seronegative	human (B57, B58)	Kaul2001a	
	<ul> <li>TSTLQEQIGW cross r</li> <li>ELISPOT was used to : HIV-1-infected female</li> </ul>	study CTL responses to a	a and B clades a panel of 54 predefined HIV-1 epitopes in 91	HIV-1-exposed, persiste	ently seronegative (HEPS) and 87	
p24 (108–117)			HIV-2 infection nbia, Bertoletti, Pers. Comm. VEEQIQW in this region, not TSTVEEQQW	human (B58) V as in the paper	Bertoletti1998a	
p24 (108–117)	<ul><li>deletion in CCR5</li><li>In Gambia there is exposeems to be protective</li></ul>	osure to both HIV-1 and	HIV-1 exposed seronegative osed African female sex workers in Gambia and HIV-2, CTL responses to B35 epitopes in exposs-reactive, [Bertoletti1998b]			
p24 (108–117)	<ul> <li>HLA-B*5801+ individ</li> <li>This can be an immuno</li> <li>HIV-2 sequence: HIV-2 epitopes</li> <li>The epitope is TSTLQI</li> </ul>	uals may have an enhance of the common of th	HIV-2 infection infected individuals have a dominant respons red potential for cross-protection between HIV A-B57 and B*5801 infected individuals, and requence TSTVEEQIQW, and the CTL from a e, and TSTVEEQIQW in HIV-2 ROD t HIV-1 and HIV-2 cross-reactive epitopes	V-1 and HIV-2 is associated with long-t	erm non-progression [Goulder1996b]	
p24 (108–117)	<ul> <li>HLA B*5801 and B35 may preferentially select HIV-1 and HIV-2 cross-reactive epitopes</li> <li>p24 (240–249 SF2) TSTLQEQIGW HIV-1 infection human (B58) Altfeld2001b</li> <li>Therapy provided during acute infection resulted in a narrower CTL response, stronger T help response, and a less diverse viral population than was see individuals treated during chronic infection</li> <li>The breadth and specificity of the response was determined using ELISPOT by studying 19 individuals with pre-seroconversion therapy (Group 1), 11 individuals with primary infection but post-seroconversion therapy (Group 2), and 10 individuals who responded to HAART given during chronic infect (Group 3), using 259 overlapping peptides spanning p17, p24, RT, gp41, gp120 and Nef</li> <li>Previously described and newly defined optimal epitopes were tested for CTL response</li> <li>Number of HLA-B58+ individuals that had a CTL response to this epitope broken down by group: 0/0 group 1, 1/1 group 2, and 0/0 group 3</li> </ul>					
p24 (108–117)		be were observed in autol	HIV-1 infection  spitope are present during the time of decreasi logous clones of subjects who were B58-posit in adult infections			

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
p24 (108–118)	• For one donor (from Zir	nbabwe) this was defined as the	HIV-1 infection g HLA-B*57 individuals, in 2 it wa optimal peptide ly related HLA molecules B*5801		Goulder1996b
p24 (108–118)	p24 (240–249 LAI) • C. Brander notes this is	TSTLQEQIGWF a B*5701 epitope	HIV-1 infection	human (B*5701)	Brander2001
p24 (108–118)	<ul><li>Epitope name: Gag-TF1</li><li>Among HIV+ individua</li></ul>	TSTLQEQIGWF  1 Is who carried HLA B57, 2/5 (40	HIV-1 infection 0%) recognized this epitope	human (B57)	Sabbaj2002b
p24 (109–117)		STLQEQIGW  with long-term non-progression TL responses in HLA B*5701 L		human (B*5701 B*5801)	Klein1998
p24 (109–117)	<ul><li>Epitope name: Gag-SW</li><li>Among HIV+ individua</li></ul>	STLQEQIGW	HIV-1 infection  (9%) recognized this epitope	human (B57)	Sabbaj2002b
p24 (118–126)	for the A3 supertype) wi Progressors had memory A positive correlation be observed, which may co	hile the effector cells of long-terry resting CD8+ T-cells that recognized tween effector CD8+ T-cells and intribute to the inability of LTNP	m nonprogressors recognized far fognized far fewer epitopes than LTN d plasma viremia and a negative co	ewer epitopes IPs orrelation between CD8+ effec	Propato2001 ested, (18 for the A2 supertype, 16 ctor T-cells and CD4+ T-cells was
p24 (121–135)	p24 (253–267) • High frequency of memory	NPPIPVGEIYKRWII ory and effector Gag-specific CT	HIV-1 infection	human (B8)	Gotch1990
p24 (121–135)	relative to B8 epitopes,	which varied over time lew of immune escape that points	HIV-1 infection th the appropriate HLA types – little s out that there may be a protective		Goulder1997a, Phillips1991 ne immunodominant B27 epitope, and that HLA-B8 individuals tend to
p24 (121–135)	p24 (121–135) • One of the 51 HIV-1 epi HLA alleles	NPPIPVGEIYKRWII topes selected by Ferrari et al. as	HIV-1 infection s good candidate CTL epitopes for	human (B8) vaccines by virtue of being co	Ferrari2000 conserved and presented by common
p24 (121–140)	p24 (253–272) • HIV-specific CTL lines	NPPIPVGEIYKRWIILGLNK developed by ex vivo stimulation		human	Lieberman1995

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
p24 (121–140)	<ul><li>Twelve subjects had CT</li><li>Two of these 12 had CT</li></ul>	NPPIPVGEIYKRWIILGLNK I CTL specific for more than 1 HI L that could recognize vaccinia-e L response to this peptide s were HLA-A2, A3, B8, B62, and	IV-1 protein expressed LAI gag	human	Lieberman1997a
p24 (121–140)	p24 (253–272 SF2) • CTL expanded ex vivo	NPPIPGEIKRWIILGNIK were later infused into HIV-1 infe	HIV-1 infection acted patients	human	Lieberman1997b
p24 (121–140)	p24 (255–274 SF2) • Gag CTL epitope precur	NPPIPVGEIYKRWIILGLNK rsor frequencies were estimated a		human ed	vanBaalen1993
p24 (121–142)	p24 (253–274 BH10)  • Gag CTL response stud	NPPIPVGEIYKRWIILGLN- KIV ied in three individuals	HIV-1 infection	human (B8)	Johnson1991
p24 (121–152)	<ul> <li>Anti-HIV lipopeptide va administered in a phase</li> <li>A CD4+ T cell prolifera</li> <li>9/12 tested mounted a C peptide was particularly</li> </ul>	I trial tive response to at least one of the	peptides no acid peptides derived from Nef e six peptides was observed in 9/ e six peptides; each of the six pep	10 vaccinees – 9/10 reacted	Gahery-Segard2000  ins modified by a palmitoyl chain was  to this peptide se in at least one individual – this
p24 (121–152)	<ul> <li>Immunization of 2/4 HI B8, B27, B35, and Bw6</li> <li>Placebo and HLA mis-n</li> </ul>	NPPIPVGEIYKRWIILGLN-KIVRMYSPTSILD popeptide HIV component: gag V seropositive HLA selected indi 2 gave a transient increase in pepthatched controls showed no chang HLA Bw62 and B35 – the two HI	peptide viduals with a 32 amino acid Gaş tide-specific bulk CTL response, ge in CTL	but they did not decrease p	Seth2000 CTL epitopes restricted by HLA A33, lasma viral load.
p24 (122–130)	<ul> <li>sex workers eventually s</li> <li>The epidemiological factoristing for a period or</li> </ul>	seroconverted, and for six of these etor associated with seroconversion	e HIV CTL reactive epitopes had on was stopping sex work and HIV	been defined while seroneg	Kaul2001c roconverted – 11/114 HEPS Nairobi gative lines when HEPS sex workers stop
24 (122, 120)	p24 (260–268 LAI)	DD IDUOD IV	HIV-1 or HIV-2 infection	L (D#2501)	
p24 (122–130)	• C. Brander notes this is	PPIPVGDIY a B*3501 epitope	TH V-1 of TH V-2 infection	human (B*3501)	Brander2001

HXB2 Location	<b>Author's Location</b>	Sequence	Immunogen	Species (HLA)	References
p24 (122–130)	p24 (245–253 HIV-2) • C. Brander notes this is	NPVPVGNIY a B*3501 epitope	HIV-1 infection	human (B*3501)	Brander2001
p24 (122–130)	p24 (260–268 LAI) • Defined as minimal pept	PPIPVGDIY tide by titration curve, I	HIV-1 or HIV-2 infection PPIPVGEIY and HIV-2 form NPVPVGNIY	human (B35) Y are also recognized	Rowland-Jones1995b
p24 (122–130)	stimulate a primary resp	onse, only secondary – the B35 presented test	in vitro stimulation timulation of CTLp using optimized peptid peptide-specific CTLp counts could be obt peptides used in control experiments showi	ained via staining with per	otide-Class I tetramers
p24 (122–130)	p24 (260–268 LAI) • Review of HIV CTL epi	PPIPVGDIY itopes	HIV-1 infection	human (B35)	McMichael1994
p24 (122–130)	<ul> <li>Seroprevalence in this co</li> <li>Most isolated HIV strain responses are frequently</li> <li>This epitope is conserve</li> </ul>	ohort is 90-95% and then sare clade A in Nairoby observed using A or D d among B and D clade	HIV-1 exposed seronegative egative prostitutes from Nairobi – these CT for HIV-1 exposure is among the highest in bi, although clades C and D are also found clade versions of epitopes eviruses Y, was preferentially recognized by CTL	the world	Rowland-Jones1998b n cross-reactive, however stronger
p24 (122–130)	<ul> <li>CD8+ T cells were foun viral load</li> <li>All three patients were F</li> <li>ELISPOT was used to to subjects showed a domin</li> <li>The subject with A*020</li> <li>Weak responses were of B*2705</li> <li>No acute response was of</li> </ul>	d prior to seroconversion  3*2705, with HLA allelest a panel of CTL epitonant response to the B*1 had a moderatly strongserved to A*301-RLRI  detected to the following	HIV-1 infection cific CTL responses were studied during act on, and there was a close temporal relations es: A1, A30/31, B*2705, B35; A1, A*0302 ppes that had been defined earlier and were 2705 epitope KRWIILGGLNK eg response to SLYNTVATL PGGKKK, A*301-QVPLRPMTYK, and B2 g epitopes: A*201-ILKEPVHGV, A*301-K IPVGEIY, B35-NSSKVSQNY, B35-VPLR	thip between the number of 1, B7, B2705; and A*0201 appropriate for the HLA has 7-TPGPGVRYPL in the su	f circulating HIV-specific T cells and , A*0301, B2705, B39 aplotypes of the study subjects – 3/3 abject who was HLA A1, A*0301, B7, QSSMTK, A*301-TVYYGVPVWK,
p24 (122–130)	<ul><li>deletion in CCR5</li><li>In Gambia there is exposeems to be protective</li></ul>	sure to both HIV-1 and itope is not conserved:	osed African female sex workers in Gambia HIV-2, CTL responses to B35 epitopes in e NPVPVGNIY, but the CTLs are cross-reac	exposed, uninfected women	n are cross-reactive, and the B35 allele

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References			
p24 (122–130)	p24 (260–268) • Epitope name: PPI	PPIPVGDIY	HIV-1 infection	human (B35)	Oxenius2000			
	<ul> <li>Patients who started th CD4 proliferative resp HAART had no HIV s undetectable</li> <li>One of two HLA B354</li> </ul>	onses and were able to me pecific CD4 proliferative among the eight study study 8 1/68, B8/35, Bw4/6, Cw4	ection (three with sustained therapy, twaintain a CTL response even with under responses and lost their CTL response subjects recognized this epitope 4/0704) was given acute and sustained	letectable viral load – three pati es when HAART was eventual	ly given and their viral loads became			
p24 (122–130)	p24 (122–130) • One of the 51 HIV-1 epHLA alleles	PPIPVGDIY pitopes selected by Ferra	HIV-1 infection ri et al. as good candidate CTL epitopo	human (B35) es for vaccines by virtue of bei	Ferrari2000 ng conserved and presented by common			
p24 (122–130)	<ul> <li>individuals treated dur</li> <li>The breadth and specifindividuals with prima (Group 3), using 259 c</li> <li>Previously described a</li> </ul>	ring chronic infection ficity of the response was ary infection but post-sero overlapping peptides spar and newly defined optima	determined using ELISPOT by study	ing 19 individuals with pre-sero individuals who responded to Nef se	HAART given during chronic infection			
p24 (122–130)	p24 (260–268)	PPIPVGDIY	HIV-1 infection, HIV-1 ex seronegative	posed human (B35)	Kaul2001a			
	<ul> <li>ELISPOT was used to HIV-1-infected female</li> </ul>	-	a panel of 54 predefined HIV-1 epitopo	es in 91 HIV-1-exposed, persis	tently seronegative (HEPS) and 87			
	• Responses in HEPS women tended to be lower, and focused on different epitopes with HLA presenting molecules that have previously been associated with reduced risk of infection, and there was a shift in the response in the HEPS women upon late seroconversion to epitopes recognized by the HIV-1 infected women							
	• 43/91 HEPS women had CD8+ responses and detection of HIV-1-specific CTL in HEPS women increased with the duration of viral exposure							
	<ul> <li>Among HLA-B35 women, 1/3 HEPS and 3/4 HIV-1 infected women recognized this epitope</li> <li>The dominant response to this HLA allele was to this epitope in the 1/3 HEPS case and in the all 3/4 responsive HIV-1 infected women</li> <li>Subject ML 857 shifted from a A*6802 DTVLEDINL and B35 (H/N)PDIVIYQY response prior to seroconversion to a B35 PPIPVGDIY and B35 VPLRPMTY response post-seroconversion</li> </ul>							
p24 (122–130)	E.'. C. N	PPIPVGDIY	HIV-1 infection	human (B35)	Sabbaj2002b			
		als who carried HLA B3	25, 2/21 (10%) recognized this epitope 5301, 0/11 (0%) recognized this epito					
p24 (122–130)	p24 <b>Vaccine</b> Vector/Type:	PPIPVGEIY  DNA prime with vaccinia	HIV-1 infection, Vaccine a MVA boost Strain: subtype A Hi	human (B35)  W component: p17, p24, polye	Hanke2000, Wee2002 pitope			

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
	which could direct the conserved, often immu Kenya. A DNA and M included in the polyepi  Multiple CD4+ or CD8 assays after vaccination	protein to the cell mer nodominant epitopes of VA prime-boost vaccin tope string [Hanke200 8+ T-cell vaccine-indu- n of 5 macaques. The	contains p24 and p17, in a reversed ord mbrane and inhibit efficient peptide process that were selected to have particularly gonation protocol using the HIVA antigen 100]. Colored responses to peptide pools were deteresponse to the Mamu A*01 SIV p27 excinated macaques, possibly because of particularly process.	ressing and class I presentation, a pood cross-reactive potential for the will be used in a phase III clinical ected using intracellular cytokine pitope p11C (CTPYDINQM), inc	s well as a polyepitope string of e A-clade epidemic in Nairobi, l trial in Kenya. This epitope is staining and IFNgamma Elispot luded in the polyepitope region, was
p24 (124–138)	p24 (256–270 LAI) • Clustering of Gag p24	IPVGEIYKRWII CTL epitopes recogni	LGL HIV-1 infection zed in 29 HIV-infected people	human (B8)	Buseyne1993b
p24 (124–138)	<ul> <li>Epitopes recognized in</li> </ul>	l cytotoxic activity aga five children were ma		ndary cultures	Buseyne1993a  b be presented by B8 in EM18
p24 (127–135)	p24 (259–267 SF2) • GDIYKRWII specific (	GDIYKRWII CTL clone also recogr	HIV-1 infection nized GEIYKRWII	human (B*0801)	McAdam1998
p24 (127–135)	p24 (261–269) • Predicted epitope based	GEIYKRWII d on B8-binding motif	HIV-1 infection s, from larger peptide NPPIPVGEIYKR	human (B8)	Sutton1993
p24 (127–135)	<ul> <li>HIV-uninfected donors</li> <li>Strong CTL responses macrophages were not</li> <li>A weak response to KI</li> </ul>	using peptide-pulsed were elicited by the ep able to prime a CTL r TPLCVSL was stimu	in vitro stimulation ges and dendritic cells to stimulate prim APC – the dendritic cells performed bet pitopes DRFYKTLRA and GEIYKRWI esponse against DRFYKTLRA lated using macrophages as the APC following previously-defined HIV epito	tter as APC for the stimulation of I when presented by either imma	primary responses ture or mature dendritic cells –
p24 (127–135)	p24 (259–267 LAI)  • Naturally occurring var	GEIYKRWII riant GDIYKRWII ma	HIV-1 infection by act as antagonist	human (B8)	Klenerman 1994
p24 (127–135)	• 95 optimally-defined p	eptides from this datal	HIV-1 infection CTL that reacted to SLYNTVATL, calling passe were used to screen for INF $\gamma$ resports, B8, B51 and responded to this epitop	nses to other epitopes	Betts2000 nunodominant
p24 (127–135)	p24 (259–267) • Longitudinal study of 0	GEIYKRWII CTL response and stud	HIV-1 infection ly of immune escape – GDIYKRWII co	human (B8) uld also stimulate CTL, reactivity	Nowak1995 fluctuated
p24 (127–135)	p24 (259–267) • Equivalent sequence G	GEIYKRWII DIYKRWII also recoş	HIV-1 infection gnized by CTL from some donors	human (B8)	McAdam1995

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
p24 (127–135)	p24 (259–267) • Epitope name: GEI	GEIYKRWII	HIV-1 infection	human (B8)	Oxenius2000
	<ul> <li>Patients who started the CD4 proliferative resperative respective respective</li></ul>	onses and were able to me pecific CD4 proliferative bjects that were HLA B8, B7/8, Cw0701/0702, Did tetramer staining stead in 8/10 clones /2, B8/13, Cw0/0701, DFTQGYFPDWQNY, and 1/12, B8/44, Cw06/0701 VDLSHFLK, and FNCG	naintain a CTL response even with unce responses and lost their CTL responses recognized this epitope R4/53, DQ7) had CTL responsiveness lily declined and at day 1340 the FLK1 R2/11, DQ6/7) had a CTL response ag	detectable viral load – three patises when HAART was eventually against epitopes FLKEKGGL, EKGGL stained cells were no leasinst epitopes FLKEKGGL, IL ed during therapy initiated at data. The response to epitopes FLKEK initiated at day 197	GPKVKQWPL, and GEIYKRWII onger detected and the escape mutant KEPVHGV, ay 390 but were restored when therapy
	<ul> <li>FLKEKGGL and a res</li> <li>Patient SC12(HLA A1 immunodominant resp</li> <li>GGKKKYKLK responsible</li> <li>Patient SC11(HLA A1</li> </ul>	sponse to GEIYKRWII the B8/39, Cw0701/0702, it can be specified by the B8, Cw0201, DR3/11,		ed therapy started during acute of KRWII, DCKTILKAL, GGKK remained on therapy for 40 days	infection and maintained an KKYKLK – GEIYKRWII and s, then reinitiated HAART at day 640
p24 (127–135)	<ul> <li>individuals treated dur</li> <li>The breadth and specifindividuals with prima (Group 3), using 259 c</li> <li>Previously described a</li> </ul>	ing chronic infection ficity of the response was ry infection but post-sero overlapping peptides spar and newly defined optima	s determined using ELISPOT by study	ring 19 individuals with pre-sero individuals who responded to Nef ise	HAART given during chronic infection
p24 (127–135)	period including therap	py with standard treatme			Oxenius2002b 7-1 infected patients were studied over a rebound rates, plateau viral loads, or
p24 (127–135)	p24 <b>Vaccine</b> Vector/Type:	GEIYKRWII  DNA prime with vaccini	HIV-1 infection, Vaccine a MVA boost Strain: subtype A H	human (B8) IV component: p17, p24, polye	Hanke2000, Wee2002 pitope

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
	which could direct the conserved, often immu Kenya. A DNA and M included in the polyep.  • Multiple CD4+ or CD3 assays after vaccinatio	protein to the cell memb nodominant epitopes that VA prime-boost vaccinat tope string [Hanke2000] 3+ T-cell vaccine-induced n of 5 macaques. The res	ontains p24 and p17, in a reversed order and inhibit efficient peptide proof to were selected to have particularly gion protocol using the HIVA antigen.  It responses to peptide pools were det ponse to the Mamu A*01 SIV p27 epated macaques, possibly because of	cessing and class I presentation, a cood cross-reactive potential for the will be used in a phase III clinical ected using intracellular cytokine pitope p11C (CTPYDINQM), inc	s well as a polyepitope string of the A-clade epidemic in Nairobi, al trial in Kenya. This epitope is staining and IFNgamma Elispot luded in the polyepitope region, was
p24 (127–136)	<ul><li>24 epitopes were descr</li><li>Serial peptide truncation</li><li>Subject 00RCH87 was</li></ul>	epitope responses in HIV ibed – 8 were novel, 8 us ons were used to define on not on HAART, viral los	HIV-1 infection  -1 infected minority women living in sed new restricting elements but were ptimal epitopes for CTL cell lines is ad 8300, CD4 count 313  8, 3/6 (50%) recognized this epitope	previously defined epitopes, and	
p24 (128–135)	p24 (260–267 LAI) • C. Brander notes this i	EIYKRWII s a B*0801 epitope		human (B*0801)	Brander2001
p24 (128–135)	p24 (260–267 LAI)  • Defined in a study of the	EIYKRWII ne B8 binding motif		human (B8)	Goulder1997g
p24 (128–135)	<ul><li>peptides in the study</li><li>Three peptides GSEEI contained the dominan</li><li>Five peptides RLRPGO</li></ul>	RSLYNTVATL (p17 res t Gag-specific epitope in GKKHYMIKHLVW (p1 EQA (p24 161-177), and	HIV-1 infection is epitope in a HIV+ Caucasian living idues 71-85), SALSEGATPQDLNTI 31 out of 44 B-clade infected indivic 7 20-36), ELRSLYNTVATLYCV (p1 I SILDIKQGKEPFRDY (p24 149-16	MLNTVG (p24 41-60), and WEK luals from Boston who showed G 7Gag 74-88), SALSEGATPQDL	ag-CTL responses NTMLNTVG (p24 41-60),
p24 (128–135)	<ul><li>study</li><li>Three peptides GSEEL contained the dominan</li><li>Five peptides RLRPGO</li></ul>	RSLYNTVATL (p17 res t Gag-specific epitope in GKKHYMIKHLVW (p1 EQA (p24 161-177), and	HIV-1 infection is epitope in a HIV+ South African – idues 71-85), SALSEGATPQDLNT! 31 out of 44 B-clade infected individ 7 20-36), ELRSLYNTVATLYCV (p1 I SILDIKQGKEPFRDY (p24 149-16	MLNTVG (p24 41-60), and WEK duals from Boston who showed G 7Gag 74-88), SALSEGATPQDL	ag-CTL responses NTMLNTVG (p24 41-60),
p24 (128–135)	p24 (SF2) • Epitope name: EI8 • This peptide elicited a	EIYKRWII weak CTL response duri	HIV-1 infection  ng acute HIV-1 infection in patient P	human (B8)	Goulder2001a

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
			IGW, ISPRTLNAW, and KAFSPEVIPM L were detectable at 5 months post-infec		ction; CTL responses to SLYNTVATL,
p24 (128–135)	<ul> <li>with viral load in patien</li> <li>Most patients have high</li> <li>In 15 of the patients, th</li> <li>4/13 patients that reacted load – these mutations</li> <li>Stimulation with HLA-</li> </ul>	nts with high CD4, but in levels of HIV-specific e proportion of IFN ga ed with EIYKRWII dis were: Patient 156 (KIV B8 p24 and Nef epitop	HIV-1 infection tudy HLA-A2, B8 and B57 CTL in 54 pa in patients with CD4 T-cells below 400 l c T-cell expansions, but many of these ce amma producing tetramer cells correlated splayed epitope mutations in a minority o YKRWMI), Patient 36 (EIYKRRII), Patie pes significantly increased Nef-specific T- ducing Nef-specific T-cells within the T-c	high tetramer frequencies were ills aren't functional with AIDS-free survival of sequences, which did not con- tent 656 (KIYKRWII, EIYERW cell numbers in 2 patients (748)	found despite high viral load relate with disease progression or viral fMI), and Patient 159 (EIYKRWVI). 8 and 1113)
p24 (128–135)	• HIV-specific CD8+ T c CD27 expression on H	ells expressed lower le IV-specific cells, sugge	HIV-1 infection e staining was used to study the function of evels of perforin than CMV-specific CD8- esting impaired maturation e activated virus-specific CD8+ T cells pro-	+ T cells from the same donor,	and this was associated with persistent
p24 (128–135)	p24 (128–135)  • B8-restricted CTL acco	EIYKRWII ounted for about 1/3 of	HIV-1 infection the total CTL response in one individual	human (B8)	Day2001
p24 (128–135)	precursor frequency (li	miting dilution assay [	HIV-1 infection nctional assays in 42 people with chronic LDA]) d to be active, and inert CTL were not for		
p24 (128–135)	<ul><li>specific T-cell response</li><li>Nef epitope recognition</li></ul>	es by Elispot and Tetra n was detected in all 4	HIV-1 infection successful anti-viral therapy but with ongoiner staining, maintained for 2-4 years aft subjects, gp120, Pol and Gag-specific in aediate maturation phenotype characterizes	ter initiation of HAART. 1 or 2 subjects.	-
p24 (129–136)	Phe, Leu or Ile at the C  This peptide induced C	term) – 53 of the 59 p TL in 1/4 HIV-1+ peo			-
p24 (129–138)	p24 (263–272 SF2) • Defined using reverse i Phe, Leu or Ile at the C		HIV-1 infection HLA-A*2402 binding peptides were pred peptides bound A*2402	human (A*2402) icted by searching for A*2402	Ikeda-Moore1997 anchors in HIV proteins (Tyr at 2, and

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
	<ul><li>This peptide induced C</li><li>IYKRWIILGL bound t obtained</li></ul>		ole tested in strength, the epitope can be processed	in a vaccinia construct and present	ed – two specific CTL clones were
p24 (129–138)		eptides from this databa	HIV-1 infection TL that reacted to SLYNTVATL, calling ase were used to screen for INFγ respon onded to IYKRWIILGL		Betts2000 odominant
p24 (130–148)	p24 (265–280 BRU) • Used as a positive cont	YKRWIILGLNKIV rol for HLA specificity		human (B27)	Dadaglio1991
p24 (131–139)	<ul><li> Of more than 150 chim</li><li> CTL responses were st epitopes that are recogn</li></ul>	npanzees that have been udied in two HIV-1 info nized in humans in the in which presents this I	HIV-1 infection h long-term survival – among them are la reported to be infected with HIV-1, onlected chimpanzees that have strong CTI context of HLA-B*27 and HLA-B*57 Patr-B*03 epitope is HLA B*2705 but the	HLA-B*27 and HLA-B*57 y one has developed AIDS responses, and they were found to	
p24 (131–140)		l cytotoxic activity agai five children were map	nst at least one HIV protein was detecte pped using synthetic peptides and second		Buseyne1993a
p24 (131–140)	<ul> <li>Increases in gamma int</li> </ul>	terferon producing cells 27 individuals, the domi	HIV-1 infection I and highly specific, and found to work s were observed in response to anti-retro inant response in gag measured by both bitope	viral therapy using single cell IFN-	gamma-production ELISPOT
p24 (131–140)	p24 (263–272 SF2) • Epitope invariant acros	KRWIILGLNK s clades A, B, C, and D	HIV-1 infection	human (B*27)	McAdam1998
p24 (131–140)	p24 (260–269 HIV-2) • C. Brander notes this is	RRWIQLGLQK s a B*2703 epitope		human (B*2703)	Brander2001
p24 (131–140)	CD8+ T cells were four viral load was also four All three patients were	nd prior to seroconvers nd B*2705, with HLA all variants KRWIILGGL	HIV-1 infection ecific CTL responses were studied durir ion, and there was a close temporal rela eles: A1, A30/31, B*2705, B35; A1, A3 NK and KRWIIMGGLNK were used – GLNK	tionship between the number of circles (*0301, B7, B2705; and A*0201, A*	culating HIV-specific T cells and 60301, B2705, B39

HXB2 Location	<b>Author's Location</b>	Sequence	Immunogen	Species (HLA)	References
	<ul> <li>subjects showed a dom</li> <li>The subject with A*020</li> <li>Weak responses were of B*2705</li> <li>No acute response was</li> </ul>	inant response to the B*2 D1 had a moderatly strong bserved to A*301-RLRF detected to the following		and B7-TPGPGVRYPL in the suits 301-KIRLRPGGK, A*301-AIFQ	bject who was HLA A1, A*0301, B7, QSSMTK, A*301-TVYYGVPVWK,
p24 (131–140)	p24 (263–272 LAI) • C. Brander notes this is	KRWIILGLNK a B*2705 epitope	HIV-1 infection	human (B*2705)	Brander2001
p24 (131–140)	<ul><li>patient a substitution of</li><li>The R264K mutations</li><li>Positions 260, 264, and</li></ul>	glycine at HIV-1 gag rewere associated with a Line 268 all lie along one asp	sidue 264 (R264G) was detected – the 268M mutation that may be compensed.	tese substitutions reduce binding satory, and R264G occurred in coein, a region that is important for	
p24 (131–140)	• HIV-specific CD8+ T c CD27 expression on H	ells expressed lower leve V-specific cells, suggest	-	8+ T cells from the same donor,	and this was associated with persistent
p24 (131–140)	<ul> <li>The HIV-1 subtype A f which could direct the conserved, often immurkenya. A DNA and M included in the polyepi</li> <li>Multiple CD4+ or CD8 assays after vaccination</li> </ul>	ocused vaccine HIVA co protein to the cell membrandominant epitopes that VA prime-boost vaccination tope string [Hanke2000]. + T-cell vaccine-induced to f 5 macaques. The response	HIV-1 infection, Vaccine MVA boost <i>Strain:</i> subtype A <i>E</i> ntains p24 and p17, in a reversed order and inhibit efficient peptide process were selected to have particularly group protocol using the HIVA antigen responses to peptide pools were detected to the Mamu A*01 SIV p27 eparted macaques, possibly because of	der relative to the Gag polyprotein bessing and class I presentation, a cood cross-reactive potential for the will be used in a phase III clinical ected using intracellular cytokine bitope p11C (CTPYDINQM), inc	to prevent myristylation of p17, s well as a polyepitope string of he A-clade epidemic in Nairobi, l trial in Kenya. This epitope is staining and IFNgamma Elispot luded in the polyepitope region, was
p24 (131–140)	<ul> <li>This is a highly conserve</li> </ul>	nors make a response to yed epitope	HIV-1 infection use progression this epitope, usually an immunodom position 2, and L in the C-term position	-	Goulder1997c, Goulder1997a

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
	KRWIILGLNK and an	R2K change, KKWIIL	scape that discusses this epitope in the GLNK, show little difference in titrat CTL for over 24 hours – minigene tra	ion curves, yet the K2 variants fa	il to bind to targets for more than 1
p24 (131–140)	p24 (260–269 HIV-2) • HIV-2, HLA-B*2703,	RRWIQLGLQK S. Rowland-Jones, Pers.	. Comm.	human (B27)	Brander1996b
p24 (131–140)	p24 (263–272 LAI) • The capacity of dendri	KRWIILGLNK tic cells to process and p	HIV-1 infection present antigen and stimulate anti-HIV	human (B27) V-1 CTL memory responses was	Fan1997 studied
p24 (131–140)	<ul><li>delivery of protein alor</li><li>Chloroquine administre pitopes were processe</li></ul>	ne ation enhanced epitope ed by classical proteason	presentation, and brefeldin A and pep	tide aldehyde inhibitors inhibited	Zheng1999 ced memory CTL response relative to l antigen presentation, suggesting
p24 (131–140)	<ul><li>cells was followed in v</li><li>Seven HIV+ people we</li></ul>	vivo ere studied, and all show	HIV-1 infection  varing MHC tetramers in combination  ved expansions of particular TCR BV  B expansions persisted for 2 to 3 year	clones, often several, relative to	
p24 (131–140)	p24 • Described in this revie	KRWIILGLNK w as the first identified I	HIV-1 infection HIV CTL epitope	human (B27)	Rowland-Jones1997
p24 (131–140)	p24 (263–272 LAI) • Clustering of Gag p24	KRWIILGLNK CTL epitopes recognize	HIV-1 infection and in 29 HIV-infected people	human (B27)	Buseyne1993b
p24 (131–140)	p24 (263–272 LAI) • Review of HIV CTL e	KRWIILGLNK pitopes	HIV-1 infection	human (B27)	McMichael1994
p24 (131–140)	p24 (263–272) • Naturally occurring va	KRWIIMGLNK riant KRWIILGLNK ma	HIV-1 infection ay act as antagonist	human (B27)	Klenerman1994
p24 (131–140)	p24 (263–272) • Naturally occurring va	KRWIIMGLNK riant KRWIILGLNK ma	HIV-1 infection ay act as antagonist	human (B27)	Klenerman1995
p24 (131–140)	<ul> <li>TCR usage showed a C</li> </ul>	CTL clonal response to t	HIV-1 infection ne indicating that new populations of his epitope that persisted over 5 years resent between 0.2 and 1% of the tota	3	Moss1995
p24 (131–140)	p24 (265–276) • Included in HLA-B27	KRWIILGLNK binding peptide compet	ition study	human (B27)	Carreno1992

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
p24 (131–140)		view of immune escape th	HIV-1 infection e variation was observed in the imn at points out that there may be a pro		Goulder1997a, Phillips1991 ive to B8 epitope 7, and that HLA-B8 individuals tend to
p24 (131–140)	B27, but doesn't chang	KRWIILGLNK were introduced and viral e viral viability in vitro view of immune escape th	-	human (B27) ed – an Arg to Lys change at anc	Goulder1997a, Nietfeld1995 hor position P2 abrogates binding to
p24 (131–140)	p24 (263–272) • Longitudinal study of C	KRWIIMGNK CTL response and immuno	HIV-1 infection e escape – the form KRWIILGNK v	human (B27) was also found, and both forms s	Nowak1995 timulate CTL
p24 (131–140)	<ul> <li>one A subtype infectio</li> <li>Pol reactivity: 8/8 had</li> <li>Gag reactivity: 7/8 reac</li> <li>Nef reactivity: 7/8 reac</li> <li>Env reactivity: 3/8 reac</li> </ul>	n from a person living in I CTL to A subtype, and 7/2 eted with A or B subtype g ted with A subtype, and 5	France originally from Togo, to diffe 8 to B subtype, and HIV-2 Pol was a gag, 3/8 with HIV-2 Gag /8 with B subtype, none with HIV-2 with B subtype, none with HIV-2 En	erent antigens expressed in vacci not tested 2 Nef	Durali 1998 , and 1 AG recombinant infections) and nia
p24 (131–140)	<ul> <li>In 4/6 cases, this was the Two of the cases had an</li> <li>The arginine to lysine seems.</li> </ul>	switch is in an anchor residual		due to severely diminished bindin	
p24 (131–140)	<ul><li>deletion in CCR5</li><li>In Gambia there is exp seems to be protective</li></ul>	osure to both HIV-1 and F	sed African female sex workers in C IIV-2, CTL responses to B35 epitop was not HIV-1 and HIV-2 cross-rea	pes in exposed, uninfected wome	Rowland-Jones1999  - these women had no delta 32  n are cross-reactive, and the B35 allele
p24 (131–140)	<ul> <li>Based on EpiMatrix pr were shown to bind to</li> <li>Two of these 12 peptid</li> </ul>	edictions, 28 peptides wer the predicted HLA molecues had been previously ide		oinding assays for potential HLA KRWILGLNK and HLA-A2 IL	Schafer1998  A2 or B27 binding, and 12 of these  KEPVHGV

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References		
p24 (131–140)	<ul><li>immunologically nor</li><li>No direct CTL were</li></ul>	mal HIV-infected (INHI) cas found in any of the six INHI	HIV-1 infection HIV-infected people who were infeses occur at a frequency between 0.1 s, but above background CTLp activative peptides based on HLA binding	and 1% in the infected populate it was founded in 3/6 INHIs			
p24 (131–140)	<ul> <li>individuals treated du</li> <li>The breadth and specindividuals with prim (Group 3), using 259</li> <li>Previously described</li> </ul>	aring chronic infection difficity of the response was d diary infection but post-seroco overlapping peptides spanni and newly defined optimal e	etermined using ELISPOT by study	ing 19 individuals with pre-sero individuals who responded to H Nef se	HAART given during chronic infection		
p24 (131–140)	<ul> <li>HIV-1-infected fema</li> <li>Responses in HEPS verduced risk of infect women</li> <li>43/91 HEPS women</li> </ul>	le Nairobi sex workers women tended to be lower, action, and there was a shift in had CD8+ responses and det d an A2 response to ILK(D/E		es in 91 HIV-1-exposed, persistent HLA presenting molecules the pon late seroconversion to epitor.  EPS women increased with the contract of the policy of t	at have previously been associated with pes recognized by the HIV-1 infected duration of viral exposure		
p24 (131–140)	p24 (131–140)	KRWIILGLNK	HIV-1 infection	human (B27)	Day2001		
p24 (131–140)	p24 (260–299)	RRWIQLGLQK	HIV-1 infection	human (B27)	Day2001		
p24 (131–140)	p24 (131–140) KRWIILGLNK HIV-1 infection human (B27) Goulder2001b  Epitope name: KK10  85% of B27+ adults have CTL that recognize this epitope, but only 2/6 children did  Responses to this dominant B27-restricted Gag epitope are present during the time of decreasing viral load in acute infection  Three children who shared B27 with their mothers did not respond to this epitope and inherited escape mutations from their mothers  A transmitted R132T anchor residue mutation abrogated binding to B27  In the three children infected with the non-binding KK10 variants, the dominant CTL specificity was still HLA-B27-restricted, but it was directed against an epitope in p17, IRLRPGGKK, only rarely recognized in adults when KRWIILGLNK is the dominant response  Mutations in this epitope were observed in autologous clones of subjects who were B27-positive with a higher frequency than those who were B27-negative (P = 0.0005)  These mutations are being sexually transmitted in adult infections						
p24 (131–140)	• Epitope name: Gag-F	KRWIILGLNK	HIV-1 infection	human (B27)	Sabbaj2002b		

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
	Among HIV+ individual	als who carried HLA B2	27, 2/3 (66%) recognized this epitope		
p24 (131–140)	there is concern proteat relevant concentrations • RTV did not reduce and (A2)).	se inhibitors may advers of RTV when the prote- tigen presentation and co processing and assemb	HIV-1 infection in the 20S proteasome in vitro, as does sely effect CTL epitope processing, but the asome is functioning in an intracellular concentration of the two immunodominarily of HLA-B35 or -A2, which are assem	his paper indicates that process context. ht Gag CTL epitopes (KRWII	ssing is not inhibited at therapeutically MGLNK (B27) and SLYNTVATL
p24 (131–140)	CTL epitopes (http://hi  60 epitope responses w magnitude of the respo CD8+ T-cells is higher  1 year post-HAART tre in PB, and 13/25 epitop Treatment interruption become undetectable ir  Breakdowns of epitope responded to A24-RW8	and lymph node (LN) Cly-web.lanl.gov/content/lere detected in both PB nse was similar in LN are in the LN. catment in five patients so the responses in the PB be following HAART induction the PB, and the addition responses were shown as (Nef), B7-IL9(gp41), A	HIV-1 infection  D8+ T-cell responses were compared in hiv-db/REVIEWS/brander2001.html) for and LN samples of the 15 patients, and and PB, but the percentage of CD8+ T cell studied, the magnitude of the CD8 T-cell ecame undetectable, in contrast to 5/26 is used resulted in increased viremia accommon of 9 novel epitope responses. for 4 individuals. Patient C displayed the \$\text{124-RL9(gp41)}, A24-YL8(gp41), and B'Y11(p17), A32-PW10(RT), A30-KY11(	r each person's class I HLA a an additional 8 responses wer lls in the LN is lower so the n response was decreased in both the LN. panied by the restoration of the greatest response to B27-KF7-TM9(Nef). Patient D also d	lleles. The detected only in LN. The total umber of HIV-specific cells per million of the LN and PB, but more dramatically the detection of 13 epitopes that had \$\text{K10(p24)}\$, and in decreasing order also displayed the greatest response to
p24 (131–140)	<ul><li>assays of target cells ex</li><li>Subject AIHP-6 (Thai, subtypes A, B, C, D, F,</li></ul>	epressing recombinant very CDF01-AE infected) re G, and H, and this epitor	HIV-1 infection isolated from individuals infected with accinia viruses expressing HIV-1 gag, er cognized this epitope. This subject show ope was perfectly preserved in all of thes quence which had a R->K mutation in p	nv, nef and pol from many cla yed cross-subtype CTL resporte but subtype A which had th	des. uses to gag constructs derived from
p24 (131–142)	p24 (265–276) • Epitope examined in th	KRWIILGLNKIV e context of peptide bind	Peptide-HLA interaction ding to HLA-B27	human (B27)	Jardetzky1991
p24 (131–142)	p24 (263–274 LAI) • The capacity of dendrit	KRWIILGLNKIV ic cells to process and p	HIV-1 infection resent antigen and stimulate anti-HIV-1	human (B27) CTL memory responses was	Fan1997 studied
p24 (131–142)	p24 (131–142) • One of the 51 HIV-1 ep HLA alleles	KRWIILGLNKIV oitopes selected by Ferra	HIV-1 infection ri et al. as good candidate CTL epitopes	human (B27) for vaccines by virtue of beir	Ferrari2000 ng conserved and presented by common

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
p24 (131–145)	within the three most re  Three peptides GSEELI contained the dominant  Five peptides RLRPGG	cognized peptides in the study RSLYNTVATL (p17 residues 71- Gag-specific epitope in 31 out of KKHYMIKHLVW (p17 20-36), EQA (p24 161-177), and SILDIK	HIV-1 infection e in a HIV+ African American living 85), SALSEGATPQDLNTMLNTV 44 B-clade infected individuals froi ELRSLYNTVATLYCV (p17Gag 74 QGKEPFRDY (p24 149-164) conta	G (p24 41-60), and WEKIF n Boston who showed Gag -88), SALSEGATPQDLN	RLRPGGKKKYKLK(p17 16-30) c-CTL responses FMLNTVG (p24 41-60),
p24 (131–145)	p24 (263–277 LAI) • Clustering of Gag p24 C	KRWIILGLNKIVMRY CTL epitopes recognized in 29 HI	HIV-1 infection IV-infected people	human (A33)	Buseyne1993b
p24 (131–145)		KRWIILGLNKIVRMY accinia HIV component: Gag ed with rec gag-vaccinia and syntepitope to be mapped	Vaccine thetic peptides	human (B27)	Nixon1988
p24 (131–145)	p24 (266–277 LAI) • Longitudinal study show	KRWIILGLNKIVMRY wing persistence of epitope despit	HIV-1 infection te CTL activity	human (B27)	Meyerhans1991
p24 (131–145)		KRWIILGLNKIVRMY reactive CTL clone, highly conso	HIV-1 infection erved epitope ar cross-reactive with HIV-2 in Row	human (B27) land-Jones98, HIV-2 form:	Nixon1990, Rowland-Jones1999 RRWIQLGLQK
p24 (131–146)	p24 (265–279) • HLA-B27 restricted epi	KRWIILGLNKIVRMYC tope also binds to HLA-A2 and I	HIV-1 infection HLA-B37 in solid phase assay	human (B27)	Bouillot1989
p24 (131–150)	<ul><li>Twelve subjects had CT</li><li>One of these 12 A-2 had</li></ul>	KRWIILGLNKIVRMYSPTSI d CTL specific for more than 1 H L that could recognize vaccinia-ed d CTL response to this peptide was HLA-A3, A32, B51, B62	IV-1 protein	human	Lieberman1997a
p24 (131–150)	p24 (265–284 SF2) • Gag CTL epitope precu	KRWIILGLNKIVRMYSPTSI rsor frequencies estimated	HIV-1 infection	human (Bw62?)	vanBaalen1993
p24 (131–152)	p24 (263–284 BH10)  • Gag CTL response stud	KRWIILGLNKIVRMYSPTS- ILD	HIV-1 infection	human (Bw62)	Johnson1991
p24 (132–145)	Gag	KWILGLNKIVRMY	HIV-1 infection ibute to oligoclonal expansions with	human in the CD57+ CD28- CD8-	Weekes1999a + CTLp populations
p24 (132–145)	-	CTL memory pools for CTL clor	HIV-1 infection a, and the proportion of CD28-CD8+ are specific for two persistent human	_	

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
		of the TCR Vbeta respo	es were studied onses were studied and was found to be highl s to this epitope were Vbeta22.1	y focused, with one TCR	beta-chain sequence tending to
p24 (134–143)	<ul><li>Seroprevalence in this c</li><li>Most isolated HIV strai</li></ul>	cohort is 90-95% and the ns are clade A in Nairob y observed using A or D	HIV-1 exposed seronegative negative prostitutes from Nairobi – these CTL air HIV-1 exposure is among the highest in the pi, although clades C and D are also found – I clade versions of epitopes ade viruses	e world	Rowland-Jones1998b  a cross-reactive, however stronger
p24 (136–145)	p24 (268–277 LAI)  • Predicted from larger pour review of HIV CTL ep  • Also P. Johnson, Pers. (	itopes	HIV-1 infection	human (Bw62)	McMichael1994
p24 (136–146)	<ul><li>A sustained Gag, Env a</li><li>A subject who was B62</li></ul>	nd Nef response was ob 2+ had CTL that recogni	HIV-1 infection long-term non-progressors were isolated and served, and clones were restricted by multipl zed this peptide, p17 KIRLRPGGKKKYKL, d two different $V\beta$ genes, further demonstrate	e HLA epitopes, indicating and one additional unknown	ng a polyclonal response own epitope
p24 (136–146)	p24 (136–146) • One of the 51 HIV-1 ep HLA alleles	LGLNKIVRMYS itopes selected by Ferra	HIV-1 infection ri et al. as good candidate CTL epitopes for v	human (B62) raccines by virtue of being	Ferrari2000 g conserved and presented by common
p24 (137–145)	<ul> <li>within the three most re</li> <li>Three peptides GSEEL contained the dominant</li> <li>Five peptides RLRPGG</li> </ul>	ccognized peptides in the RSLYNTVATL (p17 res Gag-specific epitope in KKHYMIKHLVW (p1 EQA (p24 161-177), and	HIV-1 infection his epitope in a HIV+ South African living in the study hidues 71-85), SALSEGATPQDLNTMLNTV hidues 71-85, SALSEGATPQDLNTMLNTV h	G (p24 41-60), and WER om Boston who showed G 4-88), SALSEGATPQDL	XIRLRPGGKKKYKLK(p17 16-30) Gag-CTL responses NTMLNTVG (p24 41-60),
p24 (137–145)	p24 (272–280 LAI) • C. Brander notes this is	GLNKIVRMY a B*1501 epitope	HIV-1 infection	human (B*1501)	Brander2001
p24 (137–145)	GLNKIVRMY  • As long as a strong CTI	L response to SLYNTVA	HIV-1 infection sion, but it presents a study of a shift from an ATL was evident, the epitope variants SLFNT de became undetectable, the CTL response she dominant form	VATL or SLYNTIATL do	ominated the viral population –

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
p24 (137–145)	recognized peptides in  Three peptides GSEEL contained the dominan Five peptides RLRPGO	the study  RSLYNTVATL (p17 residues t Gag-specific epitope in 31 o GKKHYMIKHLVW (p17 20-EQA (p24 161-177), and SIL	ut of 44 B-clade infected individua 36), ELRSLYNTVATLYCV (p170	LNTVG (p24 41-60), and WER als from Boston who showed G Gag 74-88), SALSEGATPQDL	KIRLRPGGKKKYKLK(p17 16-30) Gag-CTL responses
p24 (137–145)	<ul> <li>individuals treated duri</li> <li>The breadth and specifindividuals with primare (Group 3), using 259 o</li> <li>Previously described at</li> </ul>	ing chronic infection acity of the response was deter ry infection but post-seroconverlapping peptides spanning and newly defined optimal epit	rmined using ELISPOT by studyin	g 19 individuals with pre-sero ndividuals who responded to E	IAART given during chronic infection
p24 (137–145)	p24 (137–145) • No immunodominant r	GLNKIVRMY responses were detected to four	HIV-1 infection ar B62-restricted epitopes tested	human (B62)	Day2001
p24 (143–150)	p24 (273–283 IIIB) • C. Brander notes this is	RMYSPTSI s a B*5201 epitope	HIV-1 infection	human (B*5201)	Brander2001
p24 (143–150)	recognition or prevent not linked to variations		g that viral escape from the HLA-As epitope		Brander1999  I found not to adversely affect CTL se against SLYNTVATL is probably
p24 (143–150)	<ul> <li>Detection of CTL escarinfants</li> </ul>	pe mutants in the mother was	HIV-1 infection context of mother-to-infant transm associated with transmission, but t	he CTL-susceptible forms of t	Wilson1999a he virus tended to be found in infected
p24 (143–150)	p24 (143–150) • One of the 51 HIV-1 ep HLA alleles	RMYSPTSI pitopes selected by Ferrari et a	HIV-1 infection al. as good candidate CTL epitopes	human (B52) for vaccines by virtue of being	Ferrari2000 g conserved and presented by common
p24 (151–170)	p24 (283–302 SF2)	LDIRQGPKEPFRDYVDR	FYK HIV-1 infection	human	McAdam1998

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
p24 (155–177)	p24 (287–309)	QGPKEPFRDYVDRFYKTLR- AEQA	Vaccine	murine	Nakamura1997
		eptide HIV component: p24			
		his synthetic peptide generated sp		e response, and antibodies by Nakamura et al., and may not be c	ownest.
		hown to be located in positions 29		by Makamura et al., and may not be c	offect
p24 (157–178)	p24 (290–309)	PKEPFRDYVDRFYKTLRAE- OAS	HIV-1 infection	human (B14)	Musey1997
	• Cervical and peripheral	blood derived CTL clones from a	n HIV-infected woman rec	cognized this epitope	
p24 (159–168)	Gag (291–300)	EPFRDYVDRF	Vaccine	murine (H-2 <sup>d</sup> )	Billaut-Mulot2001
				Strain: LAI HIV component: Ga with IL18 showed lymphoproliferative	
	<ul> <li>Strong but non-lasting I protein boost</li> </ul>	•	·	ssay and DNA prime/DNA boost was	•
		er the multiepitopic DNA or with .18 increased T-cell responses but		duced HIV-1 specific Th1 cytokines by levels	(IL-2 and IFN-gamma)
p24 (159–178)	Gag (291–310) • HLA, viral sequence, an each HIV protein.	EPFRDYVDRFFKTLRAEQAT nd Elispot data was obtained from		human anans; Elispot data was obtained fro	Novitsky2002 m between 55 and 64 subjects for
		ghest percentage of reactive peption	les, and p24 had the highes	st magnitude of HIV-1 responses.	
		g the 8 most reactive C clade pept			
p24 (159–178)	Gag (96ZM651.8)	EPFRDYVDRFFKTLRAEQAT		human (B*44031)	Novitsky2001
				uences from a C subtype infected Bo	
		VVDRF, EPFRDYVDRFFKTLRA		nunodominant region region of Gag ATQEVKNWMTDT) with ELISPOT	
	• 3 of 6 (50%) carriers of	HLA-B*44031 showed CTL resp	onses to the peptide EPFR	DYVDRFFKTLRAEQAT	
p24 (161–170)		FRDYVDRFFK	HIV-1 infection	human	Kaul2001c
				viduals, HEPS, who eventually seroc	
	The epidemiological factorial	ctor associated with seroconversion		es had been defined while seronegati nd HIV-specific CTL activity decline	
	working for a period or  This epitope was recogn	retire nized in 1/22 HEPS sex worker co	introls MI 1732		
p24 (161–170)	p24 (subtype B, D)	FRDYVDRFYK	HIV-1 infection	human (B*1801)	Ogg1998a
p2+ (101-170)	1 . 31	this database, to be B*1801, FRI		numan (D · 1001)	0551770a

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
p24 (161–170)	p24 (subtype B, D) • C. Brander notes this is	FRDYVDRFYK a B*1801 epitope	HIV-1 infection	human (B*1801)	Brander2001
p24 (161–170)	p24 (161–170) • One of the 51 HIV-1 ep HLA alleles	FRDYVDRFYK itopes selected by Ferrar	HIV-1 infection i et al. as good candidate CTL epitopo	human (B18) es for vaccines by virtue of being	Ferrari2000 g conserved and presented by common
p24 (161–170)	p24 (293–302)	FRDYVDRFYK	HIV-1 infection, HIV-1 ex seronegative	posed human (B18)	Kaul2001a
	<ul> <li>HIV-1-infected female</li> <li>Responses in HEPS wo reduced risk of infection women</li> <li>43/91 HEPS women ha</li> <li>Among HLA-B18 women respond to FRDYVDRI</li> <li>The dominant response</li> <li>Four epitopes were confound in three different FRDYVDRF(Y/F)K also</li> </ul>	study CTL responses to a Nairobi sex workers men tended to be lower, n, and there was a shift in d CD8+ responses and doen, 3/4 HEPS and 1/9 HEFY/FK, while infected who to this HLA allele was to sidered to be "resistant exproteins: A2 ILK(D/E)Pso in p24	panel of 54 predefined HIV-1 epitops and focused on different epitopes with the response in the HEPS women up etection of HIV-1-specific CTL in HEIV-1 infected women recognized this men tended to respond to YPLTFGV of this epitope for all 3/4 HEPS cases a pitopes", as they were preferentially in VHGV in RT, A*6802 DTVLEDINI.	h HLA presenting molecules that pon late seroconversion to epitope. EPS women increased with the depitope, likelihood ratio 5.3, p vow WCY/F and for the single HIV-1 infected reactive in HEPS women and so L in Protease, B14 DLNM/TLN(I	t have previously been associated with less recognized by the HIV-1 infected uration of viral exposure alue 0.04, and HEPS women tended to women that responded to this epitope may confer resistance, and these were I/V)V in p24 and B18
p24 (161–170)	p24 Vaccine Vector/Type: D  The HIV-1 subtype A for which could direct the processory conserved, often immunication Kenya. A DNA and MV included in the polyepit  Multiple CD4+ or CD8 assays after vaccination	FRDYVDRFYK  DNA prime with vaccinia ocused vaccine HIVA corprotein to the cell membrandominant epitopes that VA prime-boost vaccination string [Hanke2000].  + T-cell vaccine-induced of 5 macaques. The respective production of the color of	HIV-1 infection, Vaccine MVA boost Strain: subtype A Hatains p24 and p17, in a reversed order ane and inhibit efficient peptide processor protocol using the HIVA antigen were selected to have particularly go on protocol using the HIVA antigen were sponses to peptide pools were determined to the Mamu A*01 SIV p27 epated macaques, possibly because of particular to the macaques of particular to t	human, macaque (B18 IV component: p17, p24, polyepter relative to the Gag polyprotein essing and class I presentation, a pod cross-reactive potential for the will be used in a phase III clinical exted using intracellular cytokine itope p11C (CTPYDINQM), inc	B) Hanke2000, Wee2002 itope to prevent myristylation of p17, s well as a polyepitope string of the A-clade epidemic in Nairobi, al trial in Kenya. This epitope is staining and IFNgamma Elispot luded in the polyepitope region, was
p24 (161–180)	p24 (293–312 SF2) • Of 25 patients, most ha	d CTL specific for more L that could recognize vL response to this peptid	accinia-expressed LAI gag le	human	Lieberman1997a

HXB2 Location	<b>Author's Location</b>	Sequence	Immunogen	Species (HLA)	References
p24 (161–180)	p24 (293–312 SF2) • CTL expanded ex vivo v	FRDYVDRFYKTLRAEQASQD were later infused into HIV-1 infe		human	Lieberman1997b
p24 (161–180)	p24 (293–312 SF2)	FRDYVDRFYKTLRAEQASQD	HIV-1 infection	human (B71)	McAdam1998
p24 (162–172)	p24 (296–306 subtype A)	RDYVDRFFKTL	HIV-1 infection	human (A*2402)	Dorrell1999
	<ul><li>in East Africa</li><li>This epitope is similar to clade sequence change f</li></ul>		-		
p24 (162–172)	p24 (296–306 subtype A) • C. Brander notes this is	RDYVDRFFKTL  an A*2402 epitope	HIV-1 infection	human (A*2402)	Brander2001
p24 (162–172)	<ul> <li>HIV-1-infected female N</li> <li>Responses in HEPS wor reduced risk of infection women</li> <li>43/91 HEPS women had</li> <li>Among HLA-A24 women tended to be reactive in N</li> <li>The dominant response to Differences in epitope spassociated with resistance</li> </ul>	Nairobi sex workers men tended to be lower, and focus a, and there was a shift in the resp al CD8+ responses and detection of en, 0/4 HEPS and 6/10 HIV-1 inf HEPS and infected women, RDY to this HLA allele was to this epit pecificity were only seen for response to HIV-1 in this cohort al with a CTL response to A*6802	HIV-1 infection, HIV-1 exposed seronegative 54 predefined HIV-1 epitopes in 91 sed on different epitopes with HLA ponse in the HEPS women upon late of HIV-1-specific CTL in HEPS wone ected women recognized this epitop VDRFFKTL in infected women onlate tope in all of the 6/10 HIV-1 infected conses restricted by class I HLA allel	presenting molecules that he seroconversion to epitopes onen increased with the durate, likelihood ratio 7.2, p vary di women es A2, A24, A*6802, B14,	ave previously been associated with recognized by the HIV-1 infected ation of viral exposure lue 0.03, and (R)YL(R/K)DQQLL and B18, previously shown to be
p24 (162–172)	p24 (293–312 LAI) • C. Brander notes this is	RDYVDRFYKTL a B*4402 epitope	HIV-1 infection	human (B*4402)	Brander2001
p24 (162–172)	p24 (162–172) • One of the 51 HIV-1 epi HLA alleles	RDYVDRFYKTL topes selected by Ferrari et al. as	HIV-1 infection good candidate CTL epitopes for va	human (B44) accines by virtue of being c	Ferrari2000 onserved and presented by common
p24 (162–172)	p24 (162–172)	RDYVDRFYKTL	HIV-1 infection	human (B44)	Day2001
p24 (162–172)	p24 <b>Vaccine</b> Vector/Type: D	RDYVDRFYKTL  NA prime with vaccinia MVA bo	HIV-1 infection, Vaccine ost <i>Strain:</i> subtype A <i>HIV comp</i>	human, macaque (B44) onent: p17, p24, polyepito	Hanke2000, Wee2002 pe

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
	which could direct the conserved, often immu Kenya. A DNA and M included in the polyep  • Multiple CD4+ or CD3 assays after vaccinatio	protein to the cell membrandominant epitopes that VA prime-boost vaccinati itope string [Hanke2000]. 8+ T-cell vaccine-induced n of 5 macaques. The resp	ntains p24 and p17, in a reversed order ane and inhibit efficient peptide proces were selected to have particularly go on protocol using the HIVA antigen were proposed to the Mamu A*01 SIV p27 epiated macaques, possibly because of p	essing and class I presentation, a od cross-reactive potential for the vill be used in a phase III clinical cted using intracellular cytokine ttope p11C (CTPYDINQM), inc	s well as a polyepitope string of the A-clade epidemic in Nairobi, I trial in Kenya. This epitope is staining and IFNgamma Elispot luded in the polyepitope region, was
p24 (162–172)	p24 (293–312 LAI)	RDYVDRFYKTL	HIV-1 infection	human (B44, A26 or B70)	Ogg1998a
p24 (163–172)	p24 (163–172) • One of the 51 HIV-1 e HLA alleles	DYVDRFYKTL pitopes selected by Ferrar	HIV-1 infection i et al. as good candidate CTL epitope	human (A24) es for vaccines by virtue of being	Ferrari2000 g conserved and presented by common
p24 (164–172)	<ul><li>assays of target cells e</li><li>The Thai subject VAIF Sequence alignments of</li></ul>	xpressing recombinant vac P-4 demonstrated broad Copf this epitope showed con	HIV-1 infection solated from individuals infected with ccinia viruses expressing HIV-1 gag, the cross-reactivity towards gag constant servation for clades B and D, and Y-2 RFFKTL are recognized equally well.	env, nef and pol from many clad ructs derived from subtypes A, F >F substitutions at position 6 for	es.
p24 (164–172)	<ul><li>in East Africa</li><li>This CTL epitope is co CTL reactivity</li><li>CTL reacted with target</li></ul>	e individuals with non-cla	rpe, and B clade sequences tend to have context A26 or B70 – the epitope ha	ve a change from F to Y, YVDRI	Dorrell1999  Type C – their infections all originated  FYKTL – both variants showed strong sition 2 and Leu at the carboxy
p24 (164–172)	Gag (298–306 subtype A)  In vitro restimulation of carrying A or D subtype	of CTL specific for dominate	HIV-1 infection, in vitro stimulation ant epitopes from infected individuals	human (A26 or B70) s is possible using recombinant n	Dorrell2001 nodified vaccinia virus Ankara (MVA)
p24 (164–172)	<ul><li>4 subjects who response</li><li>An HIV-1 B variant of</li></ul>	sed to the CTL epitope YV the epitope YVDRFYKT	and full length HIV-1 genome sequence VDRFFKTL – all were HLA-B*1510 L has been described, and was recogn 26 or B70 – HLA-B*1510 is equivalen	and also shared HLA-Cw03, sunized byCTL from an HIV-1 sub	otswanan cohort. ggesting linkage disequilibrium type A-infected patient, and the HLA

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References		
p24 (164–172)	p24 (164–172) • One of the 51 HIV-1 epi HLA alleles	YVDRFYKTL itopes selected by Ferrari	HIV-1 infection et al. as good candidate CTL epitop	human (B70) bes for vaccines by virtue of being	Ferrari2000 g conserved and presented by commor		
p24 (166–174)	p24 (298–306 LAI) • C. Brander notes this is	DRFYKTLRA a B*1402 epitope	HIV-1 infection	human (B*1402)	Brander2001		
p24 (166–174)	DRFYKILRA, a natural	lly occurring variant, was	HIV-1 infection DS Foundation ARIEL Project, a m found in mother, and is recognized s found in infant and is not recogniz	although less reactive	Wilson1996 audy		
p24 (166–174)	p24 (298–306 IIIB)  • The consensus peptide f  • The consensus peptide f		HIV-1 infection FYKTLRA FFKTLRA and it is equally reactive	human (B14)	Cao1997a		
p24 (166–174)	<ul><li>chain ζ, and transducing</li><li>The response using univ</li></ul>	g into CD8+ cells versal-receptor-bearing C in terms of kinetics and e	fficiency		Yang 1997b  The saling domain of the T cell receptor all occurring responses of CTL-clones		
p24 (166–174)		ss-reactivity could protectus is identical to the B cla	t against both A and D and confer pa	previously-defined B clade epito	Rowland-Jones1998a  opes that tended to be conserved in A subtypes are circulating		
p24 (166–174)	p24 (298–306 LAI)	DRFYKTLRA	HIV-1 infection	human (B14)	Harrer1996b		
p24 (166–174)	p24 (298–306) DRFYKTLRA HIV-1 infection human (B14) Yang1996  • CD4+ cell lines acutely infected with HIV were studied to determine their susceptibility to lysis by CTL  • Clones specific for RT lysed HIV-1 infected cells at lower levels than Env or Gag specific clones  • The distinction was thought to be due to lower expression of RT relative to Env and Gag  • CTL can lyse infected cells early after infection, possibly prior to viral production						
p24 (166–174)		appressive soluble factors	HIV-1 infection acentrations comparable to those four $\beta = MIP-1\alpha$ , MIP-1 $\beta$ , RANTES, after the HLA-matched cells		Yang 1997a		
p24 (166–174)			in vitro stimulation and dendritic cells to stimulate prima C – the dendritic cells performed bet				

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
	<ul><li>macrophages were not</li><li>A weak response to Kl</li></ul>	able to prime a CTL in LTPLCVSL was stimuted.	pitopes DRFYKTLRA and GEIYKRWI response against DRFYKTLRA llated using macrophages as the APC following previously-defined HIV epito		
p24 (166–174)	deletion in CCR5	posure to both HIV-1 a	xposed African female sex workers in G nd HIV-2, CTL responses to B35 epitopective, [Harrer1993]		
p24 (166–174)		ipe mutants in the mot	HIV-1 infection s in the context of mother-to-infant trans her was associated with transmission, bu pe mutants		Wilson1999a the virus tended to be found in infected
p24 (166–174)	<ul> <li>three most recognized</li> <li>Three peptides GSEEI contained the dominan</li> <li>Five peptides RLRPGO</li> </ul>	peptides in the study LRSLYNTVATL (p17 at Gag-specific epitope GKKHYMIKHLVW ( LEQA (p24 161-177),	HIV-1 infection In this epitope in 2/5 HIV+ individuals where the septope in 2/5 HIV+ individuals where sides 71-85), SALSEGATPQDLNTM in 31 out of 44 B-clade infected individing 17 20-36), ELRSLYNTVATLYCV (p1 and SILDIKQGKEPFRDY (p24 149-16)	MLNTVG (p24 41-60), and WEI tuals from Boston who showed Coroga 74-88), SALSEGATPQDI	KIRLRPGGKKKYKLK(p17 16-30) Gag-CTL responses LNTMLNTVG (p24 41-60),
p24 (166–174)	recognized during the	initial decline in viren	HIV-1 infection is epitope in initial control of viremia in nia not evident until 18 months post-presen		Goulder2001a everal subdominant CTL epitopes
p24 (166–174)	p24 (166–174) • One of the 51 HIV-1 e HLA alleles	DRFYKTLRA pitopes selected by Fe	HIV-1 infection rrari et al. as good candidate CTL epitop	human (B14) bes for vaccines by virtue of bein	Ferrari2000 g conserved and presented by common
p24 (166–174)	<ul> <li>individuals treated dur</li> <li>The breadth and specifindividuals with prima (Group 3), using 259 c</li> </ul>	ing chronic infection ficity of the response v ry infection but post-s overlapping peptides sp	HIV-1 infection alted in a narrower CTL response, strong was determined using ELISPOT by study eroconversion therapy (Group 2), and 10 panning p17, p24, RT, gp41, gp120 and 10 mal epitopes were tested for CTL respon	ring 19 individuals with pre-sero ) individuals who responded to F Nef	conversion therapy (Group 1), 11

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References					
	Number of HLA-B14+	individuals that had a C	TL response to this epitope broken down by	y group: 3/3 group 1, 1/2 g	group 2, and 0/0 group 3					
p24 (166–174)	p24 (298–306)	DRFFKTLRA	HIV-1 infection, HIV-1 exposed seronegative	l human (B14)	Kaul2001a					
	<ul> <li>Variants DRF(F/W)KT</li> </ul>	LRA are specific for clac	——————————————————————————————————————							
		• ELISPOT was used to study CTL responses to a panel of 54 predefined HIV-1 epitopes in 91 HIV-1-exposed, persistently seronegative (HEPS) and 87 HIV-1-infected female Nairobi sex workers								
	• Responses in HEPS we	omen tended to be lower,	and focused on different epitopes with HLz n the response in the HEPS women upon la							
	<ul> <li>43/91 HEPS women ha</li> <li>Among HLA-B14 wor to respond to DLNMM</li> <li>The dominant response</li> <li>Differences in epitope</li> </ul>	nen, 0/4 HEPS and 6/7 H ILNIV/DLNTMLNVV, w e to this HLA allele was t	etection of HIV-1-specific CTL in HEPS w IIV-1 infected women recognized this epitor while infected women tended to respond to to this epitope for all of the 6/7 HIV-1 infector in for responses restricted by class I HLA al	pe, likelihood ratio 14.4, p DRF(F/W)KTLRA ted women	value 0.004 and HEPS women tended					
p24 (166–174)	p24 (SF2) • This epitope was mapper an HLA-B60 individual	-	HIV-1 infection by identifying new HLA-B60 epitopes, and	human (B14) was one of the epitopes p	Altfeld2000b resented by another HLA molecule in					
p24 (166–174)	exogenous protein and	by a fusion protein of ar allows processing throug	HIV-1 infection izes DRFYKTLRA. n HIV protein and anthrax lethal factor (LF th the MHC class I pathway. This strategy the fixed by the strategy of the strateg	for CTL detection could a	llow antigen presentation without					
p24 (166–174)	<ul><li>T-cells, detected by int</li><li>Ghonorrhea caused the</li></ul>	racellular cytokine produ weaker HIV-1 specific C	HIV-1 infection  n sex workers caused a functional deficience ction and tetramer assays, while not affecti CTL responses in 4 HIV-1 exposed persister CTL in 2 HEPS subjects were shown to have	ng the total number of epi ntly seronegative (HEPS)	tope-specific CTLs. women to become undetectable by					
p24 (166–174)	<ul> <li>The HIV-1 subtype A is which could direct the conserved, often immurkenya. A DNA and M included in the polyepi</li> <li>Multiple CD4+ or CD8 assays after vaccination</li> </ul>	ocused vaccine HIVA co protein to the cell membi nodominant epitopes that VA prime-boost vaccinati tope string [Hanke2000]. 3+ T-cell vaccine-induced n of 5 macaques. The res	HIV-1 infection, Vaccine a MVA boost <i>Strain:</i> subtype A <i>HIV con</i> ntains p24 and p17, in a reversed order relarane and inhibit efficient peptide processing t were selected to have particularly good crition protocol using the HIVA antigen will be a responses to peptide pools were detected to ponse to the Mamu A*01 SIV p27 epitope nated macaques, possibly because of process	tive to the Gag polyproteing and class I presentation, oss-reactive potential for the used in a phase III clinical using intracellular cytokin p11C (CTPYDINQM), in	n to prevent myristylation of p17, as well as a polyepitope string of he A-clade epidemic in Nairobi, al trial in Kenya. This epitope is e staining and IFNgamma Elispot cluded in the polyepitope region, was					

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
p24 (166–174)	<ul> <li>Seroprevalence in this</li> <li>Most isolated HIV stra responses are frequentl</li> <li>This epitope is conserv</li> <li>The Clade A version or</li> </ul>	cohort is 90-95% and the ins are clade A in Nairce by observed using A or lead among B and D clade of the epitope, DRFFKL	HIV-1 exposed seronegative prostitutes from Nairobi – these neir HIV-1 exposure is among the highes obi, although clades C and D are also fou D clade versions of epitopes de viruses  FRA, was preferentially recognized by C exposed and uninfected prostitutes	e CTL may confer protection t in the world and – B clade epitopes are often	
p24 (166–175)	<ul> <li>By testing mutations in infectivity</li> </ul>	an HXB2 background,  dy overlaps the major ho	HIV-1 infection term survivor was to this highly conserve it was found that all mutations within the comology region for which highly conserve	ne epitope that abrogated CTL i	recognition also abolished viral
p24 (169–188)	<ul><li>each HIV protein.</li><li>Nef and p24 had the hi</li></ul>	and Elispot data was obt ghest percentage of rea	KNWMTDT HIV-1 infection rained from 105 HIV-1 positive Botswans ctive peptides, and p24 had the highest m clade peptides from among over 350 tes	nagnitude of HIV-1 responses.	Novitsky2002 from between 55 and 64 subjects for
p24 (173–181)	sex workers eventually	seroconverted, and for actor associated with ser r retire	HIV-1 infection aposed, persistently seronegative individuals of these HIV CTL reactive epitopes beconversion was stopping sex work and all ols ML1792	had been defined while seroneg	gative
p24 (173–181)	p24 (305–313) • Originally reported as • Thought to be HLA-Cv		HIV-1 infection t subsequently found not to be presented er and B. Walker)	human (Cw8) by cells transfected with B14	Johnson1991
p24 (173–181)	<ul> <li>and D clades – such cr</li> <li>The A subtype consens</li> <li>The D subtype consens</li> </ul>	oss-reactivity could pro sus is RAeQAtQEV sus is RAEQsQdV	HIV-1 exposed seronegative infected prostitutes from Nairobi using placet against both A and D and confer prostoring or a property of the prop	reviously-defined B clade epito stection in Nairobi where both s	subtypes are circulating
p24 (173–181)	p24 (305–313) • Study of cytokines rele • Thought to be HLA-Cy		HIV-1 infection activated CTL s originally reported (C. Brander, B. Wal	human (Cw8)  Iker, and S. Rowland-Jones, per	Price1995

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
p24 (173–181)	<ul> <li>A sustained Gag, Env ar</li> <li>Despite this being a well could recognize either it</li> </ul>	nd Nef response was ob I defined conserved epi or p24 PQDLNTMLN	HIV-1 infection ong-term non-progressors were isolated and served, and clones were restricted by multiple tope, and thought to be presented by B14, no originally reported (C. Brander, B. Walker, and thought to be presented by B14, no originally reported (C. Brander, B. Walker, and the service of the servi	le HLA epitopes, indicating one of the 11 gag-specific cl	a polyclonal response ones from a B-14 positive subject
p24 (173–181)	p24 (305–313)  • ELISPOT was used to s HIV-1-infected female 1	•	HIV-1 infection, HIV-1 exposed seronegative a panel of 54 predefined HIV-1 epitopes in 9	human (Cw8)  1 HIV-1-exposed, persistent	Kaul2001a tly seronegative (HEPS) and 87
p24 (174–184)	p24 (306–316 LAI) • C. Brander notes this is	AEQASQDVKNW a B*4402 epitope		human (B*4402)	Brander2001
p24 (174–184)	p24 (306–316 LAI) • Pers. Comm. from D. L	AEQASQDVKNW ewinsohn to C. Brander	r and B. Walker, C Brander et al., this databa	human (B*4402, B44) se, 1999	Brander1997
p24 (174–184)		igrated to the lymph no	HIV-1 infection y expanding autologous HIV-1 Gag-specific orders and transiently reduced circulating producets		
p24 (174–184)	<ul> <li>Adoptively transferred gadjacent to cells express</li> <li>The CTL clones express viral replication, sugges</li> </ul>	gene-marked HIV-specing HIV tat-fusion transped CCR5 and localized ting a possible homing	HIV-1 infection Theorem arked CD8 HIV-specific CTL fic CTL homed to specific lymph node sites, scripts, indicative of viral replication among HIV-1 infected cells expressing MIF mechanism and studying antigen specific CTL in vivo		
p24 (174–184)	CD8+ cell IFNgamma p  • In general, during the fit specificities that were not HIV-specific responses of	roduction to measure rest month of treatment vot previously detectable diminished	HIV-1 infection  es was tested in 14 HIV+ patients from an ur esponses viral load decreased and frequencies of HIV-s were newly detected, as were CMV specific use: increases or decreases in pre-existing res	specific CTL tripled and bro c CD8+ PBL – but with cont	padened – eight new HIV tinued viral suppression,
p24 (174–184)	p24 (174–184) • B44-restricted CTL resp	AEQASQDVKNW conse was strongest to t	HIV-1 infection his epitope in one individual	human (B44)	Day2001
p24 (174–184)	p24 • Epitope name: B44-AW	AEQASQDVKNW 11(p24)	HIV-1 infection	human (B44)	Altfeld2002

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
	<ul> <li>CTL epitopes (http://hi</li> <li>60 epitope responses w magnitude of the responses were compared to the response of t</li></ul>	v-web.lanl.gov/contentere detected in both Pense was similar in LN in the LN. catment in five patients be responses in the PB following HAART into the PB, and the addit responses were shown	CD8+ T-cell responses were compared in t/hiv-db/REVIEWS/brander2001.html) for B and LN samples of the 15 patients, and and PB, but the percentage of CD8+ T cell secame undetectable, in contrast to 5/26 induced resulted in increased viremia accomion of 9 novel epitope responses. In for 4 individuals. Patient B displayed the while a third response against epitope A3:	reach person's class I HLA all- an additional 8 responses were ls in the LN is lower so the nur response was decreased in bot in the LN. panied by the restoration of the greatest response to epitope B	eles. detected only in LN. The total mber of HIV-specific cells per million h LN and PB, but more dramatically detection of 13 epitopes that had 44-AW11(p24) and also responded to
p24 (175–186)	<ul> <li>500 – 3 of the men wer</li> <li>Two CTL lines from or</li> <li>Isolation of CTLs spec</li> </ul>	e analyzed in detail ar ne donor recognized th ific to HIV in both ma	HIV-1 infection If and cell-free forms, and HIV-specific CT and had broad CTL to gag, env and policis epitope It is and female urinal tracts provide evidence It issues may be correlated with lower vir	e that virus-specific lymphocy	tes come from the urogenital mucosa,
p24 (176–184)	p24 (308–316 LAI) • C. Brander notes this is	QASQEVKNW s a B*5301 epitope	HIV-1 infection	human (B*5301)	Brander2001
p24 (176–184)	<ul><li>24 epitopes were descr</li><li>Serial peptide truncatio</li><li>Subject 01RCH59 was</li><li>Among HIV+ individu</li></ul>	pitope responses in Hi ibed – 8 were novel, 8 ons were used to define Hispanic, was not on als who carried HLA 1	HIV-1 infection  IV-1 infected minority women living in the used new restricting elements but were preported optimal epitopes for CTL cell lines isolated HAART, viral load 5100, CD4 count 349, B*5301, 11/15 (73%) recognized this epitope B57, 3/6 (60%) recognized this epitope	eviously defined epitopes, and ed from 12 individuals, assaye and she also recognized PIQK	8 were previously described d by a Cr-release
p24 (176–184)	p24 (309–317 LAI)  Recognition of this per Peptide defined on the Described as B*5701 i	basis of B*5801 bindi	ng motif, yet not cross-restricted except at	human (B*5701) high concentrations	Goulder1996b
p24 (176–184)	p24 (311–319 LAI) • C. Brander notes this is	QASQEVKNW s a B*5701 epitope	HIV-1 infection	human (B*5701)	Brander2001
p24 (176–184)		ane response that was ASQEVKNW.	HIV-1 infection ency in HIV-1 infected non-progressors, 1 highly focused on four p24 epitopes that v of the LTNP's tested.		

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
p24 (176–184)	threshold of infection v KAFSPEVIPMF, TST • CTL responses are bro	without therapy, and their LQEQIGW, or QASQEV ader in B*5701+ individu	CD8+ T-cell response tends to be foc	used on peptides that contain E se that control viremia.	Migueles2001 ndividuals have viral loads below the *5701 epitopes ISPRTLNAW,
p24 (176–184)	<ul> <li>This is a relatively con</li> <li>HLA-Cw*0401 was de diminished cell-surface</li> <li>The HLA presenting m</li> </ul>	efined as the restricting ele e expression of Cw*0401 nolecule for this epitope w	ement, but cells that carry Cw*0401 v in some cells	but subsequent experiments wi	Buseyne 1997  this epitope – this could be the result of the an HLA B53+ C4- cell line and with Florence Buseyne, 2000)
p24 (176–184)	(LAI)	QASQEVKNW		human (B53)	Brander2001, Buseyne1999
	<ul><li>epitope processing that</li><li>Dendritic cells treated without protein synthem</li></ul>	t may be important in the with AZT to inhibit prote sis, while macrophages de	epitopes by antigen presenting cells (initial generation of viral specific CT) in synthesis were able to elicit a strone monstrated a decreased presentation ependent and required receptor-dependent	L g specific CTL response in QA efficiency	•
p24 (176–184)	<ul> <li>HIV-1-infected female</li> <li>Responses in HEPS we reduced risk of infection women</li> <li>43/91 HEPS women has</li> </ul>	Nairobi sex workers omen tended to be lower, a on, and there was a shift in ad CD8+ responses and de		es in 91 HIV-1-exposed, persist in HLA presenting molecules th bon late seroconversion to epito PS women increased with the o	at have previously been associated with pes recognized by the HIV-1 infected
p24 (176–184)	<ul> <li>Two of the new epitope anchor residue motif fo</li> <li>While S, T, and P coule compensatory interacti</li> </ul>	mbians, three HLA-B53 e es lacked the predicted by or B53 and the related B3: d all fit into the HLA-B35	or HLA-B53 B pocket and form a hy offinity of QATQEVKNM for B53	TQEVKNM, and bound to B5	3 with high affinity, thus extending the

	Author's Location	Sequence	Immunogen	Species (HLA)	References
	-	-	died here, but it was noted that both the A, Q B58, common HLA alleles in Africans	QATQEVKNM, and B,	QASQDVKNW, subtype version of
p24 (176–184)	Gag (SF2) • Epitope name: QW9	QASQEVKNW	HIV-1 infection	human (B57)	Goulder2001a
	<ul><li>This peptide elicited a v</li><li>Three CTL responses, t</li></ul>	o epitopes TSTLQEQIGV	g acute infection of patient PI004 W, ISPRTLNAW, and KAFSPEVIPMF, were were detectable at 5 months post-infection an		ection; CTL responses to SLYNTVATL
p24 (176–184)	(LAI)	QASQEVKNW		human (Cw4)	Brander2001, Buseyne1999
p24 (176–184)	p24 (176–184)	QASGEVKNW	HIV-1 infection, HIV-1 exposed seronegative	human (Cw4)	Kaul2001a
	<ul> <li>ELISPOT was used to s HIV-1-infected female I</li> </ul>		panel of 54 predefined HIV-1 epitopes in 91	HIV-1-exposed, persis	tently seronegative (HEPS) and 87
p24 (176–185)	p24 (311–319 SF2)	QASKEVKNWV	HIV-1 infection in a narrower CTL response, stronger T hel	human (B57)	Altfeld2001b
		y infection but post-seroc	onversion therapy (Group 2), and 10 individ-	uals who responded to	HAART given during chronic infection
	<ul> <li>Previously described an</li> </ul>	d newly defined optimal	ing p17, p24, RT, gp41, gp120 and Nef epitopes were tested for CTL response L response to this epitope broken down by g	group: 0/0 group 1, 0/0	
p24 (177–185)	<ul> <li>Previously described an</li> </ul>	d newly defined optimal	ing p17, p24, RT, gp41, gp120 and Nef epitopes were tested for CTL response	group: 0/0 group 1, 0/0 human (B53)	
p24 (177–185)	<ul> <li>Previously described an</li> <li>Number of HLA-B57+</li> <li>p24 (177–185)</li> <li>Variants A(T/S)QEVKN</li> <li>ELISPOT was used to shifty-1-infected female of Responses in HEPS wo</li> </ul>	d newly defined optimal individuals that had a CT  ATQEVKNWM  NWM are specific for the tudy CTL responses to a Nairobi sex workers men tended to be lower, a	ing p17, p24, RT, gp41, gp120 and Nef epitopes were tested for CTL response L response to this epitope broken down by g HIV-1 infection, HIV-1 exposed seronegative	human (B53)  HIV-1-exposed, persis presenting molecules the	group 2, and 1/2 group 3  Kaul2001a  tently seronegative (HEPS) and 87  nat have previously been associated with
p24 (177–185)	<ul> <li>Previously described an</li> <li>Number of HLA-B57+</li> <li>p24 (177–185)</li> <li>Variants A(T/S)QEVKN</li> <li>ELISPOT was used to s HIV-1-infected female 1</li> <li>Responses in HEPS wo reduced risk of infection women</li> <li>43/91 HEPS women had</li> <li>Among HLA-B53 women</li> </ul>	d newly defined optimal individuals that had a CT ATQEVKNWM  NWM are specific for the tudy CTL responses to a Nairobi sex workers men tended to be lower, and, and there was a shift in d CD8+ responses and deen, 1/2 HEPS and 5/9 HI	ing p17, p24, RT, gp41, gp120 and Nef epitopes were tested for CTL response L response to this epitope broken down by g  HIV-1 infection, HIV-1 exposed seronegative  A/B clades panel of 54 predefined HIV-1 epitopes in 91  and focused on different epitopes with HLA p	human (B53)  HIV-1-exposed, persis  presenting molecules the seroconversion to epite  men increased with the	group 2, and 1/2 group 3  Kaul2001a  tently seronegative (HEPS) and 87  nat have previously been associated with opes recognized by the HIV-1 infected duration of viral exposure
p24 (177–185)	<ul> <li>Previously described an</li> <li>Number of HLA-B57+</li> <li>p24 (177–185)</li> <li>Variants A(T/S)QEVKN</li> <li>ELISPOT was used to s HIV-1-infected female 1</li> <li>Responses in HEPS wo reduced risk of infection women</li> <li>43/91 HEPS women had</li> <li>Among HLA-B53 women</li> </ul>	d newly defined optimal individuals that had a CT ATQEVKNWM  NWM are specific for the tudy CTL responses to a Nairobi sex workers men tended to be lower, and, and there was a shift in d CD8+ responses and deen, 1/2 HEPS and 5/9 HI	ing p17, p24, RT, gp41, gp120 and Nef epitopes were tested for CTL response L response to this epitope broken down by g  HIV-1 infection, HIV-1 exposed seronegative  A/B clades panel of 54 predefined HIV-1 epitopes in 91  and focused on different epitopes with HLA particle response in the HEPS women upon late stection of HIV-1-specific CTL in HEPS work V-1 infected women recognized this epitope this epitope in the 1/2 HEPS case and in on HIV-1 infection, HIV-1 exposed	human (B53)  HIV-1-exposed, persis  presenting molecules the seroconversion to epite  men increased with the	group 2, and 1/2 group 3  Kaul2001a  tently seronegative (HEPS) and 87  nat have previously been associated with opes recognized by the HIV-1 infected duration of viral exposure
	<ul> <li>Previously described an</li> <li>Number of HLA-B57+</li> <li>p24 (177–185)</li> <li>Variants A(T/S)QEVKN</li> <li>ELISPOT was used to s HIV-1-infected female 1</li> <li>Responses in HEPS wo reduced risk of infection women</li> <li>43/91 HEPS women had</li> <li>Among HLA-B53 wom</li> <li>The dominant response</li> <li>p24 (313–322)</li> </ul>	Id newly defined optimal individuals that had a CT ATQEVKNWM  NWM are specific for the tudy CTL responses to a Nairobi sex workers men tended to be lower, an, and there was a shift in d CD8+ responses and deten, 1/2 HEPS and 5/9 HI to this HLA allele was to EVKNWMTETL  tudy CTL responses to a	ing p17, p24, RT, gp41, gp120 and Nef epitopes were tested for CTL response L response to this epitope broken down by g  HIV-1 infection, HIV-1 exposed seronegative  A/B clades panel of 54 predefined HIV-1 epitopes in 91  and focused on different epitopes with HLA particle response in the HEPS women upon late stection of HIV-1-specific CTL in HEPS work  V-1 infected women recognized this epitope this epitope in the 1/2 HEPS case and in on	human (B53)  HIV-1-exposed, persist presenting molecules the seroconversion to epitemen increased with the lay one of the 5/9 HIV-1 human (B53)	group 2, and 1/2 group 3  Kaul2001a  tently seronegative (HEPS) and 87  nat have previously been associated with opes recognized by the HIV-1 infected duration of viral exposure  infected women  Kaul2001a

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
p24 (191–205)	Gag (320–328 BH10, LAI)	VQNANPDCKTILKAL	HIV-1 infection	human	Maksiutov2002
	• This CTL epitope (the I			erminants with human proteins.  In overlapping this epitope is TLLV	QNANP) has similarity with growth
p24 (191–205)	p24 (191–205) • One of the 51 HIV-1 ep HLA alleles	VQNANPDCKTILKAL itopes selected by Ferrari et al.	HIV-1 infection . as good candidate CTL epit	human (B51) opes for vaccines by virtue of being	Ferrari2000 g conserved and presented by common
p24 (191–205)	p24 (323–337) • Two CTL epitopes defin	VQNANPDCKTILKAL ned (see also p17(21-35))	HIV-1 infection	human (B8)	Nixon1991
p24 (191–205)	relative to the B8 epitor	bes, which varied over time iew of immune escape that poi			Goulder1997a, Phillips1991 n the immunodominant B27 epitope, 7, and that HLA-B8 individuals tend to
p24 (191–210)	<ul><li>Twelve subjects had CT</li><li>Three of these 12 had C</li></ul>	VQNANPDCKTILKALGPA d CTL specific for more than 1 L that could recognize vaccini TL response to this peptide s were HLA-A3, A24, B8, B5	l HIV-1 protein ia-expressed LAI gag	human	Lieberman1997a
p24 (191–210)	p24 (323–342 SF2) • CTL expanded ex vivo	VQNANPDCKTILKALGPA were later infused into HIV-1 i		human	Lieberman1997b
p24 (193–201)	<ul> <li>Med. 2:405, 1996;Lanc</li> <li>15% of Japanese popula</li> <li>Of the 172 HIV-1 peptic positive individuals, and</li> </ul>	et 22:1187, 1986;Hum Immun ations carry HLA-B51 while H	nol 22:73, 1988;Hum Immund ILA-B27 and -B57 are detect residues, 33 bound to HLA-I	ol 44:156, 1995) ed in less than 0.3% B*5101, seven of these peptides we	Tomiyama1999 with a rapid progression to AIDS (Nat.
p24 (193–201)	• 95 optimally-defined pe	ptides from this database were	e used to screen for INF $\gamma$ resp	human (B51) ling into question whether it is immonses to other epitopes is epitope as well as to other epitop	
p24 (193–201)		NANPDCKTI atternal CTL responses in the cope mutants in the mother was a			Wilson1999a he virus tended to be found in infected

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
	No variants of this epit	tope were found in a non	transmitting mother that had a CTL re	esponse to this epitope	
p24 (193–201)	p24 (323–333) • Epitope name: NAN	NANPDCKTI	HIV-1 infection	human (B51)	Oxenius2000
	CD4 proliferative resp HAART had no HIV s undetectable	onses and were able to n pecific CD4 proliferative	ection (three with sustained therapy, two naintain a CTL response even with und the responses and lost their CTL response bitope but none were HLA B51+	etectable viral load – three patie	ents that had delayed initiation of
p24 (193–201)	p24 (191–205) • One of the 51 HIV-1 e HLA alleles	NANPDCKTI pitopes selected by Ferra	HIV-1 infection uri et al. as good candidate CTL epitope	human (B8) es for vaccines by virtue of being	Ferrari2000 g conserved and presented by common
p24 (195–202)	<ul><li>immunologically norm</li><li>No direct CTL were for</li></ul>	nal HIV-infected (INHI) ound in any of the six IN	HIV-1 infection for HIV-infected people who were infected second who were infected people who were infected as the second of the	and 1% in the infected population ity was founded in 3/6 INHIs	ion
p24 (195–202)	<ul><li>Epitope name: Gag-Nl</li><li>Among HIV+ individu</li></ul>		HIV-1 infection 35, 3/17 (18%) recognized this epitope	human (B35)	Sabbaj2002b
p24 (197–205)	p24 (329–337 LAI) • C. Brander notes this i	DCKTILKAL s a B*0801 epitope		human (B*0801)	Brander2001
p24 (197–205)	p24 (329–337 LAI) • Predicted epitope base	DCKTILKAL d on B8-binding motifs,	from larger peptide VQNANPDCKTII	human (B8) LKAL	Sutton1993
p24 (197–205)	p24 (329–337) • In a longitudinal study	DCKTILKAL of CTL response and in	HIV-1 infection nmune escape – the variant DCRTILKA	human (B8) AL was also found, binds to B8,	Nowak1995 but is not recognized
p24 (197–205)	p24 (329–337) • Defined as minimal ep	DCKTILKAL itope by titration and bir	nding studies	human (B8)	McAdam1995
p24 (197–205)	p24 (197–205) • Included in a study of	DCKTILKAL the B8 binding motif		human (B8)	Goulder1997g
p24 (197–205)	CD4 proliferative resp	onses and were able to n	HIV-1 infection rection (three with sustained therapy, two maintain a CTL response even with under responses and lost their CTL responses	etectable viral load – three patie	ents that had delayed initiation of
	undetectable	-	only 1 of the 7/8 study subjects that we	·	given and then vital loads occalle

HXB2 Location	<b>Author's Location</b>	Sequence	Immunogen	Species (HLA)	References			
	immunodominant respo		nd minor responses to GE	ined therapy started during acute inf IYKRWII, DCKTILKAL, GGKKK				
p24 (197–205)	p24 (197–205) • One of the 51 HIV-1 ep HLA alleles	DCKTILKAL pitopes selected by Ferrari et al. as	HIV-1 infection good candidate CTL epito	human (B8) opes for vaccines by virtue of being	Ferrari2000 conserved and presented by commo			
p24 (197–205)	p24 (197–205)  • B8-restricted CTL acco	DCKTILKAL punted for about 1/3 of the total C	HIV-1 infection ΓL response in one individ	human (B8) lual	Day2001			
p24 (197–205)	period including therap	y with standard treatment interrup	tions (STI).		Oxenius2002b infected patients were studied over ebound rates, plateau viral loads, or			
p24 (199–218)	<ul><li>each HIV protein.</li><li>Nef and p24 had the hi</li><li>This peptide was amon</li></ul>	ghest percentage of reactive peptic g the 28 most reactive C clade pep	105 HIV-1 positive Botsv des, and p24 had the highe tides from among over 35	st magnitude of HIV-1 responses.  0 tested spanning all HIV proteins.	Novitsky2002 rom between 55 and 64 subjects for			
p24 (211–230)	p24 (345–364 SF2) • Gag CTL epitope precu	LEEMMTACQGVGGPGHKARV ursor frequencies estimated, peptid		human	vanBaalen1993			
p24 (211–230)	p24 (343-362 SF2)	LEEMMTACQGVGGPGHKARV	HIV-1 infection	human (B7)	McAdam1998			
p24 (211–231)	<ul><li>Twelve subjects had C7</li><li>One of these 12 had C7</li></ul>	• 1 1						
p24 (217–227)	p24 (349–359 IIIB) • C. Brander notes this is	ACQGVGGPGHK s an A*1101 epitope	HIV-1 infection	human (A*1101)	Brander2001			
p24 (217–227)	cross-reactive and reco specific manner. Two o	gnized by clade E infected individ other HLA A*1101 clade B defined	uals. The clade E and B and I epitopes were found not	human (A*1101) ade E (CRF01). Three epitopes, ide nalogs to three more HLA A*1101 to have stimulated a response in cla VGGPGHK is most common in clace	epitopes was recognized in a clade de E infected individuals.			

subjects, and acqgvggpShk from 3/7 E clade infected Thai subjects.

(acqgvggpShk is most common and is also common in clades C and D). ACQGVGGPGHK was recognized by CTL from 4/5 B clade infected Japanese

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
			was almost identical, but bulk CTL vas due to TCR specificity.	generated from individuals did no	ot cross-react with the cross-clade
p24 (217–227)	p24 (349–359 IIIB) • HIV IIIB proteins were • ACQGVGGPSHK, a v		HIV-1 infection of CTL epitopes recognized by three was also recognized	human (A11) e lab workers accidentally infecte	Sipsas1997 d with HIV-1 IIIB
p24 (217–227)	<ul><li>peptides in the study</li><li>Three peptides GSEEL contained the dominan</li><li>Five peptides RLRPGO</li></ul>	RSLYNTVATL (p17 resion of the Gag-specific epitope in 3 GKKHYMIKHLVW (p17 EQA (p24 161-177), and	HIV-1 infection s epitope in a HIV+ Caucasian living dues 71-85), SALSEGATPQDLNT? 31 out of 44 B-clade infected indivice 20-36), ELRSLYNTVATLYCV (p1 SILDIKQGKEPFRDY (p24 149-16	MLNTVG (p24 41-60), and WEK duals from Boston who showed G 7Gag 74-88), SALSEGATPQDL	ag-CTL responses NTMLNTVG (p24 41-60),
p24 (217–227)	CD4 proliferative responsible HAART had no HIV spundetectable  Both of the 2/8 HLA-A  Patient SC19(HLA A1 ACQGVGGPGHK, AV  Patient SC18(HLA A2)	onses and were able to ma becific CD4 proliferative r A11 study subjects recogni 1/12, B8/44, Cw06/0701, /DLSHFLK, and FNCGG /11, B8/44, Cw06/0701, D	intain a CTL response even with un responses and lost their CTL respon- zed this CTL epitope DR3/7, DR52/53, DQ 2/8) had a CT EFFY that declined during therapy	detectable viral load – three patie ses when HAART was eventually FL response to epitopes FLKEKG initiated at day 197 he epitopes ACQGVGGPGHK, Q	given and their viral loads became  GL, GEIYKRWII,  OVPLRPMTYK, AVDLSHFLK, and
p24 (217–227)	p24 (216–226) • One of the 51 HIV-1 ep HLA alleles	ACQGVGGPGHK pitopes selected by Ferrari	HIV-1 infection et al. as good candidate CTL epitop	human (A11) pes for vaccines by virtue of being	Ferrari2000 conserved and presented by common
p24 (217–227)	<ul> <li>individuals treated duri</li> <li>The breadth and specifindividuals with primare (Group 3), using 259 o</li> <li>Previously described and</li> </ul>	ng chronic infection icity of the response was or ry infection but post-seroc verlapping peptides spann and newly defined optimal	determined using ELISPOT by study	ying 19 individuals with pre-seroc 0 individuals who responded to H Nef nse	AART given during chronic infection
p24 (217–227)		ACQGVGGPGHK ed epitopes [Oxenius2000 by with standard treatment		human (A11) Elispot assay, 13 chronically HIV-	Oxenius2002b  1 infected patients were studied over a

	<b>Author's Location</b>	Sequence	Immunogen	Species (HLA)	References
	STIs induced increased clearance rates.	recognition of CTL epito	pes, but there was no correlation bet	ween CTL responses with viral	rebound rates, plateau viral loads, or
p24 (221–231)	CD8+ cell IFNgamma p  • In general, during the fit specificities that were not HIV-specific responses of	production to measure responsive month of treatment virous to previously detectable with diminished	HIV-1 infection  was tested in 14 HIV+ patients from ponses all load decreased and frequencies of were newly detected, as were CMV see: increases or decreases in pre-exist	f HIV-specific CTL tripled and be specific CD8+ PBL – but with co	oroadened – eight new HIV ontinued viral suppression,
p24 (223–231)		ting that the breadth of Cl	HIV-1 infection verlapping peptides spanning all HIV rL responses are underestimated if a		Altfeld2001a  was found to react with 12 peptides ed in the study
p24 (223–231)	p24 (355–363 LAI)  • Identical twin hemophil  • One had a strong respon  • [Goulder1997a] is a revi	nse to this peptide, the oth	-	human (B7) VIII	Goulder1997e, Goulder1997a
p24 (223–231)	<ul> <li>peptides in the study</li> <li>Three peptides GSEELF contained the dominant</li> <li>Five peptides RLRPGG</li> </ul>	RSLYNTVATL (p17 resid Gag-specific epitope in 3 KKHYMIKHLVW (p17	lues 71-85), SALSEGATPQDLNTM 1 out of 44 B-clade infected individu 20-36), ELRSLYNTVATLYCV (p17	MLNTVG (p24 41-60), and WEI uals from Boston who showed C 7Gag 74-88), SALSEGATPQDL	NTMLNTVG (p24 41-60),
	infected subjects from S		SILDIKQGKEPFRDY (p24 149-164	4) contained dominant Gag-spec	inc epitopes in 32 out of 37 C-clade
p24 (223–231)	p24 (SF2) • The CTL-dominant resp peptides in the study • Three peptides GSEELF contained the dominant • Five peptides RLRPGG	GOUTH Africa  GPSHKARVL  conse was focused on this  RSLYNTVATL (p17 resid  Gag-specific epitope in 3  KKHYMIKHLVW (p17 decorated)  EQA (p24 161-177), and Secondary	HIV-1 infection epitope in a HIV+ Caucasian living lues 71-85), SALSEGATPQDLNTM 1 out of 44 B-clade infected individual 20-36), ELRSLYNTVATLYCV (p17	human (B7) g in Boston – this epitope did not MLNTVG (p24 41-60), and WEI uals from Boston who showed C Gag 74-88), SALSEGATPQDL	Goulder2000a  fall within the three most recognized  KIRLRPGGKKKYKLK(p17 16-30)  Gag-CTL responses

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
p24 (223–231)	<ul> <li>individuals treated dur</li> <li>The breadth and specifindividuals with prima (Group 3), using 259 o</li> <li>Previously described a</li> </ul>	ing chronic infection ficity of the response warry infection but post-serverlapping peptides spand newly defined optima	HIV-1 infection ed in a narrower CTL response, stronge s determined using ELISPOT by studyi oconversion therapy (Group 2), and 10 nning p17, p24, RT, gp41, gp120 and N al epitopes were tested for CTL respons TL response to this epitope broken dow	ng 19 individuals with pre-sero individuals who responded to I lef se	HAART given during chronic infection
p24 (223–231)	<ul> <li>studied in eight HIV-1</li> <li>2 to 17 epitopes were repitopes were targeted</li> <li>Subjects with chronic lands</li> <li>An acute seroconvertor</li> <li>The other acute seroco</li> </ul>	infected subjects, two we recognized in a given income by at least one person HIV-1 infection recognizer homozygous for the Boundary failed to recognite	HIV-1 infection pitopes restricted by HLA class I A and with acute infection, five with chronic, a lividual, A2-restricted CTL response te wed between 2-8 out of 11 B7-restricted with allele recognized five B7-restricted ep with acute infection and infection in the second se	and one long-term non-progress inded to be narrow and never do l epitopes pitopes tested	or (LTNP)
p24 (223–231)	<ul> <li>One individual, AC-06 interruptions (STI). He restricted by HLA-A3,</li> <li>Only two epitopes wer was the first targeted p</li> <li>3/11 HLA-B7 individual</li> </ul>	cutely HIV-infected HL. b, was homozygous at all c had only two detectable 11 by HLA-B7, and 1 be detected during acute eptide, and remained im hals had detectable B7-re		as treated during acute infection, but after STI this broadened to d gp41 epitope IPRRIRQGL artudy period.  g acute infection – 10/15 of HL	and had supervised treatment o 27 distinct epitopes including 15 ad Gag GPGHKARVL. GPGHKARVL
p24	<ul><li>study</li><li>Three peptides GSEEL contained the dominan</li><li>Five peptides RLRPGO</li></ul>	RSLYNTVATL (p17 re t Gag-specific epitope in GKKHYMIKHLVW (p1 EQA (p24 161-177), an	HIV-1 infection nis epitope in a HIV+ South African – t sidues 71-85), SALSEGATPQDLNTM n 31 out of 44 B-clade infected individu 7 20-36), ELRSLYNTVATLYCV (p17 d SILDIKQGKEPFRDY (p24 149-164	ILNTVG (p24 41-60), and WE hals from Boston who showed G Gag 74-88), SALSEGATPQDI	Gag-CTL responses LNTMLNTVG (p24 41-60),

## II-B-4 p24-p2p7p1p6 CTL Epitopes

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References			
p24-p2p7p1p6 (223–1)	Gag	GPGHKARVLA		human (B7)	De Groot2001			
,	<ul> <li>The program Epimatrix was used in conjunction with the program Conservatrix to identify conservered regions of HIV that might serve as epitopes</li> <li>A subset of the potential epitopes was identified that could bind to the appropriate HLA-allele, and 15 predicted B7 superfamily (HLA B7, B8, and B58) epitopes were identified that could stimulate IFNγ production in an ELISPOT assay</li> <li>GPGHKARVLA was confirmed as an HLA-B7 epitope in this study, and had been previously published</li> </ul>							
p24-p2p7p1p6 (225–8)	Gag (357–372 LAI)	GHKARVLAEATLSQVN	HIV-1 infection	human	Buseyne1993a			
	<ul><li>Primary assays showe</li><li>Epitopes recognized in</li></ul>		at least one HIV protein was detec using synthetic peptides and seco					
p24-p2p7p1p6 (230–7)	Gag (386–)	VLAEAMSQV	HIV-1 infection	human (A*0201)	Altfeld2001c			
	<ul> <li>Three additional previous recognized at least on maximum of 2)</li> <li>VLAEAMSQV binds</li> <li>4/22 individuals with</li> </ul>	iously described HLA-A2 epe of the 23 peptides (median to all five HLA-A2 supertype	of 2 and maximum of 6), while 6, be alleles tested: A*0201, A*0202 ognized this epitope, and it was im	the A-A2 supertype affects tested at a 18/22 chronically infected HL/12 acute infected individuals recognomerates, A*0203, A*0206 and A*6802 (high munodominant in 3/4 by ELISPOT	nized at least 1 (median of 1 and ghest affinity)			
p24-p2p7p1p6 (230–7)		VLAEAMSQV	HIV-1 infection	human (A02)	Sabbaj2002b			
(250 1)	<ul> <li>Epitope name: Gag-VV9</li> <li>Among HIV+ individuals who carried HLA A02, 3/29 (10%) recognized this epitope</li> </ul>							
p24-p2p7p1p6 (230–7)	Gag (397–405)	VLAEAMSQV	HIV-1 infection	human (A2 supertype)	Propato2001			
(230 7)	<ul> <li>Long-term nonprogressors (LTNPs) had strong memory resting CD8+ T-cell responses against the majority of epitopes tested, (18 for the A2 supertype, 16 for the A3 supertype) while the effector cells of long-term nonprogressors recognized far fewer epitopes</li> <li>Progressors had memory resting CD8+ T-cells that recognized far fewer epitopes than LTNPs</li> <li>A positive correlation between effector CD8+ T-cells and plasma viremia and a negative correlation between CD8+ effector T-cells and CD4+ T-cells was observed, which may contribute to the inability of LTNPs to clear virus</li> <li>This epitope can bind all five HLA-A2 supertypes alleles (A*0201, A*0202, A*0203, A*0206 and A*6802)</li> </ul>							

## II-B-5 p2p7p1p6 CTL Epitopes

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References				
p2p7p1p6 (5–13)	Gag (SF2)	SQVTNPANI	Vaccine	murine BALB/c (H-2D <sup>b</sup> )	Paliard1998				
	<ul> <li>Vaccine Strain: SF2 HIV component: Gag</li> <li>HIV-1(SF2)p55gag vaccination of H-2 mice activates a CTL response against this epitope</li> <li>CTL that recognized SQVTNPANI in the context of H-2D<sup>b</sup> cross-reacted with H-2 alloantigens H-2L<sup>d</sup> and an unidentified self-peptide</li> <li>A postulate: heterozygosity at the MHC level could prevent the maturation of some T cell receptor combinations for foreign peptide and self-MHC constructs because of thymic depletion and tolerance</li> </ul>								
p2p7p1p6 (18–37)			CGKEGH es and full length HIV-1 genome sec HLA-A*02011 responded to the pep						
p2p7p1p6 (42–50)	<ul> <li>immunodominant regi</li> <li>and to the Vpr binding</li> <li>p15 contributed on ave</li> <li>3 optimal CTL epitope</li> </ul>	ons targeted by CD8+ T-c s site in p6. erage 17% of the total Gag es were mapped within p1	HIV-1 infection 5-specific CD8+ T-cell IFNgamma tells were mapped to three functional g response (rage 0-100%). 5: KELYPLTSL, CRAPRKKGC, a The binding motif for B14 is C-tel	al domains: the zinc finger structur	Yu2002b ot and intracellular staining. The es, the protease cleavage site p7/p1,				
p2p7p1p6 (55–70)	p15 (446–460 BRU)  • One of 4 epitopes first	KEGHQMKDCTERQAI predicted, then subsequen	NF HIV-1 infection ntly shown to stimulate an HLA-A2	human (A2) Prestricted CTL line	Claverie1988				
p2p7p1p6 (64–71)	<ul><li>24 epitopes were descr</li><li>Serial peptide truncati</li><li>This epitope was newl</li><li>Patient 01RCH59 was</li></ul>	epitope responses in HIV- ribed – 8 were novel, 8 usons were used to define op y defined in this study	HIV-1 infection  1 infected minority women living in ed new restricting elements but were primal epitopes for CTL cell lines is C, and had a viral load of 5100 and C, HLA-B*4002	re previously defined epitopes, and solated from 12 individuals, assaye	d by a Cr-release				
			0, 3/5 (60%) recognized this epitope	e					
p2p7p1p6 (70–79)	immunodominant regi and to the Vpr binding • p15 contributed on ave • 3 optimal CTL epitope • FLGKIWPSYK was e	ons targeted by CD8+ T-c s site in p6. erage 17% of the total Gag es were mapped within p1	g response (rage 0-100%). 5: KELYPLTSL, CRAPRKKGC, a ognized by 14/57 (25%) of subjects	al domains: the zinc finger structur	Yu2002b ot and intracellular staining. The es, the protease cleavage site p7/p1,				

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
p2p7p1p6 (83–97)	Gag (453–462 BH10, LAI)	GNFLQSRPEPTAPPF	HIV-1 infection	human	Maksiutov2002
	• This CTL epitope (the H	•	-	ninants with human proteins.  Overlapping this epitope is PEPTAPle	PFLQ) has similarity with the T-cel
p2p7p1p6 (83–97)	p15 (418–433 BRU) • One of 4 epitopes first pr	GNFLQSRPEPTAPPF redicted, then subsequently	HIV-1 infection shown to stimulate an HLA-A2 1	human (A2) restricted CTL line	Claverie1988
	p2p7p1p6 (118–126) ◆ C. Brander notes that thi	KELYPLTSL s is a B*4001 epitope		human (B*4001(B60))	Brander2001
	immunodominant region and to the Vpr binding si p15 contributed on avera 3 optimal CTL epitopes Four patients who were l The binding motif for Bo Four patients who did no	s targeted by CD8+ T cells ite in p6. ge 17% of the total Gag reswere mapped within p15: KHLA-B60+ recognized KEL fo is C-term Leu and 2nd po	were mapped to three functional ponse (rage 0-100%). ELYPLTSL, CRAPRKKGC, and YPLTSL. sition Glu. gnized the 15 amino acid long persons.	human (B60, B*4001) esponses were measured by Elispot domains: the zinc finger structures d FLGKIWPSYK. eptide carrying KELYPLTSL, sugge	the protease cleavage site p7/p1,
	<ul><li>This B7 epitope is one of</li><li>A dominant B7 epitope v</li></ul>	was defined using conventio y, EpiMatrix, to identify 20		human (B7) non-progressor al sub-dominant HLA B7 epitopes wogous HIV-1, followed by B7 ancho	

## **II-B-6** Gag CTL Epitopes

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
Gag	<ul> <li>CTLs primed by HIV- p14/9</li> </ul>	virus-like particle HIV or 1 p55 gag virus-like particle	cle (VLP) vaccination recognized ep	Rhesus macaque itopes in four different 20 amino	Paliard2000 acid peptides p17/4, p17/8, p24/13 and
Gag	<ul><li>infants</li><li>No HIV+ infants had disease, and not in rap</li></ul>	no demonstrable CTL at b	HIV-1 infection ad lower Th1 responses and decrease wirth, but Th1 responses accompanied dilution using autologous B cells inf	d by CTL responses developed in	children with slowly progressive
Gag	<ul><li> The vaccine used was</li><li> Twenty HIV negative</li><li> Immunization with vC</li></ul>	a rec canarypox with HIV subjects were vaccinated CP205 induced HIV-1-spec	in phase I trial with combinations of cific ABs to gp120, V3, and p24 anti	(vCP205), alone or with p24E-V vCP205 and CLTB-36 gens, and CTL immune response	Salmon-Ceron1999  3 MN synthetic peptide (CLTB-36)) s against vCP205 were detected after AB or CTL immune responses against
Gag	• Immunization of HIV to p24 and p17 and a t	transient elevation in viral	17/p24 Ty virus-like particle (p24-V		Klein1997 lived increased proliferative response
Gag			Vaccine / component: gp120, p24 Adjuvan articles administered in MF59 emul		O'Hagan2000 vant and CTL immune responses against
Gag	standard method, lytic	units (LU20)	•		Lubaki1999 ion (LR) of net specific lysis, and the observed using ACU and LR, but not
Gag	Gag  The presence of HIV-load in untreated subjections.		HIV-1 infection e responses was positively correlated	human I with Gag-specific memory CTL	Kalams1999a and negatively correlated with viral

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
		onses were the most rea as a positive trend with	dily detected – Gag CTL responses were th Nef, Env and RT	e only responses with a sign	nificant correlation with Gag stimulated
Gag	years - LTNPs maintai	ined a low viral load, h	HIV-1 infection ified as long-term non-progressors (LTNPs) igh frequencies of CTL precursors directed ivel ongoing viral replication		
Gag			HIV-1 infection ed with their own lymphocytes, cryopreserv seen in 7/12, and an increase in the CTL re		
Gag			HIV-1 infection n between HIV Type I plasma viral load and term survivors (LTS) of HIV-1 infection	human d CTL activity directed agai	Betts1999 inst HIV-1 Pol, and stronger combined
Gag	<del>_</del>	thin a month following	HIV-1 infection ed for CTL response to HIV proteins Env, OPI) was noted in 87% of the subjects to Gag rare	~	
Gag	Env proteins		HIV-1 infection clade virus had CTL that were able to make ted to a particular protein, and the level of recognitions are supported to the support of the su		· ·
Gag	Anti-NKR IgM MAb i	masked this inhibitory	HIV-1 infection receptor (NKR+) can exhibit down regulatifunction and increased HIV-1 specific CTL to other case anti-NKR MAb brought HIV-1	activity in phytohemaggluting	
Gag	The live canarypox vac	ccine ALVAC-HIV(vCl	Vaccine rgp120 boost Strain: MN, LAI, SF2 HIV P205) carrying MN gp120, LAI gp41, Gag ar Gag CD8+ CTL were detected in 64% of t	and Protease, and boosted w	
Gag		orrelation between stro CD4 and CD8 cells, a	HIV-1 infection ng CTL memory and breadth of response in nd lower viral load	human 7-12 month old infants, and	Buseyne1998a I remaining AIDS-free for the first year
Gag	Gag (LAI) • In infants with positive subtypes	e CTL responses, most	HIV-1 infection responses showed cross-clade reactivity wit	human th somewhat diminished rec	Buseyne1998b ognition of epitopes from different
Gag		eted individuals with repelated with a CCR5 wil	HIV-1 exposed seronegative peated high-risk sexual exposure had HIV-1 dtype genotype	human specific CTL against Env, C	Goh1999 Gag, Pol, or a combination of proteins –

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
	• In this group, the high HIV-1 proteins	est CTLp frequencies w	ere directed at Gag, but the most com	amon response was to Env and four	individuals had responses to multiple
Gag	<ul> <li>A Canarypox vaccine</li> </ul>	expressing gp120, gp41	Vaccine  onent: gp120, gp41, Gag, Pro, Nef, R' , Gag, Protease, Nef and Pol CTL epicted 3-6 months after the last vaccinate	topes gave rise to CTL that could b	Evans 1999  De detected in 61% of the volunteers –
Gag	such as epitope proces identified because they	ssing, or may possibly by would be more likely	HIV-1 infection 17 or Nef and CTL epitope density was an artifact of experimental strategy to be cross-reactive with the test reages served protein and known epitopes are	for epitope definition such that conents	Kuiken1999 this may be due to a biological reason served epitopes would tend to be
Gag	<ul> <li>Priming with an HIV-I</li> <li>The proliferative response fold increase in the median</li> </ul>	DNA vaccine and boost onse to Env and Gag aft	Vaccine hia boost Strain: LAI HIV componing with a vaccinia construct induced or the DNA vaccination had a mean S Env. The T help response happened cas also enhanced	greater levels of HIV T cell immur I of 1.5-4, but after boosting with r	HIV-fowlpox virus, there was a 6-17
Gag			Vaccine N, LAI <i>HIV component:</i> gp120, gp4 g MN gp120 and LAI gp41/gag/protea		Salmon-Ceron1999  oproliferative response in healthy,
Gag	The study explores the	e use of co-stimulatory	Vaccine : Env, Gag, Pol Adjuvant: CD86, C nolecules co-expressed with an HIV- tically increased both HIV Env and G	1 immunogen in a DNA vaccine to	
Gag			HIV-1 infection release assay in bulk culture showed r , CD4 and time to death	human no correlation between CTL-activit	Aladdin1999 y (gp120, Gag, Pol and Nef) and
Gag	<ul> <li>Rhesus macaques wer finger in the nucleocap</li> <li>Env and Gag specific 0</li> <li>2/4 monkeys (MM146</li> <li>PBMC from all vaccin MM145, the animal w</li> </ul>	e vaccinated by i.m. inj psid to prevent packagin CTL but no antibody re 5 and MM143) produced nated monkeys produced with the strongest CTL re	g sponses were induced in 2/4 vaccinated antibodies against p24 and/or gp160 I IFN-gamma, in response to HIV-1 g	ed monkeys (MM145 and MM153), but no CTL response was detected p160, indicating a Th response – th	d is response was 5 times higher in

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References			
	• 6-8 weeks post-challenge with SHIV NM-3rN plasma viral loads of both MM146 and MM143 decreased near or below the detection limit							
Gag	<ul><li>superinfection with NS</li><li>Significantly decreased</li><li>Significant CD8+ med</li></ul>	SI virus If the CD4+ T-cell proving the CD4+ T-cell proving the contract of th	HIV-1 infection developed based on proviral load of cocult iral loads were found in 12 HIV+ slow pro ted against autologous cells infected with out no correlation was found between plass	ogressors relative to 10 rapid vaccinia carrying the HIV-1	progressors gag gene was observed in slow			
Gag	<ul><li>tested increased lysis b</li><li>2/10 individuals with &lt;</li></ul>	by > 5%) if the culture <200 CD4 cells/ul, and	HIV-1 infection IL12) to cultures increased HIV-specific ly was derived from HIV+ individuals who h 3/10 individuals with 200-500 CD4cells/u CD8 cells that maintained responsiveness	and CD4 cells/ul > 500 al, had an increase of >5% upo	-			
Gag		1 SF162, mediated by	HIV-1 infection ral blood mononuclear cells of four long-t CD8+ T-cells and associated with prolifer echanism is unknown					
Gag	cross-reactive CTL res clades A, B, and D; =F	D dominate the Ugand ponses in HIV infected Proteins corresponding	HIV-1 infection lan epidemic, and a vaccine trial using B c l Ugandans to A, D, and B clade recombin to the subtype of the infecting strains tend btype cross-reactivity with B clade protein	nant vaccinia viruses expressional vaccinia vaccini	ng Gag, Env, RT or Nef from HIV-1 CTL response measured by percent			
Gag	Gag • HIV-specific CTL active could be identified in t		HIV-1 infection e female reproductive tract of only 1/3 HIV women	human V-infected women who under	White2001 went a hysterectomy, although CTL			
Gag			HIV-1 infection CD4+ T-cell reservoir by autologous CD8 etroviral treatment, but this activity appear					
Gag		and Pol expressed in va	HIV-1 infection ed in long term non-progressors (LTNP) waccinia in autologous targets low viral load	human vith low viral load using limit	Jin2000a ing dilution analysis and measuring			
Gag	<ul> <li>The CTL responses as of a lower magnitude t</li> </ul>	sayed by ELISPOT and han in chronic HIV-1 i tend to be detectable in	HIV-1 exposed seronegative is about HIV-specific CTL found in the HIV-specific CTL found in the HIV-specific CTL precursor frequencies by limiting infections – the responses in HEPS cases at HEPS subjects only if they are recently expected the HEPS cases	V-1 exposed persistently serong dilution analysis indicate the below the level of detection	at CTL in HEPS individuals tend to be n by tetramer assays			

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
	and ELISPOT, and the individuals relative to • HIV-1 specific CD8+0	authors consider the p HIV-1 infected individu CTL responses in HIV-	n are associated with HIV-1 specific Clossibility that HIV-1-specific T-help recalls, who tend to have a poor HIV-1-specific tinfected individuals show reduced le EPS individuals this is considered as a	sponses improve the "quality" of secific T-help response wels of perforin, and the T cells r	the CD8+ response in HEPS  nay not mature properly, and although
Gag	<ul> <li>Using DNA that had h pseudoparticles sugge- precursor protein requ</li> </ul>	umanized codon usage sted that the greatest br	Vaccine  t: Gag, Pol, Env, Gag-Pol fusion protei , CTL responses to DNA vaccines conteadth and most potent response was to so does not form releaseable particles	taining either Gag, Pol, Gag-Pol the Gag-Pol fusion protein. The	
Gag	• 6/24 HIV uninfected i: • Reviewed in [Kuhn200]		HIV-1 exposed seronega https://example.com/initial/ini		De Maria1994, Kuhn2002 nia-expressed Nef, Gag/Pol, Env.
Gag	responses were detected	ed at all time points.  hat were not infected the	HIV-1 infection d HIV-1 specific CTL responses to vac hough born to HIV+ mothers had detec	-	
Gag	<ul> <li>remained very low in 3</li> <li>The two infants with h</li> <li>Stronger responses we</li> <li>Two babies that were n</li> </ul>	3 infants with a rapidly iigh levels of Env peption re detected after initiat not infected though bor ntly in PBMC after bird		ogressed more slowly, the HIV-spighest CTLp frequencies.	
Gag	_	from 91% and 78% of 1	HIV-1 infection TL against Env or Gag in unstimulated HIV-infected children, respectively, wi		Kuhn2002, McFarland1994 of PBMC, Gag and Env specific CTL
Gag	variable regions found	in Nef, Env and p17.	HIV-1 infection ature and included in this database tender and Protease, epitopes are more even	_	

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
Gag	cells in BALBc mice.	LFn causes exogenous 1	HIV-1 infection  n proteins are candidate HIV vaccines to protein to be taken up and processed in mid stimulate gag-specific CD4 prolifer	a class I pathway. Expressed pro	oteins from Gag p24 and Nef
Gag	<ul><li>Nef and/or Pol CTL re</li><li>The magnitude and br</li><li>Pol and Int CTL respo</li></ul>	esponses were detected it eadth of Gag and p24 T- onses correlated positive	HIV-1 infection red patients elicited gamma-IFN CD8+ n 86% of the subjects cell responses correlated with absolute by with absolute CD4+ T-cell count either CD4 counts or viral load		Edwards2002 clated with viral load
Gag	patients on successful	HAART treatment, rela	HIV-1 infection ecinia expressing Gag, Pol, Nef and En tive to autologous monocytes. Some we etection of low frequency memory cell	eak responses could only be dete	
Gag	-	s were obtained in 14 da	HIV-1 infection ion of CD8+ and CD4+ T-cells with th ays with optimized concentrations of II		
Gag	<ul> <li>was measured in an El proteins.</li> <li>All 22 patients targete recognized Nef. Robu</li> <li>Despite high HCV vir strong anti-HCV response</li> </ul>	d at least one protein. 20 st CTL activity was indeal loads, very few HCV onses were mounted.	HIV-1 and HCV co-infect ited in 22 individuals who were co-infectells using targets expressing either Gap 0/22 patients recognized RT, 17/22 patients of disease progression or viral CD8+ T-cell Elispot responses were detected in 9/17 coinfected patients, but the control of the coinfected patients, but the coinfected patients are coinfected patients.	cted with HIV-1 and hepatitis C vg, RT, Env and Nef in a vaccinia ents recognized Gag, 13/22 subjet load.  etected. In a control HCV infected.	construct, or one of seven HCV ects recognized Env and 11/22 patients d person who did not have HIV-1,
Gag	<ul><li>varied at different time</li><li>2/4 infants infected in</li></ul>	e point. Pol responses w trapartum had detectable	HIV-1 infection V-1 Gag and Env specific CTL respons ere not detected. eresponses, one note until 11 months, of V- infants that were born to HIV+ moth	one not until 42 months.	Luzuriaga1995 months of age. Levels of the responses
Gag	A safety and immunog	geniticity study of a vacc	Vaccine pp120 boost Strain: Gag, LAI; gp120 prine dosing schedule was studied in a tr fir CTL response by day 728.		
Gag	CTL responses before	and after initiation of A	HIV-1 infection RT were studied in 13 HIV-1 vertically	human / infected infants <6 months of a	Scott2001 ge, and 4 that were >6 months of age.

**Gag CTL Epitopes** 

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References		
	<ul><li>became undetectable a</li><li>One older infant, at 23 group. 3/4 infants olde</li></ul>	after successful therapy months, had CTL resp or than 6 months of age	nowed IFNgamma Elispot CD8+ T-cell r - 3 infants were coinfected with CMV a conses against all for proteins tested, Gag e responded to either Nef or Pol. ened the HIV-1-specific CTL response in	nd all 3 had CMV-specific CD8- g, Pol, Nef and Env, and had the	+ T-cell responses. lowest plasma viremia of the study		
Gag	DC cells could stimula	ate CD4+ and CD8+ T-	HIV-1 infection tigens derived from dead, apoptotic cells cells resulting in IFNgamma production ant aspect of the initial immune response	in an Elispot assay. Both HLA	Class I and class II molecules were		
Gag	boosted HIV-1 specific	c CTL responses and e nt levels and CD4 T-ce	HIV-1 infection I infected patients undergoing HAART to levated CTL responses were maintained ll count decline was observed. CD8 responses vaccinia.	up to 22 weeks after the last trea	tment interruption, but viral load		
Gag			HIV-1 infection  killing was detected in duodenal and rected CTL was different in the peripheral l				
Gag	HLA-A*0201 and HL	A-B*3501 HIV T-cell	computer prediction works, hidden Markov models, binding n epitope candidates from 533 Gag, Env ar arisons to known epitopes and between c	nd Pol sequences of which 374 v			
Gag	derived from HIV-2 and 62 from SIV. Comparisons to known epitopes and between clades were made.  Gag HIV-1 infection human (B*35) Jin2002  • Patients with HLA-B*35 variants B*3502, B*3503, B*3504, and B*5301 tend to proceed to AIDS more quickly than those with B*3501.  • Of 32 patients with HLA-B*35 alleles CD8+ CTL responses were quantified using an intracellular cytokine staining assay – 75% had responses to Pol, 69% to Gag, 50% to Nef, and 41% to Env.  • The overall magnitude of CTL responses did not differ between those bearing B*3501 and the others. A higher percentage of Gag responses was observed in those that had lower RNA levels that carried B*3501, and there was a negative association with viral load and CTL activity. The data is consistent with higher levels of CTL responses contributing to protection in B*3501 individuals, but not in B*3502, B*3503, B*3504, and B*5301 individuals.						
Gag	<ul> <li>component: gp120, gp</li> <li>HLA-B60 responses down against the MN pe</li> <li>Vaccinee 202T7 (HLA</li> </ul>	41, Gag, Pol and Nef cominated the response eptide 107-136. Low let A2, B27, C25) made	Vaccine rgp120 boost, canarypox prime with rgp epitope rich regions s against an Gag vaccine in an individual evel Gag responses were observed agains the strongest response to an epitope at po with C, and only minimally cross-reacti	I (022G0Z) who was HLA A1, At B8 and A11 epitopes, no responsitions 131-140 of Gag. The res	A11, B8, B60. The strongest response nse was observed against A1 epitopes.		

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References	
Gag	p24		Vaccine	murine (H- $2^b$ , H- $2^d$ , H- $2^k$ )	Iroegbu2000	
	• The p24 sequence is n concentrated in CTL 6	epitopes	t: p17/p24 p17 within patient, and nonsynonymoung progenicity in H-2b,d, or k mice, while			
Gag	p24		Vaccine	murine (H-2 <sup>d</sup> )	Qiu2000	
	<ul><li>Mice were injected wi</li><li>Secreted HIV-1 Gag e</li><li>IFN-gamma levels we</li></ul>	expression vectors gener ere increased compared	t: gag and 4 weeks and lymphocyte prolifer ated a stronger response than standard to an undetectable IL-4 response ag expression vaccination studies			
Gag	Gag (SF2)		Vaccine	Rhesus macaque, murine $(H-2^d)$	zurMegede2000	
	<ul> <li>immunogenicity in BA</li> <li>A CTL response in midetect a response</li> <li>Recognition of 3 diffe</li> </ul>	ALB/c and CB6F1 mice ice could be detected af erent Gag peptide pools	gag-protease gene constructs lead to ter a single immunization with codon- was observed, indicating a polyclonal detected in 4/4 rhesus monkeys, in co	optimized gag, using 2 ng of plasm		
Gag	p24 <b>Vaccine</b> Vector/Type:	coxsackievirus HIV c	Vaccine omponent: partial p24, polyepitope	murine (H-2 <sup>d</sup> )	Halim2000	
	<ul><li> This paper describes t</li></ul>	e and T help responses on the vaccine strategy and	4-P) construct was generated that can can be elicited from peptides embedde generation of constructs, and employed in MHC class I presentation in BALE	ed in a surface loop of the VP1 caps is amino-terminal fusion of Gag seq	id	
Gag	subsequent cleavage to elicit CTL responses via MHC class I presentation in BALB/c mice  Gag Vaccine murine (H-2 <sup>d</sup> ) Huang2001  Vaccine Vector/Type: DNA Strain: gag HxB2, pol NL43 HIV component: Gag, Pol  • Mice were immunized with four humanized DNA constructs: GagPol, that would form a pseudoparticle carrying Gag and Pol, Gag, Pol or a GagPol fus construct  • The GagPol pseudoparticle, Gag and GagPol fusion construct all elicited strong anti-Gag CTL, but only the GagPol fusion construct elicited strong anti-					
Gag	<ul> <li>BALB/c and C57BL/c with vaccinia expressi</li> <li>L. monocytogenes is a</li> </ul>	6 mice were immunized ing Gag	Vaccine s Strain: HXB2 HIV component: with recombinant Listeria monocytog that enters the macrophage on phocytod class II pathways	genes (Lm-Gag) expressing HIV-1 l		

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References				
	<ul> <li>CD4+ Th1 T-cells mediated the Gag specific immunological protection in mice immunized with Lm-Gag and challenged with vaccinia-Gag</li> <li>Gag-specific CTL may enhance viral clearance via IFN-gamma secretion, but are not essential for immunity;</li> </ul>								
Gag	Gag Vaccine Vector/Type:	Listeria monocytogene	Vaccine s Strain: HXB2 HIV component: G	murine $(H-2^d, H-2^b)$	Mata2000				
	<ul> <li>BALB/c and C57BL/6 with vaccinia expressing</li> </ul>		with recombinant Listeria monocytoge	nes (Lm-Gag) expressing HIV-1 H	IXB2 Gag and mice were challenged				
		• L. monocytogenes is a gram-positive bacteria that enters the macrophage on phagocytosis and lives in the cytoplasm – secreted L. monocytogenes antigens are processed and presented by both class I and class II pathways							
	• This article is a review of L. monocytogenes biology and its potential as a vaccine vector for HIV, comparing to other vector systems, and discussing CD4+ Th1 T-cells mediated Gag specific immunological protection in mice and the Gag CTL response								
Gag			Vaccine a: SF2 HIV component: codon-optimi		Otten2000				
	• CB6F1 were primed with gag DNA by im injection and challenged with vaccinia expressing Gag/Pol (rVVgag-pol)								
	• Gag-specific CTL responses were detected by IFNgamma secretion in the spleen, independent of the route (intraperitoneal, intranasal or intrarectal) of rVV gag-pol challenge								
	• The gag DNA vaccine induced CTL responses in 4/4 monkeys 2 weeks post immunization, but antibody responses were detected in only 1/4 monkeys after 3 immunizations								
	CTL cross-reactivity a	gainst Gag sequences 1	1-80, 254-323, and 421-496 was observed	ed, suggesting multiple CTL epitor	pe recognition				

## II-B-7 Gag/Pol CTL Epitopes

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References			
Gag/Pol	Gag/Pol (ARV-2 SF2) Vaccine Vector/Type:	Cowlpoxvirus Strain: A	Vaccine ARV-2,SF2 HIV component: Gag, P	Macaca nemestrina ol <i>Adjuvant:</i> IFN-gamma	Kent2000			
	<ul><li> Vaccination with FPV Macaca nemestrina</li><li> HIV-1 viral loads rema</li></ul>		creased HIV-1 specific CTL and T cell following vaccinations	ll proliferative responses to Gag/Po	ol antigens, respectively, in infected			
Gag/Pol	RT <b>Vaccine</b> Vector/Type:	DNA HIV component:	Vaccine Gag, Pol, Vif, Env Adjuvant: B7, I	murine L-12	Kim1997d			
	<ul> <li>A Gag/Pol or Env DNA vaccine, when delivered in conjunction with the plasmid encoding the co-stimulatory molecules CD86, gave a dramatic increase in both the cytotoxic and proliferative responses in mice</li> <li>When CD86 was present, CTL response could be detected even without in vitro stimulation</li> </ul>							
Gag/Pol	responses to Gag, Pol,	Env or Nef antigens	HIV-1 infection howed CD8 T cell proliferation and d stegrity of the CD8 T cell repertoire (**		Gamberg1999 six individuals showed HIV-specific tic diversity) remains intact through			
	advanced HIV infection	n, although HIV-specific	CTL activity decreases					
Gag/Pol	Vaccine Waccine Waccine Work Muthumani Work Muthumani Work Muthumani Work Work Muthumani Work Work Muthumani Work Muthumani Work Work Muthumani Work Work Muthumani Work Muthumani Work Work Muthumani Wo							
	Vpr compromised CD		and T-helper proliferative responses in of IL-12 and TNFalpha, indicative of					

## II-B-8 Protease CTL Epitopes

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
Protease (3–11)	RT (71–79 subtype A, B, D)	ITLWQRPLV		human (A*6802)	Brander2001
	• C. Brander notes this is a	an A*6802 epitope			
Protease (3–11)	<ul> <li>The HIV-1 subtype A fo which could direct the processor of the immune Kenya. A DNA and MV included in the polyepite</li> <li>Multiple CD4+ or CD8+ assays after vaccination</li> </ul>	cused vaccine HIVA contains protein to the cell membrane and odominant epitopes that were set a prime-boost vaccination protein protein [Hanke2000].  T-cell vaccine-induced response of 5 macaques. The response to	HIV-1 infection, Vaccine noost Strain: subtype A HIV comp 24 and p17, in a reversed order relative inhibit efficient peptide processing an elected to have particularly good cross occol using the HIVA antigen will be used to peptide pools were detected using the Mamu A*01 SIV p27 epitope p1 acaques, possibly because of processing	e to the Gag polyprotein to nd class I presentation, as we reactive potential for the A sed in a phase III clinical tr ng intracellular cytokine sta 1C (CTPYDINQM), include	prevent myristylation of p17, vell as a polyepitope string of A-clade epidemic in Nairobi, rial in Kenya. This epitope is aining and IFNgamma Elispot led in the polyepitope region, was
Protease (3–11)	_	ITLWQRPLV  tif, no truncations analyzed S. Rowland-Jones, pers. comm		human (A*6802, A*7401, A19)	Dong1998a
Protease (3–11)	RT (71–79 subtype A, B, D)  • C. Brander notes this is a	ITLWQRPLV	·	human (A*7401)	Brander2001
Protease (3–11)	Pol (59–65) • One of the 51 HIV-1 epir HLA alleles	ITLWQRPLV copes selected by Ferrari et al. a	HIV-1 infection s good candidate CTL epitopes for va	human (A28) ccines by virtue of being co	Ferrari2000 conserved and presented by common
Protease (3–11)	CD8+ cell IFNgamma p.  In general, during the fir specificities that were no HIV-specific responses of	roduction to measure responses st month of treatment viral load at previously detectable were ne liminished	HIV-1 infection  sted in 14 HIV+ patients from an unservice decreased and frequencies of HIV-sp wly detected, as were CMV specific Ceases or decreases in pre-existing resp	ecific CTL tripled and broa CD8+ PBL – but with conti	ndened – eight new HIV nued viral suppression,
Protease (3–11)	Pol  • ITLWQRPLV cross-reac	ITLWQRPLV ets with clades A, B and D	HIV-1 infection, HIV-1 exposed seronegative	human (A74)	Kaul2001a

HXB2 Location	<b>Author's Location</b>	Sequence	Immunogen	Species (HLA)	References
	ELISPOT was used to s     HIV-1-infected female.		a panel of 54 predefined HIV-1 epitop	es in 91 HIV-1-exposed, persiste	ently seronegative (HEPS) and 87
Protease (11–20)	for the A3 supertype) w • Progressors had memor • A positive correlation b observed, which may co	while the effector cells of the resting CD8+ T-cells the tetween effector CD8+ Tontribute to the inability	HIV-1 infection memory resting CD8+ T-cell response long-term nonprogressors recognized that recognized far fewer epitopes that local and plasma viremia and a negat of LTNPs to clear virus leles (A*0301, A*1101, A*3101, A*	d far fewer epitopes n LTNPs tive correlation between CD8+ e	es tested, (18 for the A2 supertype, 16
Protease (12–20)	for the A3 supertype) w • Progressors had memor • A positive correlation b observed, which may co	while the effector cells of the resting CD8+ T-cells the tetween effector CD8+ Tontribute to the inability	HIV-1 infection memory resting CD8+ T-cell response long-term nonprogressors recognized that recognized far fewer epitopes that c-cells and plasma viremia and a negat of LTNPs to clear virus lleles (A*0301, A*1101, A*3101, A*	d far fewer epitopes n LTNPs tive correlation between CD8+ e	es tested, (18 for the A2 supertype, 16
Protease (30–38)	<ul> <li>Seroprevalence in this c</li> <li>Most isolated HIV strain responses are frequently</li> <li>This epitope is conserved.</li> <li>The Clade A version of this epitope was recognitive.</li> </ul>	cohort is 90-95% and the ns are clade A in Nairoby observed using A or Ded among B and D clade the epitope: DTVLEDI nized by two different expressions.		se CTL may confer protection est in the world ound – B clade epitopes are often	
Protease (30–38)	<ul><li>CD8+ T cell responses</li><li>Low risk individuals die</li></ul>	tended to be to the same d not have such CD8+ c DTVLEDINL (3 individ	uals), SLYNVATL (4 individuals), LS	HIV-specific CD8 gamma-IFN r s than cervical CD8+ T cell respo	onses
Protease (30–38)	RT (85–93 subtype D) • C. Brander notes this is	DTVLEEWNL an A*6802 epitope		human (A*6802)	Brander2001
Protease (30–38)	sex workers eventually	seroconverted, and for s gnized in 3 of the 6 wor	HIV-1 infection posed, persistently seronegative indivi ix of these HIV CTL reactive epitopes nen (ML857, ML1203, and ML1707)	s had been defined while seroneg	gative

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References			
	<ul><li>escape</li><li>The epidemiological faworking for a period o</li></ul>	actor associated with seron retire	f the infecting strain had no substitute occonversion was stopping sex work a worker controls, ML851, ML1432,	and HIV-specific CTL activity de	VLEDINL, so there was no evidence for clines when HEPS sex workers stop			
Protease (30–38)	Pol (85–93)	DTVLEDINL	HIV-1 infection, HIV-1 e seronegative	exposed human (A*6802)	Kaul2001a			
	HIV-1-infected female	Nairobi sex workers	a panel of 54 predefined HIV-1 epito					
					at have previously been associated with opes recognized by the HIV-1 infected			
	<ul> <li>43/91 HEPS women had CD8+ responses and detection of HIV-1-specific CTL in HEPS women increased with the duration of viral exposure</li> <li>Among HLA-A*6802 women, 11/12 HEPS and 6/11 HIV-1 infected women recognized this epitope likelihood ratio 4.4, p value 0.08, and HEPS women tended to respond to DTVLEDINL, infected women tended to ETAYFYILKL</li> </ul>							
	<ul> <li>The dominant response to this HLA allele was to this epitope in 10 of the 11/12 HEPS cases, but in only 4 of the 6/11 HIV-1 infected women</li> <li>Differences in epitope specificity were only seen for responses restricted by class I HLA alleles A2, A24, A*6802, B14, and B18, previously shown to be associated with resistance to HIV-1 in this cohort</li> </ul>							
	• Four epitopes were considered to be "resistant epitopes", as they were preferentially reactive in HEPS women and so may confer resistance, and these were found in three different proteins: A2 ILK(D/E)PVHGV in RT, A*6802 DTVLEDINL in Protease, B14 DLN(M/T)LN(I/V)V in p24 and B18 FRDYVDRF(Y/F)K also in p24							
	<ul> <li>Subject ML 857 shifte VPLRPMTY response</li> <li>Subject ML 1203 start additional responses to</li> <li>Subject ML 1707 start RDYVDRFFKTL post</li> </ul>	d from a A*6802 DTVL post-seroconversion, an ed with CTL responses to A*6802 ETAYFILKL ved with a CTL response t-seroconversion, and the	EDINL and B35 (H/N)PDIVIYQY rd the loss of the pre-seroconversion to A*6802 DTVLEDINL and B7 FPV which became dominant, B7 TPGPG to A*6802 DTVLEDINL prior to set closs of the pre-seroconversion responsion to seroconversion, but respond	response was not due to sequence VTPQVPLR prior to seroconverse V/IRYPL, B7 IPRRIRQGL, and roconversion, and switched to A onse was not due to sequence var	e variation within these epitopes ion, and upon seroconversion acquired B7 SPRTLNAWV 6802 ETAYFILKL and A24 iation within the epitope			
Protease (30–38)	Pol  Neisseria gonorrhea ce T-cells, detected by int Ghonorrhea caused the	racellular cytokine produ e weaker HIV-1 specific	HIV-1 infection an sex workers caused a functional description and tetramer assays, while not CTL responses in 4 HIV-1 exposed p CTL in 2 HEPS subjects were shown	affecting the total number of epersistently seronegative (HEPS)	itope-specific CTLs. women to become undetectable by			
Protease (45–54)	<ul><li>for the A3 supertype)</li><li>Progressors had memo</li><li>A positive correlation</li></ul>	while the effector cells or ory resting CD8+ T-cells between effector CD8+	f long-term nonprogressors recognize that recognized far fewer epitopes th	ed far fewer epitopes an LTNPs	pes Propato2001 pes tested, (18 for the A2 supertype, 16 effector T-cells and CD4+ T-cells was			

<b>HXB2</b> Location	<b>Author's Location</b>	Sequence	Immunogen	Species (HLA)	References
	• This epitope can bind th	ree of the five HLA-A2 s	supertypes alleles (A*0201, A*020 2,	A*0203, A*0206 and A*6802)	,
Protease (75–84)	<ul> <li>Binding affinity to A*02</li> </ul>	CTL in PBMC from 5/6 nly conserved region of p could stimulate CTL: VI 201 was measured, C_1/2	seronegative donors		Konya1997
Protease (76–84)	<ul> <li>criteria, and 30 of these</li> <li>Three additional previous recognized at least one of maximum of 2)</li> <li>LVGPTPVNI binds to 4</li> </ul>	bound to HLA-A*0201 - usly described HLA-A2 e of the 23 peptides (media /5 HLA-A2 supertype all ronic HIV-1 infection rec	HIV-1 infection  the A2-supermotif pattern conserved in 20/30 bound to at least 3/5 of HLA-2 pitopes were added to the set of 20, and of 2 and maximum of 6), while 6/12 leles: A*0201, A*0202, A*0206 (high cognized this epitope by ELISPOT epitope	A2 supertype alleles tested nd 18/22 chronically infected F2 acute infected individuals reco	ILA-A2 individuals had CTL that ognized at least 1 (median of 1 and
Protease (76–84)	<ul><li>for the A3 supertype) with</li><li>Progressors had memory</li><li>A positive correlation be</li></ul>	hile the effector cells of ly resting CD8+ T-cells th	HIV-1 infection nemory resting CD8+ T-cell responses long-term nonprogressors recognized fat recognized far fewer epitopes than cells and plasma viremia and a negativ of LTNPs to clear virus	far fewer epitopes LTNPs	es tested, (18 for the A2 supertype, 16

## II-B-9 Protease-RT CTL Epitopes

HXB2 Location	<b>Author's Location</b>	Sequence	Immunogen	Species (HLA)	References		
Protease-RT (95–5)	Gag (175–184)	CTLNFPISPI	HIV-1 infection	human (A2 supertype)	Propato2001		
	• The epitope starts in Pro	otease and ends in RT					
	• Long-term nonprogresso	ors (LTNPs) had strong i	nemory resting CD8+ T-cell responses	against the majority of epitopes t	tested, (18 for the A2 supertype, 16		
	for the A3 supertype) w	hile the effector cells of	long-term nonprogressors recognized f	far fewer epitopes			
	• Progressors had memor	y resting CD8+ T-cells th	nat recognized far fewer epitopes than l	LTNPs			
	• A positive correlation be	etween effector CD8+ T-	cells and plasma viremia and a negativ	ve correlation between CD8+ effect	ctor T-cells and CD4+ T-cells was		
	observed, which may co	ontribute to the inability	of LTNPs to clear virus				
	• This epitope can bind al	l five HLA-A2 supertype	es alleles (A*0201, A*0202, A*0203, A	A*0206 and A*6802)			
Protease-RT (96–5)	Pol (176–184)	TLNFPISPI	HIV-1 infection	human (A2 supertype)	Propato2001		
	• Long-term nonprogresso	ors (LTNPs) had strong i	nemory resting CD8+ T-cell responses	against the majority of epitopes t	tested, (18 for the A2 supertype, 16		
	for the A3 supertype) w	hile the effector cells of	long-term nonprogressors recognized f	far fewer epitopes			
	<ul> <li>Progressors had memory</li> </ul>	y resting CD8+ T-cells th	nat recognized far fewer epitopes than l	LTNPs			
• A positive correlation between effector CD8+ T-cells and plasma viremia and a negative correlation between CD8+ effector T-cells and CD4+							
	observed, which may co	ontribute to the inability	of LTNPs to clear virus				
		•	supertypes alleles (A*0201, A*020 2,	A*0203, A*0206 and A*6802)			
			* **				

## II-B-10 RT CTL Epitopes

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
RT (3–12)	RT (LAI)  Recognized by CTL fr Highly conserved acro	_	HIV-1 infection EILKEPVGHGV was also recognized	human (A2, B61)	vanderBurg1997
RT (3–12)	<ul> <li>A subset of the potent epitopes could stimula</li> </ul>	ial epitopes was identified ate IFN $\gamma$ production in an	n with the program Conservatrix to ider that could bind to the appropriate HLA ELISPOT assay 7 epitope in this study, it had been prev	A-allele, and 15 predicted B7 st	uperfamily (HLA B7, B8, and B58)
RT (5–29)	RT (160–184 HXB2)  • One of five epitopes d	IETVPVKLKPGMDG WPLTEE efined for RT-specific CTI	PKVKQ- HIV-1 infection  L clones in this study	human (B8)	Walker1989
RT (18–26)	RT (185–193 LAI) • C. Brander notes this is	GPKVKQWPL is a B*0801 epitope		human (B*0801)	Brander2001
RT (18–26)			HIV-1 infection wed transactive inhibition of specific C h a discussion of antagonism	human (B8) TL-mediated lysis	Meier1995, Menendez-Arias1998
RT (18–26)	RT (173–181)  • Included in a study of • Article reviewed in [N		h a discussion of antagonism	human (B8)	Goulder1997g, Menendez-Arias1998
RT (18–26)	RT (185–193 LAI) • Predicted epitope base	GPKVKQWPL ed on B8-binding motifs, f	rom larger peptide IETVPVKLKPGM	human (B8) DGPKVKQWPLTEE	Sutton1993
RT (18–26)			HIV-1 infection  found in viral PBMC DNA and RNA a discussion of antagonism	human (B8)	Klenerman1995, Menendez-Arias1998
RT (18–26)	<ul> <li>HIV-uninfected donor</li> <li>Strong CTL responses macrophages were not</li> <li>A weak response to K</li> </ul>	s using peptide-pulsed AF were elicited by the epitor table to prime a CTL resp LTPLCVSL was stimulate	in vitro stimulation and dendritic cells to stimulate primar PC – the dendritic cells performed bette opes DRFYKTLRA and GEIYKRWII onse against DRFYKTLRA ed using macrophages as the APC lowing previously-defined HIV epitope	er as APC for the stimulation of when presented by either imma	primary responses ture or mature dendritic cells –

HXB2 Location	<b>Author's Location</b>	Sequence	Immunogen	Species (HLA)	References
RT (18–26)	RT (185–193) • Epitope name: GPK	GPKVKQWPL	HIV-1 infection	human (B8)	Oxenius2000
	<ul> <li>Patients who started the CD4 proliferative resp</li> </ul>	onses and were able to ma	ction (three with sustained therapy, two with aintain a CTL response even with undetectab responses and lost their CTL responses when	ole viral load – three pat	ients that had delayed initiation of
	<ul> <li>Patient SC2 (HLA A1 peptides – FLKEKGG FLKENGGI was foun</li> <li>Patient SC11(HLA A1</li> </ul>	L tetramer staining steadil d in 8/10 clones l, B8, Cw0201, DR3/11, Ε	4/53, DQ7) had CTL responsiveness against ly declined and at day 1340 the FLKEKGGL DR52, DQ2/7) started therapy early, remained	stained cells were no led on therapy for 40 days	longer detected and the escape mutant s, then reinitiated HAART at day 640
RT (18–26)	Pol • CTL responses were s	GPKVKQWPL tudied by tetramer staining	WPL, and GEIYKRWII throughout and rece HIV-1 infection g in 41 patients with combination therapy – a gen-specific cells capable of differentiating in	human (B8) activated CD8+ T-cells	Seth2001 decline as the viral load drops in
RT (18–26)	<ul> <li>individuals treated dur</li> <li>The breadth and specifindividuals with prima (Group 3), using 259 c</li> <li>Previously described a</li> </ul>	ring chronic infection ficity of the response was our firm infection but post-serod overlapping peptides spant and newly defined optimal	HIV-1 infection d in a narrower CTL response, stronger T held determined using ELISPOT by studying 19 is conversion therapy (Group 2), and 10 individing p17, p24, RT, gp41, gp120 and Nef epitopes were tested for CTL response L response to this epitope broken down by gr	individuals with pre-ser duals who responded to	oconversion therapy (Group 1), 11 HAART given during chronic infection
RT (18–26)			HIV-1 infection, HIV-1 exposed seronegative , C, and D panel of 54 predefined HIV-1 epitopes in 91	human (B8)  HIV-1-exposed, persis	Kaul2001a stently seronegative (HEPS) and 87
RT (18–26)	RT (18–26)  • B8-restricted CTL acc	GPKVKQWPL ounted for about 1/3 of the	HIV-1 infection e total CTL response in one individual	human (B8)	Day2001
RT (18–26)	RT • Epitope name: GPK • Using previously defin	GPKVKQWPL	HIV-1 infection  O, Oxenius 2001a] in an IFN gamma Elispot as	human (B8)	Oxenius2002b
	period including thera	py with standard treatmen			-
RT (18–27)	Pol	GPKVKQWPLT	with the program Conservatrix to identify c	human (B7, B8)	De Groot2001

HXB2 Location	<b>Author's Location</b>	Sequence	Immunogen	Species (HLA)	References		
	epitopes were identified	that could stimulate IFNγ	t could bind to the appropriate H broduction in an ELISPOT assay ntified HLA-B8 epitope, and new	•	uperfamily (HLA B7, B8, and B58)  ope in this study		
RT (33–41)	RT (33–41 LAI) • C. Brander notes this is a	ALVEICTEM an A*0201 epitope	HIV-1 infection	human (A*0201)	Brander2001		
RT (33–41)	<ul> <li>Patient 201#5, (A*0201)</li> <li>M41L gave an increased</li> <li>Three additional A*0201</li> <li>M41L occurred at ancho</li> </ul>	, was found by ELISPOT t A2 binding score (http://bi individuals and one B27 i r positions p2 and p9 in sev	HIV-1 infection on induced by nucleosidee reverse o recognize the mutated peptide a imas.dcrt.nih.gov/molbio/hla_bin ndividual did not respond to this veral computer predicted RT epito reased the predicted binding affin	after zidovudine treatment, but no d) compared to the wildtype RT s epitope before or after treatment opes (33-41, 32-41, and 40-49)	•		
RT (33–41)	RT (33–41)  Of 98 patients in cross-sopatients, respectively)  New clusters of epitopes	•		human (A2) immunogenic than Integrase and	Haas1998 Protease (81%, 51%, and 24% of 37		
RT (33–41)	RT (33–41) ALVEICTEM HIV-1 infection human (A2) Day2001  • The CTL response to optimally defined CTL epitopes restricted by HLA class I A and B alleles in individuals who coexpressed HLA A2, A3, and B7 w studied in eight HIV-1-infected subjects, two with acute infection, five with chronic, and one long-term non-progressor (LTNP)  • 2 to 17 epitopes were recognized in a given individual, A2-restricted CTL response tended to be narrow and never dominated the response, and 25/27 epitopes were targeted by at least one person  • SLYNTVATL was the dominant A2 epitope recognized in patients with chronic infection, except for Subject 11841 who recognized 5/8 epitopes and w had a dominant A-2 response to ALVEICTEM						
RT (33–43)	<ul><li>patients, respectively)</li><li>New clusters of epitopes</li></ul>	were defined utilizing diff			Haas1998 Protease (81%, 51%, and 24% of 37		
RT (33–43)	RT (33–43) • C. Brander notes this is a	ALVEICTEMEK an A*0301 epitope	HIV-1 infection	human (A*0301)	Brander2001		
RT (33–43)	studied in eight HIV-1-ir • 2 to 17 epitopes were recepitopes were targeted by	affected subjects, two with a cognized in a given individ- y at least one person	HIV-1 infection ses restricted by HLA class I A an acute infection, five with chronic, sual, A2-restricted CTL response t 8 A3 epitopes, but none was clean	and one long-term non-progressorended to be narrow and never do			

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
RT (38–52)	A live attenuated bacte	CTEMEKEGKISKIGP Salmonella HIV component: rial vaccine, Salmonella SL320 B/c mice (<15% lysis assayed by	61-pHART, with an inserted H	murine $(H-2^d)$ IV epitope in the Lpp-OmpA-HIV	Burnett2000 fusion protein, induced a specific
RT (38–52)	<ul> <li>Murine and human hel</li> </ul>		-	murine $(H2^k)$ Domain of RT and is a helper and C	De Groot1991, Menendez-Arias1998 TL epitope.
RT (38–52)	RT (205–219)  • Murine and human hel • Epitope noted in a revi		HIV-1 infection to be located in the "fingers" do	human (broad)  Domain of RT and is a helper and C	Hosmalin 1990, Menendez-Arias 1998 TL epitope.
RT (39–47)	• The new assay is CTL		s based on the discovery that C	C3H/HeJ mice L recognition of peptide-MHC cla TL develop adhesive properties up by CAA	
RT (39–47)	single mutations which restored by an addition • 2E and 9I are anchor re	n did not alone abrogated CTL all substitution, and (iii) someti	activity did abrogate activity witness there was recognition of to M in the third position, it enhances	then combined, (ii) loss of recogni wo single substitutions as well as	Leggatt1998 combinations were observed: (i) two tion of a single substitution could be the combination of those substitutions polymorphism at this site is important
RT (42–50)	RT (42–50 LAI) • C. Brander notes this i	EKEGKISKI s a B*5101 epitope	HIV-1 infection	human (B*5101)	Brander2001
RT (42–50)	patients, respectively)	EKEGKISKI -sectional analysis, 78% had C es were defined utilizing differe		human (B51) immunogenic than Integrase and l	Haas1998 Protease (81%, 51%, and 24% of 37
RT (57–65)	for the A3 supertype)  • Progressors had memo  • A positive correlation observed, which may of	while the effector cells of long- ry resting CD8+ T-cells that re	term nonprogressors recognize cognized far fewer epitopes that and plasma viremia and a negative NPs to clear virus	nd far fewer epitopes an LTNPs ative correlation between CD8+ ef	Propato2001 s tested, (18 for the A2 supertype, 16 fector T-cells and CD4+ T-cells was

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
RT (73–82)			HIV-1 infection ent mutation induced by nucleoside rever		
			recognized before and after zidovudine transfer epitopes and was predicted to reduce		
RT (73–82)	RT (228–237) • Epitope name: A3-KK	KLVDFRELNK	HIV-1 infection	human (A3)	Yu2002a
	<ul> <li>CTL responses in 18 a</li> <li>One individual, AC-06 interruptions (STI). He restricted by HLA-A3,</li> <li>0/14 HLA-A3 positive</li> </ul>	acutely HIV-infected HLA- 6, was homozygous at all the e had only two detectable C , 11 by HLA-B7, and 1 by e individuals had detectable	A3 (n=7) or -B7 (n=4) or both -A3 and B aree class I alleles (A3, B7, Cw7), was tree? TL responses during acute infection, but HLA-Cw7.  A3-restricted responses to this epitope duals began to have detectable responses to	eated during acute infection t after STI this broadened during acute infection, but	on and had supervised treatment to 27 distinct epitopes including 15
RT (93–101)	(LAI)	GIPHPAGLK		(A3)	Altfeld2000a, Brander2001
RT (93–101)	RT (248–257) • Epitope name: A3-GK	GIPHPAGLK	HIV-1 infection	human (A3)	Yu2002a
	restricted by HLA-A3, • 0/14 HLA-A3 positive	, 11 by HLA-B7, and 1 by individuals had detectable	CTL responses during acute infection, but HLA-Cw7.  A3-restricted responses to this epitope duals began to have detectable responses to	luring acute infection, but	
RT (93–102)	Pol (240–249 93TH25 subtype CRF01)	3 GIPHPAGLKK	HIV-1 exposed seronegative	human (A11)	Sriwanthana2001
	• Epitope name: P248-2				
	<ul> <li>Epitope name: P248-2</li> <li>This was a study of HI</li> <li>HLA-A11 is very com and CTL responses we</li> <li>This epitope was weak</li> </ul>	IV-1 exposed persistently someon in this population, and ere found in 8/8 HIV+ cont	eronegative (HEPS) female sex workers in discovery discovery was enriched among the HEPS sexwork rols, and 0/9 HIV- women that were not early subject 265 who was HLA A2/A11 and some subject 265 who was HLA	kers – weak CTL response exposed	hailand es were detected in 4/7 HEPS women

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
RT (98–113)	Pol (254–264 BH10, LAI)	AGLKKKKSVTVLDVGD	HIV-1 infection	human	Maksiutov2002
	• This CTL epitope (the H	ntigenic similarity matrix to co IIV-1 LAI fragment with high s d leukocyte-cell adhesion mole	imilarity to a human protein ov	verlapping this epitope is GLKK	KKSVTVL) has similarity with the
RT (98–113)	immunologically norma		cur at a frequency between 0.1	and 1% in the infected population	Bernard1998 biting immune dysregulation – such on
RT (103–117)		KKSVTVLDVGDAYFS x rare long-term survivor HIV-i nd in any of the six INHIs, but a		human (Cw4) ted for many years without exhi ity was founded in 3/6 INHIs	Bernard1998 biting immune
RT (107–115)	RT (262–270 IIIB) • C. Brander notes this is	TVLDVGDAY a B*3501 epitope		(B*3501)	Brander2001
RT (107–115)	RT (262–270 IIIB)	TVLDVGDAY	HIV-1 infection	human (B35)	Menendez-Arias1998, Wilson1996
	<ul> <li>TVLDMGDAC is a natu</li> </ul>	rally occurring variant that is le	ess reactive	ther-infant HIV transmission stu (Asp-110) in the active site of I	•
RT (107–115)	• Detection of CTL escapinfants	TVLDVGDAY ternal CTL responses in the core mutants in the mother was ass at gave a positive CTL response	sociated with transmission, but		Wilson1999a  ne virus tended to be found in infected
RT (107–115)	Pol (262–270) • One of the 51 HIV-1 epi HLA alleles	TVLDVGDAY topes selected by Ferrari et al. a	HIV-1 infection as good candidate CTL epitope	human (B35) s for vaccines by virtue of being	Ferrari2000 conserved and presented by commor
RT (107–115)	<ul> <li>individuals treated durin</li> <li>The breadth and specific individuals with primary (Group 3), using 259 ov</li> <li>Previously described and</li> </ul>	g chronic infection  ity of the response was determit  infection but post-seroconverserlapping peptides spanning p1  d newly defined optimal epitope	ined using ELISPOT by studying ion therapy (Group 2), and 10 7, p24, RT, gp41, gp120 and Nes were tested for CTL respons	ng 19 individuals with pre-seroc individuals who responded to H. ef	Altfeld2001b erse viral population than was seen in onversion therapy (Group 1), 11 AART given during chronic infection oup 2, and 0/1 group 3
RT (107–115)	• Epitope name: Pol-TY9	TVLDVGDAY	HIV-1 infection	human (B35)	Sabbaj2002b

HXB2 Location	<b>Author's Location</b>	Sequence	Immunogen	Species (HLA)	References
	Among HIV+ individu	als who carried HLA E	335, 8/21 (38%) recognized this epitope		
RT (107–115)	responded to Gag, 8/1 CD8+ T-cells in one w T-cells in breast milk f carry known B35 epito The frequencies of res	1 responded to Pol, 7/1 roman, and another work from a volunteer who wope TVLDVGDAY.  ponses in the two comp	HIV-1 infection 5 HIV-1 infected women from the US a 1 women to Nef, and 2/5 women to Env nan had cytolytic responses measured b as HLA A3, A11, B35, B51 induced IFI partments differed, and 2/4 women that r ponses in peripheral blood cells.	peptide pools. These responses y Cr-release. Ngamma after stimulation with	were shown to be primarily due to either of two overlapping peptides that
RT (108–118)			in vitro stimulation rimary CTL induction after repeated stir IC derived from uninfected individual	human (A*0201) mulations with peptide	vanderBurg1996
RT (108–118)	monthly into six HIV-i  1/6 showed increased on o change – pulsed DO  VLDVGDAYFSV is a	infected patients env-specific CTL and in Cs were well tolerated conserved HLA-A2 ep	HIV-1 infection and from HLA-identical siblings, pulsed whereased lymphoproliferative responses, itope included in this study – 4/6 patienter two had the sequences EEDVGDAY	2/6 showed increase only in protest had this sequence as their HI	oliferative responses, and 3/6 showed V direct sequence, but only one of
RT (108–118)	RT (267–277)  • Binds HLA-A*0201 –  • VLDVGDAYFSV is in		in vitro stimulation itro stimulation of PBMC from an HIV	human (A2) negative donor	vanderBurg1995
RT (108–118)	Pol (263–273) • One of the 51 HIV-1 e HLA alleles	VLDVGDAYFSV pitopes selected by Feri	HIV-1 infection rari et al. as good candidate CTL epitopo	human (A2, A*0201) es for vaccines by virtue of bein	
RT (108–122)	immunologically norm	nal HIV-infected (INHI)	LDE HIV-1 infection ivor HIV-infected people who were infector ocases occur at a frequency between 0.1 NHIs, but above background CTLp active	and 1% in the infected populat	
RT (113–120)	<ul> <li>(Nat. Med. 2:405, 199</li> <li>15% of Japanese popu</li> <li>Of the 172 HIV-1 pept positive individuals, and</li> </ul>	6;Lancet 22:1187, 1986 lations carry HLA-B51 tides with HLA-B*5101 nd six were properly pro	HIV-1 infection h slow progression to AIDS, while HLA 6;Hum Immunol 22:73, 1988;Hum Imm while HLA-B27 and -B57 are detected l anchor residues, 33 bound to HLA-B* cocessed d among B subtype sequences, DAYFS	nunol 44:156, 1995) in less than 0.3% 5101, seven of these peptides w	with a rapid progression to AIDS

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
RT (116–135)	<ul><li>each HIV protein.</li><li>Nef and p24 had the high</li></ul>	hest percentage of reactive peptic	105 HIV-1 positive Botswanans; Edes, and p24 had the highest magnit	ude of HIV-1 responses.	Novitsky2002 om between 55 and 64 subjects for
RT (117–126)	Pol (264–273 93TH253 subtype CRF01)  • Epitope name: P272-281  • This was a study of HIV-  • HLA-A11 is very comm and CTL responses were	SVPLDESFRK  1 -1 exposed persistently seronegate on in this population, and was enterfound in 8/8 HIV+ controls, and	tive (HEPS) female sex workers in Carriched among the HEPS sexworker to 10/9 HIV- women that were not exp	human (A11)  Chiang Mai, northern Thails s – weak CTL responses we cosed	ere detected in 4/7 HEPS women,
RT (117–126)	Pol (264–273 93TH253 subtype CRF01)  HLA-A11 CRF01 (called Thailand, of whom more 77 possible HLA-A11 epepitopes for CTL respon This is one of the new A	SVPLDESFRK  d subtype E in Bond et al.) epitope than half were HLA-A11 positive bitopes were first defined using E ses from 8 HLA-A11 positive FS 11 epitopes identified through the	HIV-1 infection  pes were identified that stimulated Cove EpiMatrix, these were screened for books, six were novel, six were previous estreamlined EpiMatrix method, and A and B, and exact matches were un	human (A11)  CTL from HIV+ female sex binding to A11 finding and 2 busly identified and 3/8 tested FSWs recognized.	Bond2001 workers (FSW) from Northern 26 bound, and 12 of these were
RT (118–127)	RT (273–282 SF2)  • A CTL clone responsive • 4/7 B35-positive individe • A K to E substitution at • [Menendez-Arias 1998],	VPLDKDFRKY  to this epitope was obtained uals had a CTL response to this eposition 5 abrogates specific lysic in a review, notes that a Glu to Ly	HIV-1 infection	human (B*3501)	
RT (118–127)	RT (273–282 IIIB)  • C. Brander notes this is a	VPLDEDFRKY	HIV-1 infection	human (B*3501)	Brander2001
RT (118–127)	Pol (273–282)  CD8+ T-cells that bound A significant increase in healthy individuals CD28-CD45RA- cells ar	VPLDKDFRKY I one of six HIV-specific B*3501 CD28-CD45RA- cells and a decre likely to be effector cells and h	HIV-1 infection -epitope tetramers did not express C rease of CD28+CD45RA+ cells wa nave high levels of perforin in their o nically infected HIV-1-infected patie	s observed in chronically H cytoplasm	
RT (118–127)	(SF2) • Epitope name: HIV-B35	VPLDEDFRKY 01-SF2-4	HIV-1 infection	human (B*3501)	Tomiyama2000b

HXB2 Location	<b>Author's Location</b>	Sequence	Immunogen	Species (HLA)	References
	B*3501 VPLDEDFRKY epitope IPLTEEAEL	Y tetramer binding did no	ot inhibit CTL activity of a clone tha	t react with both HLA-B*3501 than	n HLA-B*5101 presentation of the
RT (118–127)	RT (273–282 IIIB) • Binds HLA-B*3501	VPLDEDFRKY	HIV-1 infection	human (B*3501, B35)	Shiga1996
RT (118–127)	• 3/9 CTL epitopes had supeptide to B35 and was	iously described HIV-1 lubstitutions that were mo shown to be an escape m/10 of the B35+ individu	B35 CTL epitopes were obtained in re common in B35+ individuals than	n in B35- individuals – only one of	these reduced the binding of the
RT (118–127)	<ul><li>VPLDKDFRKY, a varia</li><li>VPHDEDFRKY, a varia</li></ul>	ant found in HIV MN, wa ant found in HIV YU2, w	2	human (B35) e lab workers accidentally infected v	Sipsas1997 with HIV-1 IIIB
RT (118–127)	<ul> <li>individuals treated durin</li> <li>The breadth and specific individuals with primary (Group 3), using 259 ov</li> <li>Previously described an</li> </ul>	g chronic infection bity of the response was of infection but post-seroc erlapping peptides spand d newly defined optimal	HIV-1 infection I in a narrower CTL response, strong determined using ELISPOT by study conversion therapy (Group 2), and 10 ting p17, p24, RT, gp41, gp120 and 10 epitopes were tested for CTL response The response to this epitope broken do	ving 19 individuals with pre-serocor 0 individuals who responded to HA. Nef nse	nversion therapy (Group 1), 11 ART given during chronic infection
RT (118–127)	<ul><li> Epitope name: Pol-VY1</li><li> Among HIV+ individua</li></ul>		HIV-1 infection , 5/21 (24%) recognized this epitope	human (B35)	Sabbaj2002b
RT (126–135)	HIV-seropositive for 6 y	rears and had not receive ome CTL epitopes are po	HIV-1 infection recombinant vaccinia-RT-infected B-d any antiretroviral therapy porly presented on the surface of infe		
RT (127–135)			HIV-1 infection the A2-supermotif pattern conserved - 20/30 bound to at least 3/5 of HLA		Altfeld2001c ences – 233 peptides met this

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
	recognized at least one maximum of 2)  • 2/22 individuals with c  • 0/12 acutely infected in	of the 23 peptides (me hronic HIV-1 infection dividuals recognized t	a2 epitopes were added to the set of 20, a dian of 2 and maximum of 6), while 6/1 recognized this epitope in ELISPOT his epitope alleles: A*0201, A*0202,A*0203, A*02	2 acute infected individuals reco	ognized at least 1 (median of 1 and
RT (127–135)	for the A3 supertype) v • Progressors had memore • A positive correlation be observed, which may c	while the effector cells ry resting CD8+ T-cell between effector CD8+ ontribute to the inability	HIV-1 infection g memory resting CD8+ T-cell response of long-term nonprogressors recognized s that recognized far fewer epitopes than T-cells and plasma viremia and a negati ty of LTNPs to clear virus types alleles (A*0201, A*0202, A*0203,	far fewer epitopes LTNPs ve correlation between CD8+ ef	es tested, (18 for the A2 supertype, 16
RT (128–135)	• Epitope name: Pol-TI8	TAFTIPSI	HIV-1 infection	human (A*0217, B*5101)	Sabbaj2002b
	<ul> <li>24 epitopes were descr</li> <li>Serial peptide truncation</li> <li>Patient 01RCH46 was B*4002, and KETINEI</li> </ul>	ibed – 8 were novel, 8 ons were used to define Hispanic, on HAART, EAA p24(70-78), HLA	V-1 infected minority women living in the used new restricting elements but were propriated epitopes for CTL cell lines isolated and had a viral load of 21000 and CD4 cm B*4002 at 202, 7/36 (19%) recognized this epitoper	previously defined epitopes, and ated from 12 individuals, assaye count of 623 – she also recognize	d by a Cr-release ed GELDRWEKI, p17(11-19), HLA
RT (128–135)	RT (295–302 IIIB) • C. Brander notes this is	TAFTIPSI a B*5101 epitope	HIV-1 infection	human (B*5101)	Brander2001
RT (128–135)	<ul> <li>Med. 2:405, 1996;Land</li> <li>15% of Japanese popul</li> <li>Of the 172 HIV-1 pepti positive individuals, an</li> </ul>	cet 22:1187, 1986;Hun ations carry HLA-B51 des with HLA-B*5101 d six were properly pro	HIV-1 infection In slow progression to AIDS, while HLA- Immunol 22:73, 1988; Hum Immunol 4 while HLA-B27 and -B57 are detected anchor residues, 33 bound to HLA-B*5 Decessed d among B subtype sequences, but TAF	4:156, 1995) in less than 0.3% 5101, seven of these peptides we	
RT (128–135)	RT (295–302) • Epitope name: P5 • The epitope TAFTIPSI	TAFTIPSI was recognized by pat	HIV-1 infection ient 246#1 in a study of the effects of the	human (B*5101) erapy escape mutations on CTL	Samri2000 recognition

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
RT (128–135)	Cohort Study. 64 signi-B15. Fifteen of these particular HLA molector TAFTIPSI was one of of HLA-B*5101 indiv	ficant associations betwo were in positions with k ules flanked known epitotwo epitopes characterize iduals had substitutions in	HIV-1 infection amined relation to HLA alleles found i gen polymorphisms at particular position nown epitopes, 4 in anchor residues, 11 ppes and may relate to processing. ed in detail. C-terminal I135x substitution this position, while only 127/431 (29 to abrogate binding to HLA-B*5101.	ons and HLA alleles were detect I in other positions. Six addition tions were associated with peopl	ed, for HLA-B7, -B12, -B35 and all polymorphic sites associated with e who carried HLA-B5 – 39/40 (98%)
RT (128–135)	RT (295–302 IIIB)	TAFTIPSI	HIV-1 infection e of CTL epitopes recognized by 3 lab	human (B51)	Menendez-Arias1998, Sipsas1997
	<ul> <li>TAFTIPST, a variant f</li> <li>TAFTIPSV, a variant f</li> <li>TVFTIPSI, a variant f</li> <li>[Menendez-Arias 1998]</li> </ul>	ound in HIV-1 CAM1, w ound in HIV-1 VE1RT, v ound in HIV-1 MANC, v	was also recognized but 100-fold more p was also recognized, but 10-fold more p was also recognized this epitope includes a region near the	peptide was needed peptide was needed	
RT (128–135)	<ul> <li>95 optimally-defined p</li> </ul>	peptides from this databatiduals that responded to	HIV-1 infection FL that reacted to SLYNTVATL, calling se were used to screen for INFγ respon SLYNTVATL recognized additional H	ises to other epitopes	
RT (128–135)	CD4 proliferative resp HAART had no HIV s undetectable	onses and were able to n pecific CD4 proliferative	HIV-1 infection  Section (three with sustained therapy, two naintain a CTL response even with under responses and lost their CTL responses on the poitope but none were HLA B51+	etectable viral load - three patie	ents that had delayed initiation of
RT (128–135)	CD8+ cell IFNgamma • In general, during the specificities that were HIV-specific response.	production to measure r first month of treatment not previously detectable s diminished	HIV-1 infection  es was tested in 14 HIV+ patients from esponses viral load decreased and frequencies of e were newly detected, as were CMV sponse: increases or decreases in pre-exist.	HIV-specific CTL tripled and b pecific CD8+ PBL – but with co	roadened – eight new HIV ontinued viral suppression,

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
RT (128–135)	responded to Gag, 8/1 CD8+ T-cells in one w • T-cells in breast milk f carry known B51 epito • The frequencies of res	I responded to Pol, 7/11 wo oman, and another woman rom a volunteer who was H pe TAFTIPSI. ponses in the two compartm	HIV-1 infection IV-1 infected women from the US a men to Nef, and 2/5 women to Env had cytolytic responses measured b LA A3, A11, B35, B51 induced IF tents differed, and 2/4 women that res in peripheral blood cells.	peptide pools. These responses by Cr-release.  Ngamma after stimulation with e	were shown to be primarily due to either of two overlapping peptides that
RT (151–159)	<ul><li>15% of Japanese popu</li><li>Of the 172 HIV-1 pept positive individuals, ar</li></ul>	ides with HLA-B*5101 and six were properly process	le HLA-B27 and -B57 are detected hor residues, 33 bound to HLA-B*.	5101, seven of these peptides we	Tomiyama1999  The reactive with CTL from 3 B*5101
RT (153–165)	RT (308–320) • Epitope defined in the	WKGSPAIFQSSMT context of the Pediatric AII	HIV-1 infection OS Foundation ARIEL Project, a mo	human (B7) other-infant HIV transmission stu	Brander1995b ady
RT (153–165)	Pol (308–320) • One of the 51 HIV-1 ephLA alleles	WKGPAIFQSSMT pitopes selected by Ferrari e	HIV-1 infection et al. as good candidate CTL epitopo	human (B7) es for vaccines by virtue of being	Ferrari2000 g conserved and presented by common
RT (153–167)	from 7 proteins, sugge	sting that the breadth of CT	HIV-1 infection erlapping peptides spanning all HIV L responses are underestimated if a AIFQSSMTKI were recognized		Altfeld2001a was found to react with 12 peptides ed in the study
RT (156–164)	• Only 1/7 B35-positive	SPAIFQSSM  ve to this epitope was obtain individuals had a CTL resp ], in a review, notes that this		human (B*3501)	Menendez-Arias1998, Tomiyama1997
RT (156–164)	RT (311–319 SF2)  • Binds HLA-B*3501  • [Menendez-Arias1998]	SPAIFQSSM  ], in a review, notes that this	HIV-1 infection	human (B35) in the active site of RT	Menendez-Arias1998, Shiga1996
RT (156–164)	Pol (311–319)	SPAIFQSSM	HIV-1 infection	human (B35)	Ferrari2000 g conserved and presented by common
RT (156–164)			HIV-1 infection minant response in a rapid progress ominant HLA A*0201 epitope SLY		

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
	<ul><li>Despite the initial narro</li><li>No HIV-specific lymph</li></ul>	w response to two epito oproliferative responses	ponse at the time of the initial drop in opes, no other CTL responses developes were detected in this patient, and neu (spaifqCsm, spSifqssm), but the bindi	ed atralizing antibody response was	weak
RT (156–164)	<ul> <li>This individual had a desubdominant response to</li> </ul>	ominant response to IPI to SPAIFQSSM – durin	HIV-1 infection acute infection through death, and had RRIRQGL with strong in vivo activate g the course of disease progression (4 TL clones specific for IPRRIRQGL pe	ed responses and in vitro stimulat Years), the functional CTL respo	
RT (156–164)	<ul> <li>individuals treated duri</li> <li>The breadth and specification individuals with primar (Group 3), using 259 ov</li> <li>Previously described an</li> </ul>	ng chronic infection city of the response way y infection but post-ser verlapping peptides spand newly defined optima	s determined using ELISPOT by study	ving 19 individuals with pre-sero O individuals who responded to F Nef nse	IAART given during chronic infection
RT (156–164)	<ul> <li>One individual, AC-06, interruptions (STI). He restricted by HLA-A3,</li> <li>1/11 HLA-B7 individual</li> </ul>	utely HIV-infected HL. was homozygous at all had only two detectable 11 by HLA-B7, and 1 bals had detectable B7-re		vas treated during acute infection n, but after STI this broadened to acute infection – 10/15 of HL	and had supervised treatment
RT (156–165)			HIV-1 infection  th can be induced by nucleosidee reverse from the effects of therapy escape mutation		Samri2000
RT (156–165)	RT (311–319 SF2)  • Pers. Comm. from C. F	SPAIFQSSMT  Hey and D. Ruhl to C. B		human (B7)	Brander1997, Menendez-Arias1998
RT (156–165)	RT (311–319 SF2)  • Epitope name: P4  • A panel of 16 epitopes CD8+ cell IFNgamma		HIV-1 infection es was tested in 14 HIV+ patients fror esponses	human (B7) m an unselected Caucasian popu	Mollet2000 lation treated with HAART, using

HXB2 Location	<b>Author's Location</b>	Sequence	Immunogen	Species (HLA)	References
	specificities that were a HIV-specific responses	not previously detectab diminished	viral load decreased and frequencies of I le were newly detected, as were CMV sponse: increases or decreases in pre-existing	ecific CD8+ PBL – but with co	ontinued viral suppression,
RT (156–165)	<ul> <li>A subset of the potenti epitopes could stimula</li> </ul>	al epitopes was identifite IFN $\gamma$ production in a	on with the program Conservatrix to idented that could bind to the appropriate HLA an ELISPOT assay identified HLA-B7 epitope in this study		
RT (156–165)	Cohort Study. 64 signi -B15. Fifteen of these particular HLA molecu	ficant associations between in positions with a les flanked known epit with a S162x (18/33) s	HIV-1 infection xamined relation to HLA alleles found in veen polymorphisms at particular positior known epitopes, 4 in anchor residues, 11 copes and may relate to processing. ubstitution had higher viral loads than the	ns and HLA alleles were detect in other positions. Six addition	ed, for HLA-B7, -B12, -B35 and nal polymorphic sites associated with
RT (158–166)	RT (325–333 LAI) • C. Brander notes this is	AIFQSSMTK s an A*0301 epitope	HIV-1 infection	human (A*0301)	Brander2001
RT (158–166)	<ul> <li>The HIV-1 subtype A is which could direct the conserved, often immuted Kenya. A DNA and M included in the polyepi</li> <li>Multiple CD4+ or CD8 assays after vaccination</li> </ul>	Procused vaccine HIVA of protein to the cell memoral modominant epitopes the prime-boost vaccing tope string [Hanke2006] T-cell vaccine-induction of 5 macaques. The results of the protein for the protein of the prote	HIV-1 infection, Vaccine hia MVA boost <i>Strain:</i> subtype A <i>HIV</i> contains p24 and p17, in a reversed order abrane and inhibit efficient peptide proces hat were selected to have particularly goo ation protocol using the HIVA antigen wi 0]. hed responses to peptide pools were detect esponse to the Mamu A*01 SIV p27 epite cinated macaques, possibly because of pro-	relative to the Gag polyprotein ssing and class I presentation, and cross-reactive potential for the ill be used in a phase III clinicated using intracellular cytokine ope p11C (CTPYDINQM), inc	n to prevent myristylation of p17, as well as a polyepitope string of the A-clade epidemic in Nairobi, al trial in Kenya. This epitope is estaining and IFNgamma Elispot cluded in the polyepitope region, was
RT (158–166)	RT (325–333 LAI) • C. Brander notes this is	AIFQSSMTK s an A*1101 epitope	HIV-1 infection	human (A*1101)	Brander2001
RT (158–166)	cross-reactive and reco specific manner. Two o	gnized by clade E infe other HLA A*1101 cla nonly found in viruses i	HIV-1 infection *1101 epitopes were generated for clade cted individuals. The clade E and B analo de B defined epitopes were found not to h representing subtypes A-E. It was strongly	ogs to three more HLA A*1101 have stimulated a response in cl	epitopes was recognized in a clade ade E infected individuals.

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References				
RT (158–166)	RT (325–333)	AIFQSSMTK	HIV-1 infection	human (A*1101, A3, A*0301, A*6801)	Menendez-Arias1998, Threlkeld1997				
	• Study of the fine specificity of an A3-like super-type epitope (the A3 super-type includes A*0301, A*1101, A*3301, A*3301, and A*6801)								
			ic or hydroxyl containing anchor residue at po						
	A11 or A*6801		loned CTL lines were also derived from HIV-						
	molecule, A3 or A11		nd natural variants indicate that the same amin	•					
			of the A3 superfamily: A*0301, A*1101, and epitope – AIFQRSMTR can also bind to two						
RT (158–166)	RT	AIFQSSMTK	HIV-1 infection	human (A11)	Wagner1998a				
, ,			ow that the mediators of both the cytolytic (go were used as markers) anti-viral responses ar						
RT (158–166)	RT (325–333 LAI)	AIFQSSMTK	Peptide-HLA interaction	human (A11)	Menendez-Arias1998, Zhang1993				
	<ul> <li>Exploration of A11 bin</li> </ul>	ding motif, based on N	ixon et al. 1991						
RT (158–166)	RT (325-333 LAI)	AIFQSSMTK	HIV-1 infection	human (A11)	McMichael1994				
	<ul> <li>Review of HIV CTL ep</li> </ul>	oitopes							
RT (158–166)	Pol (305–313 93TH253 subtype CRF01)		HIV-1 infection, HIV-1 exposed seronegative	human (A11)	Sriwanthana2001				
	• Epitope name: P313-32		( (HEDC) ( 1 1 1 1	CI. M. 4 TI.	1 1				
			y seronegative (HEPS) female sex workers in and was enriched among the HEPS sexworker						
			ontrols, and 0/9 HIV- women that were not ex		referenced in 177 TEE 5 Women,				
			study subject 128 who was HLA A11/A33	•					
	<ul> <li>This epitope was strong</li> </ul>	gly reactive in HIV+ stu	dy subjects 053 and 184 who carried HLA-A	11					
RT (158–166)	Pol (305–313 93TH253 subtype CRF01)		HIV-1 infection	human (A11)	Bond2001				
			t al.) epitopes were identified that stimulated	CTL from HIV+ female se	x workers (FSW) from Northern				
	Thailand, of whom mor		A11 positive ned using EpiMatrix, these were screened for l	hinding to A11 finding and	26 hound, and 12 of these were				
			positive FSWs, six were novel, six were previ		20 bound, and 12 of these were				
			nethod to be likely to bind to A11, and it serve		s, it was one of the six A11 epitopes				
	that had been previously								
	• 6/8 tested FSWs recogn	1 1							
	<ul> <li>An HLA-A11 tetramer populations after in vitr</li> </ul>	_	ope, which was recognized by two subjects – ε	and both subjects had expan	nded tetramer staining T-cell				

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
	This epitope was highlight	y conserved in other su	btypes, and exact matches were commo	n	
RT (158–166)	Cohort Study. 64 signit-B15. Fifteen of these particular HLA molecu	ficant associations between in positions with later flanked known epit with a K166x (4/19) s	HIV-1 infection  xamined relation to HLA alleles found in ween polymorphisms at particular position known epitopes, 4 in anchor residues, 11 copes and may relate to processing.  substitution had higher viral loads than the	ons and HLA alleles were detected in other positions. Six addition	ted, for HLA-B7, -B12, -B35 and nal polymorphic sites associated with
RT (158–166)	<ul><li>specific T-cell response</li><li>Nef epitope recognition</li></ul>	es by Elispot and Tetrain was detected in all 4 s	HIV-1 infection uccessful anti-viral therapy but with ong mer staining, maintained for 2-4 years af subjects, gp120, Pol and Gag-specific in ediate maturation phenotype characteriz	fter initiation of HAART.  1 or 2 subjects.	•
RT (158–166)	<ul> <li>AIFQSSMTR and AIL</li> </ul>	QSSMTK, naturally or	HIV-1 infection  AIDS Foundation ARIEL Project, a moccurring variants, were found in infant, a was found in infant and is not recognized	and are recognized	Wilson1996 tudy
RT (158–166)		of a subset of As is AI	HIV-1 infection ses is AIFQSSMTK FQASMTK and it is less able to stimula FQSSMTK and is as reactive as the orig		Cao1997a
RT (158–166)	<ul> <li>Detection of CTL escar infants</li> </ul>	pe mutants in the moth	HIV-1 infection in the context of mother-to-infant transr er was associated with transmission, but CTL response: AIFQSSMTR mutants		Wilson1999a the virus tended to be found in infecte
RT (158–166)	<ul> <li>individuals treated duri</li> <li>The breadth and specifindividuals with primare (Group 3), using 259 o</li> <li>Previously described as</li> </ul>	ng chronic infection icity of the response wary infection but post-se verlapping peptides spand and newly defined optim	HIV-1 infection ted in a narrower CTL response, stronger as determined using ELISPOT by studying roconversion therapy (Group 2), and 10 anning p17, p24, RT, gp41, gp120 and Natal epitopes were tested for CTL response TTL response to this epitope broken down	ng 19 individuals with pre-sero individuals who responded to I lef se	econversion therapy (Group 1), 11 HAART given during chronic infection
RT (158–166)	RT (158–166) • The CTL response to o	AIFQSSMTK ptimally defined CTL of	HIV-1 infection epitopes restricted by HLA class I A and with acute infection, five with chronic, a	human (A3) I B alleles in individuals who co	Day2001 pexpressed HLA A2, A3, and B7 was

HXB2 Location	<b>Author's Location</b>	Sequence	Immunogen	Species (HLA)	References
	epitopes were targeted	I by at least one person d at least 1 A3 epitope, u	lividual, A2-restricted CTL response te up to 8 A3 epitopes, but none was clear dominant epitope		minated the response, and 25/27
RT (158–166)	<ul> <li>One individual, AC-06 interruptions (STI). He restricted by HLA-A3</li> <li>0/14 HLA-A3 positive</li> </ul>	acutely HIV-infected HL 6, was homozygous at all e had only two detectable 11 by HLA-B7, and 1 to e individuals had detectal	HIV-1 infection  A-A3 (n=7) or -B7 (n=4) or both -A3 a I three class I alleles (A3, B7, Cw7), wa e CTL responses during acute infection by HLA-Cw7. ble A3-restricted responses to this epito iduals began to have detectable responses	as treated during acute infection  a, but after STI this broadened to  ppe during acute infection, but o	and had supervised treatment o 27 distinct epitopes including 15
RT (158–166)	for the A3 supertype) • Progressors had memo • A positive correlation observed, which may	while the effector cells of ory resting CD8+ T-cells between effector CD8+ contribute to the inability	HIV-1 infection g memory resting CD8+ T-cell response of long-term nonprogressors recognized that recognized far fewer epitopes that T-cells and plasma viremia and a negat of LTNPs to clear virus alleles (A*0301, A*1101, A*3101, A*3	far fewer epitopes a LTNPs ive correlation between CD8+ e	es tested, (18 for the A2 supertype, 16
RT (158–166)	Pol (313–321) • One of the 51 HIV-1 e HLA alleles	AIFQSSMTK pitopes selected by Ferra	HIV-1 infection ari et al. as good candidate CTL epitope	human (A3, A11) es for vaccines by virtue of bein	Ferrari2000 g conserved and presented by common
RT (158–166)	Pol (325–333)	AIFQSSMTK	HIV-1 infection, HIV-1 ex	posed human (A3, A11, A3	3) Kaul2001a
	<ul> <li>HIV-1-infected female</li> <li>Responses in HEPS w reduced risk of infecti women</li> <li>43/91 HEPS women h</li> <li>Among HLA-A3 wom</li> </ul>	study CTL responses to e Nairobi sex workers comen tended to be lower on, and there was a shift and CD8+ responses and nen, 2/2 HEPS and 3/3 H		h HLA presenting molecules that con late seroconversion to epitop EPS women increased with the d pitope	at have previously been associated with pes recognized by the HIV-1 infected curation of viral exposure
RT (158–166)	RT (325–333) • Epitope defined in the	AIFQSSMTK context of the Pediatric	HIV-1 infection AIDS Foundation ARIEL Project, a mo	human (A3.1) other-infant HIV transmission st	Brander1995b audy
RT (158–166)	-		HIV-1 infection FL that reacted to SLYNTVATL, calling use were used to screen for INFγ response.	-	Betts2000 nunodominant

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
	• 1/11 of the A2+ individ	luals was HLA A3 and reacted wit	th this epitope as well as two other A	A3.1 epitopes	
RT (158–166)	RT (325–333 LAI) • Defined as minimal per	AIFQSSMTK otide by titration curve, S. Rowlan	d-Jones, Pers. Comm.	human (A33)	Rowland-Jones1995a
RT (158–166)	<ul><li>sex workers eventually</li><li>The epidemiological fa working for a period or</li></ul>	seroconverted, and for six of these ctor associated with seroconversion	HIV-1 infection esistently seronegative individuals, He HIV CTL reactive epitopes had be on was stopping sex work and HIV-s ontrols, ML1668	en defined while seronegati	ive
RT (158–166)	<ul> <li>CD8+ cell IFNgamma j</li> <li>In general, during the fi specificities that were n HIV-specific responses</li> </ul>	production to measure responses arst month of treatment viral load of not previously detectable were new diminished	HIV-1 infection  ted in 14 HIV+ patients from an uns decreased and frequencies of HIV-sp wly detected, as were CMV specific of ases or decreases in pre-existing resp	pecific CTL tripled and broacCD8+ PBL – but with conti	adened – eight new HIV inued viral suppression,
RT (158–166)	<ul> <li>CD8+ T cells were four viral load was also four</li> <li>All three patients were</li> <li>ELISPOT was used to the subjects showed a domnown</li> <li>The subject with A*020</li> <li>Weak responses were of B*2705</li> <li>No acute response was</li> </ul>	nd prior to seroconversion, and the ad B*2705, with HLA alleles: A1, A lest a panel of CTL epitopes that h inant response to the B*2705 epito 11 had a moderatly strong respons bserved to A*301-RLRPGGKKK detected to the following epitopes	and been defined earlier and were appope KRWIILGGLNK	between the number of cir B7, B2705; and A*0201, A propriate for the HLA haple FPGPGVRYPL in the subject	*0301, B2705, B39 otypes of the study subjects – 3/3 ect who was HLA A1, A*0301, B7,
RT (158–182)	RT (325–349 PV22)  • HIV-1 specific CTLs re	AIFQSSMTKILEPFRKQNP- DIVIYQ lease $\gamma$ -IFN, and $\alpha$ - and $\beta$ -TNF	HIV-1 infection	human (A11)	Jassoy1993
RT (158–182)	RT (325–349)  • Study of cytokines relea	AIFQSSMTKILEPFRKQNP- DIVIYQ ased by HIV-1 specific activated C		human (A11)	Price1995
RT (164–172)			HIV-1 infection resting CD8+ T-cell responses again n nonprogressors recognized far few		Propato2001 tested, (18 for the A2 supertype, 16

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References	
	<ul> <li>A positive correlation observed, which may of</li> </ul>	between effector CD8+ 'contribute to the inability	that recognized far fewer epitopes that T-cells and plasma viremia and a negator of LTNPs to clear virus alleles (A*0301, A*1101, A*3101, A*	ative correlation between CD8+ et	ffector T-cells and CD4+ T-cells was	
RT (173–181)	RT (173–181 LAI) • C. Brander notes this i	KQNPDIVIY s an A*3002 epitope		human (A*3002)	Brander2001, Goulder2001a	
RT (173–181)	RT KQNPDIVIY HIV-1 infection human (A*3002) Goulder2001a  • Epitope name: KY9 (RT-53)  • HLA-A*3002 is very common in African populations, 50% of Zimbabweans express HLA-A30, 44% in African Zulu, so five new HIV epitocharacterized that are presented by this HLA molecule  • A rapid method was developed combining ELISPOT with intracellular IFN-γ staining of PBMCs to map optimal epitopes, then HLA presen were defined – this method was completed within 48 to 72 hours of receipt of blood  • Two individuals were studied: Subject 199 (HLA A*0201/*3002 B*4402/51 Cw2/5), a Caucasian, and Subject 6007 (HLA A*3002/ B53/*5 African-Caribbean  • In both HLA-A*3002 individuals the response to RSLYNTVATLY was dominant  • In subject 199 four additional A*3002 epitopes were identified  • Three quantitative assays, ELISPOT, precursor frequency and chromium release, confirmed a hierarchy of response: RY11 (p17) > KY9 (gp (RT-53) > IY9 (gp41)					
RT (175–183)	RT (328–336 IIIB)  • A CTL clone responsive  • 3/7 B35-positive individe  • D to E, or V to I, subst	iduals had a CTL respon		human (B*3501) and binding to B*3501	Tomiyama1997	
RT (175–183)	RT (328–336 IIIB) • C. Brander notes this i	NPDIVIYQY s a B*3501 epitope	HIV-1 infection	human (B*3501)	Brander2001	
RT (175–183)	RT (342–350 LAI) • C. Brander notes this i	HPDIVIYQY s a B*3501 epitope	HIV-1 infection	human (B*3501)	Brander2001	
RT (175–183)	<ul><li>A significant increase healthy individuals</li><li>CD28-CD45RA- cells</li></ul>	in CD28-CD45RA- cells are likely to be effector	HIV-1 infection fic B*3501-epitope tetramers did not est and a decrease of CD28+CD45RA+ cells and have high levels of perforintlls in chronically infected HIV-1-infection	cells was observed in chronically in their cytoplasm		
RT (175–183)	Cohort Study. 64 signi -B15. Fifteen of these	ficant associations between the positions with k	HIV-1 infection amined relation to HLA alleles found een polymorphisms at particular posit nown epitopes, 4 in anchor residues, opes and may relate to processing.	ions and HLA alleles were detect	ed, for HLA-B7, -B12, -B35 and	

<b>HXB2</b> Location	<b>Author's Location</b>	Sequence	Immunogen	Species (HLA)	References
	B*35 subtypes. D177x		erized in detail. D177x substitutions are k ciated with people who carried HLA-B*3 ations.		
RT (175–183)	RT (342–350 LAI) • Review of HIV CTL e	HPDIVIYQY pitopes	HIV-1 infection	human (B35)	McMichael1994
RT (175–183)	RT (329–337) • NPDIVIYQY preferre	HPDIVIYQY d sequence for some CT	HIV-1 infection L clones, HIV-2 NPDVILIQY is also reco	human (B35) ognized	Rowland-Jones 1995b
RT (175–183)	• 3/9 CTL epitopes had peptide to B35 and wa	eviously described HIV- substitutions that were n is shown to be an escape in 8/10 of the B35+ indiv	B35 CTL epitopes were obtained in 10 nore common in B35+ individuals than in	B35- individuals – only one	of these reduced the binding of the
RT (175–183)	stimulate a primary res	sponse, only secondary – of the B35 presented test	in vitro stimulation stimulation of CTLp using optimized pep peptide-specific CTLp counts could be opeptides used in control experiments sho	obtained via staining with per	ptide-Class I tetramers
RT (175–183)	RT (328–336 IIIB)	NPDIVIYQY	HIV-1 infection	human (B35)	Menendez-Arias1998, Shiga1996
			cted in a long-term survivor, however it h tutions reduce binding [Menendez-Arias		al progressors – it is cross-reactive with
RT (175–183)	RT (328–336 IIIB)	NPDIVIYQY	HIV-1 infection	human (B35)	Menendez-Arias1998, Sipsas1997
	<ul><li>NPDIIIYQY, a variant</li><li>NPEIVIYQY, was also</li><li>NPDLVIYQY, was also</li><li>[Menendez-Arias 1998]</li></ul>	found in HIV-1 JRCSF, o recognized o recognized ], in a review, notes that I in a long-term survivor	e of CTL epitopes recognized by 3 lab we was also recognized the YXDD motif, highly conserved amor, however it has since been found in norm	ng polymerases, overlaps this	with HIV-1 IIIB s epitope – CTL activity to this epitope
RT (175–183)	RT  • A CTL response was f	NPDIVIYQY  ound in exposed but unit	HIV-1 exposed seronegative	human (B35)	Menendez-Arias1998, Rowland-Jones1998a topes that tended to be conserved in A

- and D clades such cross-reactivity could protect against both A and D and confer protection in Nairobi where both subtypes are circulating
- The A subtype consensus is HPDIVIYQY

HXB2 Location	<b>Author's Location</b>	Sequence	Immunogen	Species (HLA)	References
		, in a review, notes that in a long-term survivor	the YXDD motif, highly conserved and, however it has since been found in no		
RT (175–183)	<ul><li>Seroprevalence in this of</li><li>Most isolated HIV strain</li></ul>	cohort is 90-95% and th ins are clade A in Nairo y observed using A or I	HIV-1 exposed seronegation negative prostitutes from Nairobi – the neir HIV-1 exposure is among the higher obi, although clades C and D are also for Clade versions of epitopes de D NPEIVIYQY	se CTL may confer protection est in the world	Rowland-Jones1998b  n cross-reactive, however stronger
RT (175–183)	<ul><li>deletion in CCR5</li><li>In Gambia there is exposeems to be protective</li></ul>	osure to both HIV-1 and pitope is not conserved:	posed African female sex workers in G d HIV-2, CTL responses to B35 epitopo e NPDVILIQY, but the CTLs are cross-	es in exposed, uninfected women	n are cross-reactive, and the B35 allele
RT (175–183)	<ul> <li>CD8+ T cells were fou viral load was also four</li> <li>All three patients were</li> <li>ELISPOT was used to a subjects showed a dom</li> <li>The subject with A*020</li> <li>Weak responses were of B*2705</li> <li>No acute response was</li> </ul>	nd prior to seroconversiond  B*2705, with HLA alletest a panel of CTL epit inant response to the B*01 had a moderately strubserved to A*301-RLR detected to the following	HIV-1 infection ecific CTL responses were studied duri ion, and there was a close temporal rela- eles: A1, A30/31, B*2705, B35; A1, A copes that had been defined earlier and *2705 epitope KRWIILGGLNK ong response to SLYNTVATL EPGGKKK, A*301-QVPLRPMTYK, a ng epitopes: A*201-ILKEPVHGV, A*2 PIPVGEIY, B35-NSSKVSQNY, B35-V	ationship between the number of *0301, B7, B2705; and A*0201 were appropriate for the HLA hand B7-TPGPGVRYPL in the sum of the sum of the HLA hand B7-TPGPGVRYPL in the sum of the sum of the HLA hand B7-TPGPGVRYPL in the B7-TPGPGVRYPL in the B	, A*0301, B2705, B39 aplotypes of the study subjects – 3/3 abject who was HLA A1, A*0301, B7, QSSMTK, A*301-TVYYGVPVWK,
RT (175–183)	<ul> <li>sex workers eventually</li> <li>HPDIVIYQY or NPDI seroconversion, 7 mont</li> <li>20/20 sequences of the 857 – this was the only</li> <li>The epidemiological fa working for a period or</li> </ul>	seroconverted, and for VIYQY was recognized hs infecting strain had thre case in the study where ctor associated with ser- retire	HIV-1 infection sposed, persistently seronegative indivisity of these HIV CTL reactive epitopered in 1 of the 6 women (ML857), and the essubstitutions in this epitope, all 20 versions are a virus carrying an unrecognized form reconversion was stopping sex work an econtrol sex workers, ML887	s had been defined while serone, he response was present in the la- were NpQiIiyqy, and this form w n of the epitope broke through	gative st available sample prior to ras not recognized by CTL from ML

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References		
RT (175–183)	<ul> <li>individuals treated during</li> <li>The breadth and specification individuals with primar (Group 3), using 259 over Previously described and arrangements.</li> </ul>	ng chronic infection city of the response was of y infection but post-serocy verlapping peptides spanned newly defined optimal	determined using ELISPOT by studyi	ng 19 individuals with pre-seroc individuals who responded to H fef	AART given during chronic infection		
RT (175–183)	Pol (342–350)  • Variants (H/N)PDIVIY  • ELISPOT was used to s HIV-1-infected female	study CTL responses to a	HIV-1 infection, HIV-1 exp seronegative /B clades panel of 54 predefined HIV-1 epitope		Kaul2001a ntly seronegative (HEPS) and 87		
	reduced risk of infectio women  • 43/91 HEPS women ha  • Among HLA-B35 wom  • The dominant response infected women  • Subject ML 857 shifted	n, and there was a shift in d CD8+ responses and de nen, 2/3 HEPS and 1/4 HI to this HLA allele was to I from a A*6802 DTVLE	and focused on different epitopes with the response in the HEPS women up etection of HIV-1-specific CTL in HE IV-1 infected women recognized this to this epitope in only one of the 2/3 H DINL and B35 (H/N)PDIVIYQY resulted loss of the pre-seroconversion response.	PS women increased with the depitope EPS cases, and was not to this e ponse prior to seroconversion to	pitope in the one responsive HIV-1 a B35 PPIPVGDIY and B35		
RT (175–183)	Epitope name: Pol-HY     Among HIV+ individual		HIV-1 infection (4/21 (19%) recognized this epitope	human (B35)	Sabbaj2002b		
RT (175–183)	<ul> <li>Among HIV+ individuals who carried HLA B35, 4/21 (19%) recognized this epitope</li> <li>Pol NPDIVIYQY HIV-1 infection human (B35) Sabbaj2002a</li> <li>IFNgamma T-cell responses in breast milk of 5 HIV-1 infected women from the US and 6 from Zambia were tested with using Elispot. 11/11 women responded to Gag, 8/11 responded to Pol, 7/11 women to Nef, and 2/5 women to Env peptide pools. These responses were shown to be primarily due to CD8+ T-cells in one woman, and another woman had cytolytic responses measured by Cr-release.</li> <li>T-cells in breast milk from a volunteer who was HLA A3, A11, B35, B51 induced IFNgamma after stimulation with a peptide that carries known B35 epitope NPDIVIYQY.</li> <li>The frequencies of responses in the two compartments differed, and 2/4 women that responded to epitopes in Nef 101-205 and Pol 601-710 showed responses in breast milk but no detectable responses in peripheral blood cells.</li> </ul>						
RT (175–183)	The HIV-1 subtype A for which could direct the processor conserved, often immure Kenya. A DNA and MV	ocused vaccine HIVA cor protein to the cell membra nodominant epitopes that	HIV-1 infection, Vaccine MVA boost <i>Strain:</i> subtype A <i>HI</i> trains p24 and p17, in a reversed order and inhibit efficient peptide processor were selected to have particularly goon protocol using the HIVA antigen where the selected to have particularly goon protocol using the HIVA antigen where the selected to have particularly goon protocol using the HIVA antigen where the selected to have particularly goon protocol using the HIVA antigen where the selected to have particularly goon protocol using the HIVA antigen where the selected to have particularly goon protocol using the HIVA antigen where the selected to have particularly goon protocol using the HIVA antigen where the selected to have particularly goon protocol using the HIVA antigen where the selected to have particularly goon protocol using the HIVA antigen where the selected to have particularly goon protocol using the HIVA antigen where the selected to have particularly goon protocol using the HIVA antigen where the selected to have particularly goon protocol using the HIVA antigen where the selected to have particularly goon protocol using the HIVA antigen where the selected to have particularly goon protocol using the HIVA antigen where the selected to have particularly goon protocol using the HIVA antigen where the selected to have particularly goon protocol using the HIVA antigen where the selected to have particularly goon protocol using the HIVA antigen where the selected to have particularly goon protocol using the HIVA antigen where the selected the selected to have particularly goon protocol using the HIVA antigen where the selected	r relative to the Gag polyprotein essing and class I presentation, as od cross-reactive potential for th	tope to prevent myristylation of p17, s well as a polyepitope string of e A-clade epidemic in Nairobi,		

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
	assays after vaccinatio	n of 5 macaques. The respo	esponses to peptide pools were detense to the Mamu A*01 SIV p27 eped macaques, possibly because of	oitope p11C (CTPYDINQM), inc	luded in the polyepitope region, was
RT (175–184)	RT (175–184 LAI)	NPDIVIYQYM	HIV-1 infection	human (B51)	Samri2000
	<ul><li>Patient 246#1 (B51), v</li><li>The resistance mutation</li></ul>	vas found by ELISPOT to re		ated peptide after zidovudine trea	
RT (175–199)	RT (342–366 LAI)  • One of five enitones de	NPDIVIYQYMDDLYVG EIGQHR efined for RT-specific CTL o	SSDL- HIV-1 infection	human (A11)	Menendez-Arias1998, Walker1989
RT (179–187)	RT Vaccine Vector/Type:  This epitope was show	VIYQYMDDL vaccinia HIV component:	Vaccine polyepitope nted to appropriate CTL clones up	human (A*0201) on infection of human target cells	Hanke1998a, Hanke1998b s with vaccinia virus Ankara (VVA)
RT (179–187)	into a patient – they we treatment had no impa	ere well tolerated, but the Sl ct upon viral load and CD4	LYNTVATL clone was shown by to		Tan1999 FL and VIYQYMDDL were infused ninated through apoptosis, and the
RT (179–187)	<ul> <li>The proteasome is inhithe proteasome to creater.</li> <li>IFN-gamma induction the presentation of the pathways</li> <li>ILKEPVHGV seems to the pathways</li> </ul>	ibited by lactacystin treatme te an immunoproteasome of the immunoproteasome a A*0201 ILKEPVHGV epit o be processed by the classi	and lactacystin inhibition increases	stion of proteasome subunits, LMs the presentation of the A*0201 vithin pol proteins, showing the two YQYMDDL appears to be destroy	
RT (179–187)			HIV-1 infection sponse and confers drug resistance spitope includes catalytic residue:		Harrer1996a, Menendez-Arias1998
RT (179–187)	RT (346–354 LAI)  • C. Brander notes this i	VIYQYMDDL	HIV-1 infection	human (A*0201)	Brander2001

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
RT (179–187)	RT (346–354)	VIYQYMDDL	HIV-1 infection	human (A*0201)	Brander1998a, Menendez-Arias1998
	<ul> <li>VIYQYMDDL, and the Only one subject had only one subject had only subjects were part of the In the review [Menence</li> </ul>	nere was no correlation b CTL against all three epi the San Francisco City C dez-Arias 1998] the autho M6V abolish CTL activ	CTL responses against the p17 SLYNTVAT etween viral load and recognition of a spectopes linic Cohort, the ARIEL project and from the response to the substitution of three residues in ity, and M6V confers resistance to 3TC – states.	cific epitope or evidence of in the Boston area n this epitope can confer resis	nmune escape stance to RT inhibitors (1, 3, and 6) –
RT (179–187)	RT • Epitope name: RT VL	VIYQYMDDL	HIV-1 infection	human (A*0201)	Altfeld2001c
	<ul> <li>criteria, and 30 of thes</li> <li>Three additional previindividuals had CTL tileast 1 (median of 1 and 1)</li> </ul>	se bound to HLA-A*020 ously described HLA-A2 hat recognized at least or and maximum of 2)	d the A2-supermotif pattern conserved in n 1 – 20/30 bound to at least 3/5 of HLA-A2 2 epitopes were added to the set of 20, include of the 23 peptides (median of 2 and max HLA-A2 patients with chronic HIV-1 infect	2 supertype alleles tested luding RT VL9, and 18/22 ch ximum of 6), while 6/12 acute	ronically infected HLA-A2 e infected individuals recognized at
RT (179–187)	RT (346–354) • Epitope name: VL9	VIYQYMDDL	HIV-1 infection	human (A*0201)	Dela Cruz2000
	epitope-specific lysis l	by CD8+ CTL	I-terminus of the HLA-A2 heavy chain, or primary responses in vitro	tethering the epitopes to the	target chain, resulted in
RT (179–187)	<ul><li>immunodominance1</li><li>immunoproteasome. 7</li><li>ILKEPVHGV was eff</li><li>by the MB1 subunit of</li></ul>	74 cells were used that lands and these genes could be addiciently presented in TAF of the protease, and could	HIV-1 infection 0201 HIV epitopes was shown to use differ ack TAP1 and TAP2 genes, as well as the I led back through transfection to study proc 2-1 and -2 transfected cells while VIYQYN be expressed in the presence of the proteased by lactacystin in a wild type cell line.	LMP2 and LMP7 genes that cessing.  MDDL and SLYNTVATL we	encode the beta-subunits of the re not. VIYQYMDDL was destroyed
RT (179–187)	<ul> <li>The HIV-1 subtype A which could direct the conserved, often immu Kenya. A DNA and M</li> </ul>	focused vaccine HIVA co protein to the cell memb anodominant epitopes that	HIV-1 infection, Vaccine a MVA boost <i>Strain:</i> subtype A <i>HIV co</i> ontains p24 and p17, in a reversed order re- orane and inhibit efficient peptide processinat were selected to have particularly good of tion protocol using the HIVA antigen will.  ].	elative to the Gag polyprotein ng and class I presentation, as cross-reactive potential for th	to prevent myristylation of p17, s well as a polyepitope string of e A-clade epidemic in Nairobi,

HXB2 Location	<b>Author's Location</b>	Sequence	Immunogen	Species (HLA)	References
	assays after vaccination	of 5 macaques. The r	ed responses to peptide pools were detect esponse to the Mamu A*01 SIV p27 epit cinated macaques, possibly because of processing the process of the process	ope p11C (CTPYDINQM), in	cluded in the polyepitope region, was
RT (179–187)		oss-reactivity could pro	HIV-1 exposed seronegative infected prostitutes from Nairobi using potect against both A and D and confer pro IYQYMMDL	reviously-defined B clade epit	
RT (179–187)	<ul> <li>A polyepitope vaccine</li> <li>HHD mice have a transexpressed in the mice</li> <li>CTL responses to Gag observed in HIV polyto</li> <li>No CTL immune responses 180-189 (VLEWR)</li> <li>Sixteen HLA A2+ patienthe polytope – one indi</li> </ul>	was generated in a vac gene of HLA A2 links (77-85) SLYNTVATL, ope HHD-vaccinated n nses were generated a FDSRL) ents were tested for the vidual recognized all s te than one epitope, bu	Vaccine nia boost HIV component: polyepitope cinia construct that contiguously encoded do to the transmembrane and cytotoxic do Pol (476-484) ILKEPVHGV, gp120 (12) nice, and these responses were enhanced a gainst HLA A2-restricted HIV epitopes N eir ability to make CTL responses by pept even of these epitopes; 7 patients had CT t they were not able to test all peptides fo LA-A2 patients	omains of H-2D $^d$ – this transge 0-128) KLTPLCVTL, and Net with vaccinia boost Nef 157-166 (PLTFGWCYKL) cide restimulation in culture wi L cultures able to recognize at	ene is the only MHC molecule  f (190-198) AFHHVAREL were  h, Pol 346-354 (VIYQYMDDL), and th the epitopes selected for inclusion is t least one of the epitopes, and 6 of
RT (179–187)	<ul> <li>1/28 individuals tested VIYQYIDDL, but faile</li> </ul>	produced HIV-1 RT-sp d to recognize the wile	HIV-1 infection mivudine, and is in the middle of the HL. pecific CTL that recognized the peptide re dtype epitope VIYQYMDDL i-VIYQYVDDL responses maybe helpfu	epresenting the lamivudine esc	•
RT (179–187)	RT (179–187) • Of 98 patients in crosspatients, respectively)	VIYQYMDDL sectional analysis, 789	HIV-1 infection % had CTL against pol – RT was more in	human (A2) nmunogenic than Integrase and	Haas1998 I Protease (81%, 51%, and 24% of 37
RT (179–187)	<ul> <li>HLA-A11 is very command CTL responses were</li> </ul>	V-1 exposed persistent non in this population re found in 8/8 HIV+ o	HIV-1 infection  ly seronegative (HEPS) female sex worker, and was enriched among the HEPS sextentrols, and 0/9 HIV- women that were not subject 144 who carried HLA-A2	vorkers – weak CTL responses	

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
RT (179–187)	Pol (339–347 93TH253 subtype CRF01)	VIYQYMDDL	HIV-1 infection	human (A2)	Bond2001
	epitopes in this group, al	though E clade version	ex workers (FSW) from Northern Thailar ons of previously defined B-clade A2 and on of this epitope, which is identical to the	d A24 epitopes were also tested	l.
			s, and exact matches were very uncommo		eisioii vii Qimbbb
RT (179–187)	studied in eight HIV-1-in	fected subjects, two cognized in a given ir	HIV-1 infection epitopes restricted by HLA class I A and with acute infection, five with chronic, a ndividual, A2-restricted CTL response te	nd one long-term non-progress	or (LTNP)
RT (179–187)	<ul> <li>there is concern protease relevant concentrations of RTV did not alter the prethe MB1 beta subunit, ar destroyed by MB1 in the</li> </ul>	inhibitors may adve- of RTV when the protessentation two RT A2 ad VIYQYMDDL who constitutive protease processing and assem	HIV-1 infection  y in the 20S proteasome in vitro, as does rsely effect CTL epitope processing, but teasome is functioning in an intracellular 2 epitopes processed by distinct pathway, hich is dependent on IFNgamma induction ome. hbly of HLA-B35 or -A2, which are asser-	this paper indicates that procest context. s: ILKEPVHGV, generated by on of LMP7 which replaces ME	the constitutive proteasome containing in the immunoproteasome, and is
RT (179–187)	<ul><li>Seroprevalence in this co</li><li>Most isolated HIV strain</li></ul>	short is 90-95% and to sare clade A in Nair observed using A or	HIV-1 exposed seronegative prostitutes from Nairobi – thes their HIV-1 exposure is among the higher obi, although clades C and D are also for D clade versions of epitopes clade viruses	e CTL may confer protection st in the world	
RT (179–187)	<ul> <li>Epitope name: LR26</li> <li>The stability of peptide by SLYNTVATL (p17), SLI (GILGFVFTL), while Refer to the four high-affinity peless than an hour.</li> <li>HLA-A2.1 transgenic mas adjuvants.</li> </ul>	oinding to HLA-A2.1 LNATDIAV (gp41) a GPGRAFVTI and VI ptides formed stable ice were immunized	Vaccine  Adjuvant: P30, incomplete Freund's adward determined for six HLA-A2.1 pept nd LLWKGEGAV (RT) all bound with Parameters with half-lives ranging between the six HIV-1 peptides and P30, as a stong CTL response in Cr-release assays e combination was used.	ides included in this vaccine straigh affinity comparable to a integrative binding activity = 0.0 and 32 hours, while the load universal T-helper epitope, we	ady – ILKEPVHGV (RT), fluenza epitope reference 01). ow affinity peptides had half lives of ith IFA or Montanide or microspheres

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References		
RT (179–187)	<ul><li>Epitope name: LR26</li><li>When HIV-1 peptides v</li></ul>	were used to vaccinate HLA			Peter2002  The observed when the peptides were ination [Peter2001], IL-12 can		
	counteract immunodon	ninance in BALB/c mice, so	it was given with the multiple e	pitope vaccination, and was instead			
RT (180–189)	RT (LAI)	IYQYMDDLYV	HIV-1 infection	human (A*0201)	Menendez-Arias1998, vanderBurg1997		
		om a progressor, spans impo mined that this was an epitop	rtant RT functional domain be recognized by a long-term sur	rvivor			
RT (181–189)				human (A*0201) side reverse transcriptase inhibitors	Samri2000		
	patient 250#0 (HLA-A	*0201), but neither were rec	ognized by patient 201#5 (also l	ation YQYVDDLYV and for the w HLA-A*0201) binding affinity for A2 (http//bima			
RT (192–201)	patients, respectively)	DLEIGQHRTK sectional analysis, 78% had as were defined utilizing diff		human (A3) e immunogenic than Integrase and F	Haas1998 Protease (81%, 51%, and 24% of 37		
RT (192–216)	RT (359–383 HXB2)	DLEIGQHRTKIEELRQI RWGLTT		human (Bw60)	Menendez-Arias1998, Walker1989		
	One of five epitopes de	fined for RT-specific CTL cl	ones in this study				
RT (192–216)	RT (191–215)	DLEIGQHRTKIEELRQI RWGFTT		human (polyclonal)	Haas 1997, Menendez-Arias 1998		
	• Polyclonal CTL recognition switched from RT 191-215 to RT 514-524 when AZT therapy selected for the resistance mutation, and presumably the escape variant, RT T215Y						
RT (198–212)	an HLA-B60 individua	1		human ness, and was one of the epitopes pre and optimal epitope were not deter	Altfeld2000b sented by another HLA molecule in mined		
RT (201–209)	patients, respectively)	KIEELRQHL sectional analysis, 78% had es were defined utilizing diff		human (A2) e immunogenic than Integrase and F	Haas 1998 Protease (81%, 51%, and 24% of 37		

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References		
RT (201–210)	<ul> <li>A subset of the potenti epitopes could stimula</li> </ul>	al epitopes was identifie te IFN $\gamma$ production in arewly identified as a HLA	on with the program Conservatrix to ide d that could bind to the appropriate HI n ELISPOT assay L-B58 epitope in this study, it had been	LA-allele, and 15 predicted B7 sup	perfamily (HLA B7, B8, and B58)		
RT (202–210)	RT (202–210 LAI) • C. Brander notes this i	IEELRQHLL s a B*4001 epitope		human (B*4001)	Altfeld2000b, Brander2001		
RT (202–210)	<ul> <li>RT (SF2) IEELRQHLL HIV-1 infection human (B60) Altfeld2001b</li> <li>Therapy provided during acute infection resulted in a narrower CTL response, stronger T help response, and a less diverse viral population than was seen individuals treated during chronic infection</li> <li>The breadth and specificity of the response was determined using ELISPOT by studying 19 individuals with pre-seroconversion therapy (Group 1), 11 individuals with primary infection but post-seroconversion therapy (Group 2), and 10 individuals who responded to HAART given during chronic infection (Group 3), using 259 overlapping peptides spanning p17, p24, RT, gp41, gp120 and Nef</li> <li>Previously described and newly defined optimal epitopes were tested for CTL response</li> <li>Number of HLA-B60+ individuals that had a CTL response to this epitope broken down by group: 0/2 group 1, 1/1 group 2, and 0/0 group 3</li> </ul>						
RT (202–210)			HIV-1 infection dy identifying new HLA-B60 epitopes I very common in Asian populations	human (B60(B*4001)	Altfeld2000b		
RT (202–210)			HIV-1 infection to five B61-restricted epitopes tested n another subject, and the B60-restricted	human (B60/B61) ed responses together contributed	Day2001 over one-third of the total CTL		
RT (203–212)			HIV-1 infection  Ing-term survivor in two samples taken EPVGHGV and TWETWWTEYW wer		Menendez-Arias1998, vanderBurg1997		
RT (209–220)	patients, respectively)	·	HIV-1 infection had CTL against pol – RT was more is	human (A2) mmunogenic than Integrase and P	Haas 1998 rotease (81%, 51%, and 24% of 37		
RT (243–252)	RT (LAI)  • Recognized by CTL fr	PIVLPEKDSW	HIV-1 infection	human (B*5701) also recognized	Menendez-Arias1998, vanderBurg1997		

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References				
RT (243–252)	RT (LAI)	PIVLPEKDSW	HIV-1 infection	human (B*5701)	Menendez-Arias1998, vanderBurg1997				
		_	ose CTL response persisted for more not reduce affinity, but abrogated CT		V3M reduced affinity but was well				
RT (243–252)	RT (410–419) • Epitope name: PIV	PIVLPEKDSW	HIV-1 infection	human (B57)	Oxenius2000				
	CD4 proliferative responsible TAART had no HIV spundetectable	onses and were able to main pecific CD4 proliferative re	tion (three with sustained therapy, two ntain a CTL response even with und esponses and lost their CTL response type but none were HLA B57+	detectable viral load – three patien					
RT (243–252)	RT	PIVLPEKDSW	HIV-1 infection	human (B57)	Oxenius2002b				
	period including therap	by with standard treatment i			l infected patients were studied over a ebound rates, plateau viral loads, or				
RT (244–252)	<ul><li>RT (399–407)</li><li>Subtype of B57 not det</li><li>C. Brander notes this is</li></ul>			human (B*5701)	Brander2001				
RT (244–252)	RT (244–252 LAI)	IVLPEKDSW	HIV-1 infection	human (B*5701, B*5801)	Klein1998				
	• This peptide was defined as the optimal epitope								
		B57 has been associated with long-term non-progression in the Amsterdam cohort.  B17							
	<ul> <li>B57 has been associate</li> </ul>								
	<ul><li>B57 has been associate</li><li>The most pronounced 0</li></ul>	CTL responses in HLA B*:	5701 LTS were to RT and Gag	ponse that was dominated by rea	ctivity to the epitope – two variants				
	<ul> <li>B57 has been associate</li> <li>The most pronounced 0</li> <li>B57 restricted CTL reswere found in this LTS</li> </ul>	CTL responses in HLA B*: sponses are targeted at mult : ITLPEKESW, which bou	5701 LTS were to RT and Gag iple proteins, but one LTS had a resp nd to B*5701 with similar affinity a	as the index peptide but was an es	ctivity to the epitope – two variants cape mutant that was not recognized				
	<ul> <li>B57 has been associate</li> <li>The most pronounced 0</li> <li>B57 restricted CTL reswere found in this LTS by CTL, and IMLPEK</li> </ul>	CTL responses in HLA B*5 sponses are targeted at mult :: ITLPEKESW, which bou DSW, which bound to B*5	5701 LTS were to RT and Gag iple proteins, but one LTS had a respond to B*5701 with similar affinity a 701 with reduced affinity but could state to the same of th	s the index peptide but was an es	scape mutant that was not recognized				
	<ul> <li>B57 has been associate</li> <li>The most pronounced (</li> <li>B57 restricted CTL reswere found in this LTS by CTL, and IMLPEK</li> <li>In an additional HIV+</li> </ul>	CTL responses in HLA B*5 sponses are targeted at mult :: ITLPEKESW, which bou DSW, which bound to B*5	5701 LTS were to RT and Gag iple proteins, but one LTS had a resp nd to B*5701 with similar affinity a	s the index peptide but was an es	scape mutant that was not recognized				
	<ul> <li>B57 has been associate</li> <li>The most pronounced 0</li> <li>B57 restricted CTL reswere found in this LTS by CTL, and IMLPEK</li> <li>In an additional HIV+index peptide</li> </ul>	CTL responses in HLA B*; sponses are targeted at mult :: ITLPEKESW, which bou DSW, which bound to B*5' LTS, only the variant IELP	5701 LTS were to RT and Gag iple proteins, but one LTS had a respond to B*5701 with similar affinity a 701 with reduced affinity but could state to the same of th	s the index peptide but was an es	scape mutant that was not recognized				
RT (244–252)	<ul> <li>B57 has been associate</li> <li>The most pronounced 0</li> <li>B57 restricted CTL reswere found in this LTS by CTL, and IMLPEK</li> <li>In an additional HIV+index peptide</li> </ul>	CTL responses in HLA B*; sponses are targeted at mult :: ITLPEKESW, which bou DSW, which bound to B*5' LTS, only the variant IELP	5701 LTS were to RT and Gag iple proteins, but one LTS had a respond to B*5701 with similar affinity a 701 with reduced affinity but could set EKDSW was found, and this epitop	s the index peptide but was an es	scape mutant that was not recognized				
RT (244–252)	<ul> <li>B57 has been associate</li> <li>The most pronounced 0</li> <li>B57 restricted CTL reswere found in this LTS by CTL, and IMLPEK</li> <li>In an additional HIV+index peptide</li> <li>This epitope was recog</li> <li>Pol (244–252)</li> <li>Combined tetramer and</li> </ul>	CTL responses in HLA B*sponses are targeted at mult in ITLPEKESW, which bound to B*sponses are targeted at mult in ITLPEKESW, which bound to B*sponses are targeted at multiple bound to B*sponses and the context of both IVLPEKDSW intracellular cytokine state.	5701 LTS were to RT and Gag tiple proteins, but one LTS had a respond to B*5701 with similar affinity a roll with reduced affinity but could straightful EKDSW was found, and this epitop the HLA-B*5701 and B*5801  HIV-1 infection ning was used to study the function	human (B*5801) of circulating CD8+ T cells spec	d less affinity for B*5701 than the  Appay2000 cific for HIV and CMV				
RT (244–252)	<ul> <li>B57 has been associate</li> <li>The most pronounced 0</li> <li>B57 restricted CTL reswere found in this LTS by CTL, and IMLPEK</li> <li>In an additional HIV+index peptide</li> <li>This epitope was recog</li> <li>Pol (244–252)</li> <li>Combined tetramer and</li> <li>HIV-specific CD8+ T of</li> </ul>	CTL responses in HLA B*S sponses are targeted at mult ETLPEKESW, which boun DSW, which bound to B*5' LTS, only the variant IELP spized in the context of both IVLPEKDSW d intracellular cytokine stain cells expressed lower levels	5701 LTS were to RT and Gag iple proteins, but one LTS had a respond to B*5701 with similar affinity a 701 with reduced affinity but could set to be	human (B*5801) of circulating CD8+ T cells spec	d less affinity for B*5701 than the  Appay2000 cific for HIV and CMV				
RT (244–252)	<ul> <li>B57 has been associate</li> <li>The most pronounced 0</li> <li>B57 restricted CTL restricted CTL restricted CTL, and IMLPEK</li> <li>In an additional HIV+index peptide</li> <li>This epitope was recognology</li> <li>Combined tetramer and HIV-specific CD8+ To CD27 expression on H</li> </ul>	CTL responses in HLA B*; sponses are targeted at mult in ITLPEKESW, which bound to B*5' LTS, only the variant IELP sponses in the context of both IVLPEKDSW distracellular cytokine statically expressed lower levels IV-specific cells, suggesting	5701 LTS were to RT and Gag iple proteins, but one LTS had a respond to B*5701 with similar affinity a 701 with reduced affinity but could set to be	human (B*5801) of circulating CD8+ T cells from the same donor, a	d less affinity for B*5701 than the  Appay2000 dific for HIV and CMV and this was associated with persistent				

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
RT (244–252)	suppression of replication	n. The "EpiNef" construct w			Guillon2002 on kinetics on CTL mediated affect a target cell line; the target cells
RT (244–252)	B14-restricted Rev-SAE co-incubated with CD4+ in ten days of culture. W	PVPLQL specific CD8 T-cel cultures innoculated with H hen the RT epitope was clon	l clone TCC108, and the B57-red IV-1 at low MOI. Co-incubation ed into the Nef gene of the infec	with the Rev-specific CTL result ting strain, another early expresse	vanBaalen2002  ed until after 24 hours. The c CD8 T-cell clone TCL1C11 were ded in two logs less HIV-1 production ed protein, it proved as effective as are important for vaccine design.
RT (245–252)	<ul><li>with viral load in patient</li><li>Most patients have high</li></ul>	s with high CD4, but in patie levels of HIV-specific T-cell		high tetramer frequencies were fells aren't functional	Kostense2001 ositive cells were inversely correlated ound despite high viral load
RT (259–267)	<ul> <li>for the A3 supertype) wh</li> <li>Progressors had memory</li> <li>A positive correlation be observed, which may con</li> <li>This epitope can bind for</li> <li>Tetramer staining with A HIV-specific sells in LTN</li> </ul>	resting CD8+ T-cells that re tween effector CD8+ T-cells thribute to the inability of LT ar of the five HLA-A2 supert 2, beta2microglobulin, and e	term nonprogressors recognized cognized far fewer epitopes than and plasma viremia and a negation of the collear virus supples alleles (A*0201, A*020 2, either SLYNTVATL, KLVGKLN atted effector cells were the minor	I far fewer epitopes In LTNPs In LTNPs Ive correlation between CD8+ eff A*0203, A*0206 and A*6802) IWA, or LTFGWCFKL revealed to	s tested, (18 for the A2 supertype, 16 Sector T-cells and CD4+ T-cells was
RT (260–271)	RT (415–426 IIIB) • C. Brander notes this is a	LVGKLNWASQIY a B*1501 epitope	HIV-1 infection	human (B*1501)	Brander2001
RT (260–271)	RT (260–271) • No immunodominant res	LVGKLNWASQIY  sponses were detected to four	HIV-1 infection B62-restricted epitopes tested	human (B62)	Day2001
RT (260–271)	RT (415–426 IIIB)  • P. Johnson, Pers. Comm.	LVGKLNWASQIY	HIV-1 infection	human (Bw62)	Brander1996b, Menendez-Arias1998
RT (263–271)	RT (263–271 LAI) • C. Brander notes this is a	KLNWASQIY an <b>A*3002</b> epitope		human (A*3002)	Brander2001, Goulder2001a
RT (263–271)	RT • Epitope name: KY9 (RT-	KLNWASQIY -35)	HIV-1 infection	human (A*3002)	Goulder2001a

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
	<ul> <li>characterized that are p</li> <li>A rapid method was de were defined – this me</li> <li>Two individuals were s African-Caribbean</li> <li>In both HLA-A*3002 i</li> <li>In subject 199 four add</li> </ul>	presented by this HLA neveloped combining ELL thod was completed with studied: Subject 199 (Historial A*3002 epitope	ISPOT with intracellular IFN-γ stainin thin 48 to 72 hours of receipt of blood LA A*0201/*3002 B*4402/51 Cw2/5 to RSLYNTVATLY was dominant	ng of PBMCs to map optimal epit ), a Caucasian, and Subject 6007	opes, then HLA presenting molecules (HLA A*3002/ B53/*5801 Cw4/7) an
RT (263–271)	<ul> <li>CTL epitopes (http://hi</li> <li>60 epitope responses w magnitude of the responses were compared to the response of t</li></ul>	and lymph node (LN) C iv-web.lanl.gov/content/ were detected in both PB onse was similar in LN a in the LN. eatment in five patients pe responses in the PB b following HAART resu , and the addition of 9 n e responses were shown	studied, the magnitude of the CD8 T-c became undetectable, in contrast to 5/2 alted in increased viremia accompanied	for each person's class I HLA all and an additional 8 responses were cells in the LN is lower so the nursell response was decreased in both 6 in the LN.  d by the restoration of the detection the greatest response to B27-KK	deles. detected only in LN. The total mber of HIV-specific cells per million th LN and PB, but more dramatically on of 13 epitopes that had become
RT (266–285)	Pol (421–440)  HLA, viral sequence, a each HIV protein.  Nef and p24 had the hi	WASQIYPGIKVRQ and Elispot data was obt	LCKLLRG HIV-1 infection ained from 105 HIV-1 positive Botsward positive peptides, and p24 had the highest C clade peptides from among over 350	human anans; Elispot data was obtained t magnitude of HIV-1 responses.	
RT (268–282)	from 7 proteins, sugges	sting that the breadth of	KL HIV-1 infection c overlapping peptides spanning all HI CTL responses are underestimated if GSPAIFQSSMTKI were recognized		
RT (269–277)	cross-reactive and reco specific manner. Two of • QIYAGIKVK is comm	known clade B HLA A <sup>3</sup> egnized by clade E infectother HLA A*1101 clad	*1101 epitopes were generated for clace ted individuals. The clade E and B and B defined epitopes were found not to epresenting subtypes A, B and E. It was s.	alogs to three more HLA A*1101 b have stimulated a response in cl	epitopes was recognized in a clade ade E infected individuals.

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References			
	• QIYAGIKVK had the highest A*1101 binding affinity, but qiyagikvR and qiyPgikvR (the most common C and D clade variant both bound to A*1101) QIYAGIKVK and qiyagikvR were both cross-presented by a clone from a B clade infection, but qiyPgikvR was not.							
RT (269–277)	(LAI)	QIYPGIKVR		(A3)	Altfeld2000a, Brander2001			
RT (269–277)	<ul><li>studied in eight HIV-1-</li><li>2 to 17 epitopes were repitopes were targeted</li></ul>	infected subjects, two we ecognized in a given ind by at least one person	HIV-1 infection pitopes restricted by HLA class I A and with acute infection, five with chronic, a lividual, A2-restricted CTL response ter p to 8 A3 epitopes, but none was clearly	nd one long-term non-progressonded to be narrow and never do	or (LTNP)			
RT (269–277)	<ul> <li>One individual, AC-06 interruptions (STI). He restricted by HLA-A3,</li> <li>1/14 HLA-A3 positive</li> </ul>	cutely HIV-infected HLA, was homozygous at all had only two detectable 11 by HLA-B7, and 1 b individuals had detectab	HIV-1 infection  A-A3 (n=7) or -B7 (n=4) or both -A3 at three class I alleles (A3, B7, Cw7), was e CTL responses during acute infection, by HLA-Cw7.  Dle A3-restricted responses to this epito duals began to have detectable responses	as treated during acute infection, but after STI this broadened to pe during acute infection, but o	and had supervised treatment o 27 distinct epitopes including 15			
RT (271–279)	(LAI) • C. Brander notes this is	YPGIKVRQL s a B*4201 epitope	HIV-1 infection	human (B*4201)	Brander2001			
RT (271–279)	<ul> <li>YHKIKVRQL is a natu</li> </ul>	urally occurring variant	HIV-1 infection  occurring variants that are both reactive that has not been tested  AIDS Foundation ARIEL Project, a mo		Menendez-Arias1998, Wilson1996			
RT (271–279)	Pol (438–446 IIIB)  This study describes m  Detection of CTL escapinfants	YPGIKVRQL aternal CTL responses i pe mutants in the mothe nat gave a positive CTL	HIV-1 infection n the context of mother-to-infant transm r was associated with transmission, but response: YPGIKVKQL, YAGIKVRQ	human (B42) mission the CTL-susceptible forms of t	Wilson1999a			
RT (293–301)	<ul><li>An I to V substitution a</li><li>An I to V substitution a</li></ul>	individuals had a CTL r at position 5 abrogates s at position 1, P to Q at p at position 1 did not alter	esponse to this epitope specific lysis, but not binding to B*350 osition 2, and E to K at 5, abrogates spe		Menendez-Arias1998, Tomiyama1997			

HXB2 Location	<b>Author's Location</b>	Sequence	Immunogen	Species (HLA)	References					
RT (293–301)	Pol (448–456 SF2-24)	IPLTEEAEL	HIV-1 infection	human (B*3501 AND B*5101)	Tomiyama2000b					
	• Epitope name: HIV-B35	• Epitope name: HIV-B35-SF2-24								
			n HLA-B*3501 and HLA-B*5101 ar		single CTL clone					
	<ul> <li>IPLTEEAEL binds appr</li> </ul>	oximately four times more tightly	y to HLA-B*3501 than HLA-B*510	1.						
RT (293–301)	Pol (489–456)	IPLTEEAEL	HIV-1 infection	human (B*3501, B*5301, B*5101, B*0702)	Ueno2002					
	Valpha12.1 and Vbeta5.	6 was shown recognize the epitop ad B*0702 in cytolytic CTL assay	both HLA-B*3501 and -B*5101 to a pe in either HLA-B*3501 and -B*51 as, demonstrating that this single TC	01. Furthermore, this TCR	also recognized the peptide					
RT (293–301)	(SF2)	IPLTEEAEL	HIV-1 infection	human (B35)	Kawana1999					
,	HLA B35 is associated	with rapid disease progression		,						
			epitopes were obtained in 10 HLA	B35+ and 19 HLA B35- in	dividuals					
			non in B35+ individuals than in B35-							
	associated pattern of mu	itation								
RT (293–301)	RT (448–456 SF2)	IPLTEEAEL	HIV-1 infection	human (B35, B51)	Menendez-Arias1998, Shiga1996					
	• Binds HLA-B*3501 and	l B*5101			6					
	• Reviewed in [Menendez	z-Arias1998], this epitope lies in t	the thumb region of RT							
RT (293–301)	Pol (447–455)	IPLTEEAEL	HIV-1 infection, HIV-1 exposed seronegative	human (B51)	Kaul2001a					
	• ELISPOT was used to study CTL responses to a panel of 54 predefined HIV-1 epitopes in 91 HIV-1-exposed, persistently seronegative (HEPS) and 87									
	HIV-1-infected female N									
RT (294–318)	RT (461–485 HXB2)	PLTEEAELELAENREILKE-	HIV-1 infection	human (A2)	Menendez-Arias1998,					
	One of five epitopes def	PVHGVY Walker1989  • One of five epitopes defined for RT-specific CTL clones in this study								
RT (308–317)	RT (LAI)	EILKEPVGHV	HIV-1 infection	human (A*0201)	Menendez-Arias1998, vanderBurg1997					
		m a long-term survivor, SPIETVI m a progressor, EELRQHLLRW	PVKL was also recognized and TWETWWTEYW were also re	cognized	validerBurg1991					
RT (309–317)	RT (476–484 LAI)	ILKEPVHGV	HIV-1 infection	human	Luzuriaga2000					
(	<ul> <li>Longitudinal study of 8 peripheral blood cells. 6 Three HLA-A*0201 chi</li> </ul>	infants with prolonged viral supp 5/8 were studied using a Chromiu ldren were tested using SLYNTV	pression due to combination antiretro m release assay and no response was ATL or ILKEPVHGV HLA A*020 n stimulated in vitro for a week.	oviral therapy showed no H s detected using Gag expres	IV-1 specific CTL responses in ssed in vaccinia in the target cells.					

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
		children with suppressed cells at a frequency of 0.1	HIV viral replication who was co-info.4% in the PBMC.	ected with HIV and EBV, while I	HIV-tetramer negative, had
RT (309–317)			HIV-1 infection and highly specific, and found to work were observed in response to anti-retro		
RT (309–317)	responses in patients w		HIV-1 infection py (IDV, 3TC and ZDV) sometimes s to but there is a stable population of te e level of detection		
RT (309–317)	ILKEPVHGV • 71% of the 28 HIV-1 in (SLYNTVATL) and 21 • There were no difference	afected HLA-A*02 positi children by the pol tetrar ces observed in children t	HIV-1 infection  A *02+ children by tetramer staining we children recognized both epitopes, ner (ILKEPVHGV) hat had therapy versus those that did CD28-, CD45RO+, CD45RA- HLAD	with cells from 26 children stair	
RT (309–317)	<ul> <li>CD8+ T cells were four viral load was also four</li> <li>All three patients were</li> <li>ELISPOT was used to a subjects showed a dom</li> <li>The subject with A*020</li> <li>Weak responses were of B*2705</li> <li>No acute response was</li> </ul>	nd prior to seroconversion and B*2705, with HLA alleled test a panel of CTL epitopinant response to the B*201 had a moderatly strong observed to A*301-RLRP detected to the following	es: A1, A30/31, B*2705, B35; A1, A pes that had been defined earlier and to 705 epitope KRWIILGGLNK g response to SLYNTVATL	tionship between the number of *0301, B7, B2705; and A*0201, were appropriate for the HLA happend B7-TPGPGVRYPL in the substitution of the	A*0301, B2705, B39 plotypes of the study subjects – 3/3 oject who was HLA A1, A*0301, B7, eSSMTK, A*301-TVYYGVPVWK,
RT (309–317)	low CD4 counts, but C	D8 T cell mediated effect D8+ cells may be present	HIV-1 infection galovirus specific CTL were detected or activity was not seen but may lack direct effector activity is		
RT (309–317)	The proteasome is inhib		HIV-1 infection sing and could influence immunodon nent, and gamma IFN induces expres		Sewell1999 P2 and LMP7, which combine with

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
	the presentation of the pathways  • ILKEPVHGV seems	the A*0201 ILKEPVHGV s to be processed by the cl		within pol proteins, showing the tw /IYQYMDDL appears to be destro	
RT (309–317)	for direct antigen de	livery to the cytoplasm for		•	Loing2000 e parent peptide to create a lipopeptide he parent peptide
RT (309–317)	<ul><li>ELISPOT was used people</li><li>The highest CTL free</li></ul>	to assay the CD8 T cell re equency was directed at epuls, higher numbers of spo	Vaccine IV component: Gag, Pol, Nef, Env sponse to the HIV-1 proteins Gag, Pol itopes in Pol t-forming T cells were directed again	-	
RT (309–317)	cells was followed in • Seven HIV+ people	n vivo were studied, and all shov	HIV-1 infection y using MHC tetramers in combinati yed expansions of particular TCR BV B expansions persisted for 2 to 3 yea	/ clones, often several, relative to u	
RT (309–317)	95 optimally-defined	l peptides from this databa	HIV-1 infection ΓL that reacted to SLYNTVATL, call use were used to screen for INFγ resp EPVHGV, and neither of these two re	ponses to other epitopes	Betts2000 nunodominant
RT (309–317)			HIV-1 infection herapy (HAART) reduced CD8+ cel replicating viral populations are necessity		Gray1999 tected by tetramer staining were likely of HIV-1 specific CTL
RT (309–317)	<ul><li>between HIV Gag an</li><li>Inclusion of both the</li></ul>	nd Pol specific CTL effect e p17 SLYNTVATL and R	HIV-1 infection  ss-sectional study of 14 untreated HI or cells (CTLe) and viral load T ILKEPVHGV epitopes gives a goode and CD4 count or clearance rate or	od representation of HLA A*0201-	
RT (309–317)	RT Vaccine Vector/Type This epitope was sho	ILKEPVHGV :: vaccinia HIV compone	Vaccine ent: polyepitope resented to appropriate CTL clones to	human (A*0201)	Hanke1998a, Hanke1998b s with vaccinia virus Ankara (VVA)

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
RT (309–317)	RT (476–484)	ILKEPVHGV	in vitro stimulation	human (A*0201)	Konya1997, Menendez-Arias1998
	<ul><li> This epitope was inclu</li><li> Binding affinity to A*0</li></ul>	ded as a positive control 0201 was measured, $C_1/$	$2\max \mu M = 12$		
RT (309–317)	RT (468–476)	ILKEPVHGV	in vitro stimulation	human (A*0201)	vanderBurg1996
			and associated with immunogenicity i derived from uninfected individual	in transgenic HLA-A*0201/K <sup>b</sup>	mice
RT (309–317)	RT (468–476) • Binds HLA-A*0201 –	ILKEPVHGV CTL generated by in vitro	in vitro stimulation o stimulation of PBMC from an HIV n	human (A*0201) egative donor	vanderBurg1995
RT (309–317)	RT (476–484)	ILKEPVHGV	HIV-1 infection	human (A*0201)	Menendez-Arias1998, Pogue1995
	Mutational study: posi	tion 1 I to Y increases con	nplex stability with HLA-A*0201		
RT (309–317)	RT (476–484)	ILKEPVHGV	HIV-1 infection	human (A*0201)	Goulder1997e, Goulder1997a, Menendez-Arias1998
	• [Goulder1997a] is a re	view of immune escape th	nat summarizes this study		
	<ul><li>71% of an additional s</li><li>Those individuals with</li><li>[Goulder1997a] is a re</li></ul>	et of 22 HIV-1 infected H a pol ILKEPVHGV resp	onse to SLYNTVATL indicated his viru LA-A*0201 positive donors preferenti- onse tended to have mutations in or arc nat summarizes this study	ally responded to gag SLYNTV	
RT (309–317)	were prepared that can PBMCs.  • Three patients only sta Gag epitope (0.28%)	stain CTL lines specific f	HIV-1 infection which permits quantification of specification of specification of specification in the specification of specification of specification in the specification in th	nd can quantify HIV-specific Conference of tetramer staining to	D8+ cell lines in freshly isolated to the Pol epitope (0.77%), less to the
RT (309–317)	RT (476–484)	ILKEPVHGV	in vitro stimulation	human (A*0201)	Menendez-Arias1998, Walter1997
	• The HLA-A2-peptide	complex elicited HLA-A2	pressed in E. coli were refolded in the per peptide-specific CTL response in cells are could provide an alternate to intracel	s lacking HLA-A2	
RT (309–317)	Class I HLA-restricted • 17/18 asymptomatic pa	l anti-HIV CD8+ T cells atients had a CTL respons	HIV-1 infection 'NTVATL or ILKEPVHGV were used e to one or both epitopes – 72% had a fic CTL were apparently memory cells	CTL response to SLYNTVATL	

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
RT (309–317)	<ul><li>VIYQYMDDL, and the</li><li>Only one subject had G</li></ul>	ere was no correlation be CTL against all three epiton he San Francisco City Cli	HIV-1 infection TL responses against the p17 SLYNTVA tween viral load and recognition of a spopes nic Cohort, the ARIEL project and from	ecific epitope or evidence of in	
RT (309–317)	<ul><li>seven patients, and the</li><li>Levels of CTL effector</li></ul>	B*3501 epitope DPNPQ rs typically decline for 5-7	HIV-1 infection ARV therapy using HLA-tetramer comp EVVL in one additional patient days and then rebound, fluctuating dur ponential decay with a median half-life	ing the first two weeks of ther	
RT (309–317)	RT (476–484 LAI) • C. Brander notes this i	ILKEPVHGV s a A*0201 epitope	HIV-1 infection	human (A*0201)	Brander2001
RT (309–317)	epitope-specific lysis b		HIV-1 infection, in vitro stimulation terminus of the HLA-A2 heavy chain, o	human (A*0201) or tethering the epitopes to the	Dela Cruz2000 target chain, resulted in
RT (309–317)	RT (309–317) • Epitope name: P1 • The epitope was recogrecognition	ILKEPVHGV	HIV-1 infection at not in another A*0201+ patient, 201#5	human (A*0201) 5, in a study of the effects of the	Samri2000 herapy escape mutations on CTL
RT (309–317)	T-cells from HIV-1 inf	ected individuals at levels	in vitro stimulation HIV-1 sequences, upon infection of ma comparable to the response seen to HIV HIV-1 sequences can also stimulate HI	V carried in vaccinia vectors	
RT (309–317)	High frequencies of circular	rculating CD8+ T-cells we	HIV-1 infection ssors, no correlation between plasma vi- ere HIV-1 specific, and the majority of the only 2 subjects (patient 3 and 19) tested	hese responses were to gag-po	
RT (309–317)	by therapy, using a tetr	amer assay	HIV-1 infection in long term non-progressors (LTNP) w ow viral load, while HAART patients ha	•	
RT (309–317)	Pol (476–484) • Combined tetramer and	ILKEPVHGV d intracellular cytokine st	HIV-1 infection aining was used to study the function of	human (A*0201) circulating CD8+ T cells spec	Appay2000 cific for HIV and CMV

HXB2 Location	<b>Author's Location</b>	Sequence	Immunogen	Species (HLA)	References
	CD27 expression on	HIV-specific cells, sugge	vels of perforin than CMV-specific CD sting impaired maturation activated virus-specific CD8+ T cells p		•
RT (309–317)	<ul><li> Optimal expansion o in the absence of CD</li><li> Those CTL that didn</li></ul>	of HIV-1-specific memory 04+ T cell help to a variab o't respond to CD40LT co	HIV-1 infection virus-specific memory CTL was studied CTL depended on CD4+ T cell help in the degree in most of patients and Expand with IL2 present, and IL15 mulation was the universal tetanus help	n 9 of 10 patients – CD40 ligand to produced by dendritic cells also c	contributes
RT (309–317)	• Epitope name: RT2	mice were injected with b	Vaccine Intous bacteriophage major coat protein Dacteriophage antigens expressing a Th		Guardiola2001 e ILKEPVHGV, and epitope-specific
RT (309–317)	immunodominance. immunoproteasome.  • ILKEPVHGV was e by the MB1 subunit	.174 cells were used that These genes could be ad fficiently presented in TA of the protease, and could	HIV-1 infection f0201 HIV epitopes was shown to use d lack TAP1 and TAP2 genes, as well as ded back through transfection to study pP-1 and -2 transfected cells while VIYO be expressed in the presence of the prored by lactacystin in a wild type cell lin	the LMP2 and LMP7 genes that e processing. QYMDDL and SLYNTVATL wer oteasome inhibitor lactacystin, but	encode the beta-subunits of the re not. VIYQYMDDL was destroyed
RT (309–317)	monocyte-derived m • HLA-A*0201 CTL r	acrophages MDM in the	were reconstituted with HLA-A*0201 p basal ganglia to provide a mouse model by tetramer staining in the spleen in seve	l of HIV-1 encephalitis.	
RT (309–317)	<ul> <li>Ten naturally occurring gamma-IFN and cyto</li> </ul>	otoxic functions through	Vaccine  nt: RT Adjuvant: CFA itope VLMWQFDSRL were tested for vaccination of HLA-A*0201 transgenic ceine responses, and was a positive con-	mice.	Boissonnas2002  I for their ability to induce
RT (309–317)	Pol (468–476)	ILKEPVHGV	Vaccine : HIV-1 divided into a 32 plasmids in a	murine (A*0201)	Singh2002, Sykes1999

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
	<ul> <li>epidermal gene gun withe proteasome.</li> <li>A single immunization</li> <li>Immunodominant epitresponses and stimulat</li> <li>The presence of multip</li> </ul>	ith an ubiquitin express  with the UB-HIV-1 lil opes SLYNTVATL (Ga ted CTL that were func ole plasmids HLA-A*0	HLA-A*0201 alpha1 and alpha2 and Esion library of 32 plasmids that spanned brary vaccine induced potent, stable and ag), ILKEPVHGV(Pol), RIQRGPGRAF tional in a Cr-release assay and against 201-restricted CTL epitopes did not dec a based on mixtures of either 16 or 32 pe	the HIV-1 genome. Ubiquitin to multivalent CTL responses aga FVTIGK(P18) and AFHHVARE wild type antigen. crease CTL immunogenicity, and	inst all library members.
RT (309–317)	<ul> <li>The HIV-1 subtype A which could direct the conserved, often immu Kenya. A DNA and M included in the polyepi</li> <li>Multiple CD4+ or CD3 assays after vaccinatio</li> </ul>	focused vaccine HIVA protein to the cell men inodominant epitopes to IVA prime-boost vaccinitope string [Hanke2008+ T-cell vaccine-induction of 5 macaques. The result of the string focus	HIV-1 infection, Vaccine mia MVA boost <i>Strain:</i> subtype A <i>H</i> contains p24 and p17, in a reversed ordenbrane and inhibit efficient peptide prochat were selected to have particularly gonation protocol using the HIVA antigen [0]. Deed responses to peptide pools were determined by the manual of the manual A*01 SIV p27 epcinated macaques, possibly because of particularly processes and provided the macaques of processes and provided the processes and	er relative to the Gag polyproteinessing and class I presentation, a pod cross-reactive potential for the will be used in a phase III clinic exceeded using intracellular cytoking polyproteines part (CTPYDINQM), included the control of the control	n to prevent myristylation of p17, as well as a polyepitope string of he A-clade epidemic in Nairobi, al trial in Kenya. This epitope is e staining and IFNgamma Elispot cluded in the polyepitope region, was
RT (309–317)	<ul> <li>tetramer staining or CI</li> <li>In general, during the specificities that were HIV-specific responses</li> </ul>	D8+ cell IFNgamma pr first month of treatmen not previously detectab s diminished	HIV-1 infection  eles was tested in 14 HIV+ patients from the production to measure responses to viral load decreased and frequencies on the were newly detected, as were CMV sonse: increases or decreases in pre-exist	f HIV-specific CTL tripled and l specific CD8+ PBL – but with co	oroadened – eight new HIV ontinued viral suppression,
RT (309–317)	• Epitope name: Pol-IV	ILKEPVHGV	HIV-1 infection A02, 9/29 (31%) recognized this epitope	human (A02)	Sabbaj2002b
RT (309–317)	<ul><li> HHD mice have a tran expressed in the mice</li><li> CTL responses to Gag</li></ul>	was generated in a vac sgene of HLA A2 linke (77-85) SLYNTVATL	Vaccine nent: polyepitope ceinia construct that contiguously encoded to the transmembrane and cytotoxic of Pol (476-484) ILKEPVHGV, gp120 (1) nice, and these responses were enhanced	domains of H- $2D^d$ – this transge 20-128) KLTPLCVTL, and Net	ne is the only MHC molecule

HXB2 Location	<b>Author's Location</b>	Sequence	Immunogen	Species (HLA)	References
	Nef 180-189 (VLEWF • Sixteen HLA A2+ pati the polytope – one ind	RFDSRL) ents were tested for the ividual recognized all ser than one epitope, but	gainst HLA A2-restricted HIV epitopes eir ability to make CTL responses by pe seven of these epitopes; 7 patients had C t they were not able to test all peptides ients	eptide restimulation in culture wi	th the epitopes selected for inclusion in least one of the epitopes, and 6 of
RT (309–317)	patients had very simil HIV-1 infected patient	ar complementarity-de s aree patients showed sin	HIV-1 infection ras examined in three patients and ident termining regions – clonal expansion o milar sensitivity to mutation in the epito m)	f RT-HIV-specific CTL can conti	ribute to the skewed TCR repertoire in
RT (309–317)	_		HIV-1 infection which inhibits CTL killing of HIV-infection efficiently than anti-gag clones, correlation	_	Collins1998 of RT
RT (309–317)	RT (476–484 LAI)  • The capacity of dendri	ILKEPVHGV tic cells to process and	HIV-1 infection present antigen and stimulate anti-HIV	human (A2) 7-1 CTL memory responses was s	Fan1997 studied
RT (309–317)	<ul> <li>monthly into six HIV-i</li> <li>1/6 showed increased on ochange – pulsed DO</li> <li>ILKEPVHGV is a con</li> </ul>	nfected patients env-specific CTL and in Cs were well tolerated served HLA-A2 epitop	HIV-1 infection ed from HLA-identical siblings, pulsed increased lymphoproliferative responses be included in this study – 5/6 patients h the form ILREPVHGV and had no det	2, 2/6 showed increase only in propagation and this sequence as their HIV di	oliferative responses, and 3/6 showed
RT (309–317)	RT (476–484)  • CTL clones recognize	ILKEPVHGV naturally processed pe	HIV-1 infection ptide – peptide abundance corresponded	human (A2)	Menendez-Arias1998, Tsomides1994
RT (309–317)	RT (476–484) • A CTL response was f	ILKEPVHGV ound in exposed but un oss-reactivity could pro sus is ILKDPVHGV	HIV-1 exposed seronegat hinfected prostitutes from Nairobi using otect against both A and D and confer p	ive human (A2) previously-defined B clade epit	
RT (309–317)			HIV-1 infection uses and some As have the sequence ILL viruses, ILKDPVHGV, is not cross-rea		Cao1997a, Menendez-Arias1998
RT (309–317)	RT (476–484) • CD4+ cell lines acutel	ILKEPVHGV y infected with HIV we	HIV-1 infection ere studied to determine their susceptibitells at lower levels than Env or Gag spe	human (A2) ility to lysis by CTL	Menendez-Arias1998, Yang1996

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References				
			expression of RT relative to Env and Gag , possibly prior to viral production						
RT (309–317)		suppressive soluble factor	HIV-1 infection oncentrations comparable to those found in rs – MIP-1 $\alpha$ , MIP-1 $\beta$ , RANTES, after an in HLA-matched cells		Yang1997a				
RT (309–317)	RT (309–317) • Two clones were obtain	ILKEPVHGV ned with different TCR u	HIV-1 infection sage, $V_{\beta}1$ and $V_{\beta}21$	human (A2)	Menendez-Arias1998, Moss1995				
RT (309–317)	RT (476–484)	ILKEPVHGV	HIV-1 infection	human (A2)	Menendez-Arias1998, Musey1997				
	<ul> <li>Cervical CTL clones fr</li> </ul>	om an HIV-infected wor	nan recognized this epitope						
RT (309–317)	RT (476–484 LAI)	ILKEPVHGV	HIV-1 infection	human (A2)	Menendez-Arias1998, Tsomides1991				
	<ul> <li>Precise identification o</li> </ul>	f the nonamer that binds	to A2						
RT (309–317)	RT (476–484 LAI)	ILKEPVHGV	Peptide-HLA interaction	human (A2)	Connan1994, Menendez-Arias1998				
	• Promotes assembly of	• Promotes assembly of HLA-A2 molecules in T2 cell lysates							
RT (309–317)	RT (510–518) • Studied in the context of	ILKEPVHGV of HLA-A2 peptide bind	in vitro stimulation	human (A2)	Parker1992				
RT (309–317)	natural attenuated strai	n of HIV-1 which was No		•	Dyer1999 (SBBC) who had been infected with a				
RT (309–317)	<ul> <li>Some of these patients had prolonged high levels of CTL effector and memory cells despite low viral load</li> <li>RT (476–484) ILKEPVHGV in vitro stimulation human (A2) Zarling1999</li> <li>This study compares the ability of macrophages and dendritic cells to stimulate primary responses in CD8+ lymphocytes isolated from HLA-appropriate HIV-uninfected donors using peptide-pulsed APC – the dendritic cells performed better as APC for the stimulation of primary responses</li> <li>Strong CTL responses were elicited by the epitopes DRFYKTLRA and GEIYKRWII when presented by either immature or mature dendritic cells – macrophages were not able to prime a CTL response against DRFYKTLRA</li> <li>A weak response to KLTPLCVSL was stimulated using macrophages as the APC</li> <li>No detectable response was observed for the following previously-defined HIV epitopes: KIRLRPGGK, ILKEPVHGV, IRLRPGGK, GPKVKQWPL</li> </ul>								
RT (309–317)	<ul> <li>Based on EpiMatrix pr were shown to bind to</li> <li>Two of these 12 peptid</li> </ul>	edictions, 28 peptides we the predicted HLA molec es had been previously ic	computer prediction ediction to identify possible HLA-B27 and ere synthesized and tested using T2 bindin cule dentified as CTL epitopes: HLA-B27 KRV but is found only in a small number of B	ng assays for potential HLA WILGLNK and HLA-A2 I	A A2 or B27 binding, and 12 of these				

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References			
RT (309–317)	<ul> <li>criteria, and 30 of thes</li> <li>Three additional previor recognized at least one maximum of 2)</li> <li>This peptide binds to f</li> </ul>	all peptides which carried e bound to HLA-A*0201 busly described HLA-A2 of the 23 peptides (medi- our HLA-A2 supertype a	HIV-1 infection  the A2-supermotif pattern conserved – 20/30 bound to at least 3/5 of HLA epitopes were added to the set of 20, an of 2 and maximum of 6), while 6/1  lleles: A*0201, A*0202, A*0206 (high	-A2 supertype alleles tested and 18/22 chronically infected 12 acute infected individuals rec	HLA-A2 individuals had CTL that			
	<ul><li>RT IV9 was recognize</li><li>1/13 patients with acut</li></ul>							
RT (309–317)	Pol (subtype A)  This study examines C sex workers eventually  ILKDPVHGV or ILKI seroconversion, 12 mo  20/20 sequences of the	ILKDPVHGV TL responses in HIV expressions seroconverted, and for see EPVHGV was recognized in this entire infecting strain had no see the second service of the second second service of the second service of the second service of the second second service of the second second service of the second	HIV-1 infection posed, persistently seronegative individual in these HIV CTL reactive epitopes I in 1 of the 6 women (ML1760), and abstitutions in this epitope, all were II conversion was stopping sex work and	s had been defined while serone the response was present in the LKDPVHGV, so there was no e	gative last available sample prior to vidence for escape			
	working for a period or retire  This epitope was recognized by 4/22 HEPS control sex workers: ML887, ML1192, ML1250, and ML1749							
RT (309–317)	CD4 proliferative resp HAART had no HIV s undetectable • One of the 2/8 HLA-A • Patient SC9 (HLA A1/	onses and were able to m pecific CD4 proliferative 2+ study subjects recogn (2, B8/13, Cw0/0701, DR TQGYFPDWQNY, and O	aintain a CTL response even with und responses and lost their CTL response ized this CTL epitope 2/11, DQ6/7) had a CTL response aga	letectable viral load – three paties when HAART was eventually ainst epitopes FLKEKGGL, ILI	y given and their viral loads became			
RT (309–317)	<ul><li>with viral load in patie</li><li>Most patients have hig</li></ul>	nts with high CD4, but in h levels of HIV-specific T	HIV-1 infection by HLA-A2, B8 and B57 CTL in 54 p patients with CD4 T-cells below 400 F-cell expansions, but many of these company of these company of the producing tetramer cells correlate.	high tetramer frequencies were ells aren't functional	Kostense2001 positive cells were inversely correlated found despite high viral load			
RT (309–317)	Pol • CTL responses were st response to therapy, bu • 6/10 A*0201+ individu	ILKEPVHGV audied by tetramer staining at the overall level of antiguals had HIV-specific tetr	HIV-1 infection g in 41 patients with combination the	human (A2) rapy – activated CD8+ T-cells d ating into effectors stays consta	Seth2001 ecline as the viral load drops in nt and new epitopes may be recognized			

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
	<ul> <li>Prior to therapy, the me recognizing the epitope</li> </ul>		cells that recognized the immunodomi	nant epitope SLYNVATL was	six-fold greater than the percentage
RT (309–317)	<ul> <li>individuals treated duri</li> <li>The breadth and specific individuals with primar (Group 3), using 259 or</li> <li>Previously described ar</li> </ul>	ng chronic infection city of the response wa y infection but post-ser verlapping peptides spa ad newly defined optima	s determined using ELISPOT by studyi	ng 19 individuals with pre-sero individuals who responded to ef e	HAART given during chronic infection
RT (309–317)	<ul> <li>HIV-1-infected female</li> <li>Responses in HEPS wo reduced risk of infection women</li> <li>43/91 HEPS women ha</li> <li>Among HLA-A2 women women, SL(F/Y)NTVA</li> <li>The dominant response</li> <li>Four epitopes were confound in three different FRDYVDRF(Y/F)K also Differences in epitope sassociated with resistant</li> <li>Subject ML 1250 had a</li> </ul>	study CTL responses to Nairobi sex workers men tended to be lowern, and there was a shift d CD8+ responses and en, 7/10 HEPS and 14/2 TL in infected women to this HLA allele was sidered to be "resistant proteins: A2 ILK(D/E) so in p24 specificity were only se ce to HIV-1 in this coh n A2 response to ILK(I) n A2 response to ILK(I) n A2 response to ILK(I)	a panel of 54 predefined HIV-1 epitopes, and focused on different epitopes with in the response in the HEPS women up detection of HIV-1-specific CTL in HE 6 HIV-1 infected women recognized the to this epitope in all 7/10 HEPS cases be epitopes", as they were preferentially respectively. A*6802 DTVLEDINL en for responses restricted by class I HI	rs in 91 HIV-1-exposed, persist HLA presenting molecules the on late seroconversion to epitode PS women increased with the is epitope, and ILK(D/E)PVHotation only 5 of the 14/26 HIV-eactive in HEPS women and sein Protease, B14 DLN(M/T)LA alleles A2, A24, A*6802, Ethich switched to SL(F/Y)NTV	nat have previously been associated with opes recognized by the HIV-1 infected duration of viral exposure GV tended to be more reactive in HEPS of the infected women of may confer resistance, and these were N(I/V)V in p24 and B18 and B18, previously shown to be water formula of the infected women of the inf
RT (309–317)	<ul> <li>HLA-A11 is very command CTL responses were</li> </ul>	V-1 exposed persistently non in this population, re found in 8/8 HIV+ co	HIV-1 infection  y seronegative (HEPS) female sex work and was enriched among the HEPS sex ontrols, and 0/9 HIV- women that were ly subject 144 who carried HLA-A2	workers – weak CTL response	

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
RT (309–317)	Pol (93TH253 subtype CRF01)	ILRIPVHGV	HIV-1 infection	human (A2)	Bond2001
	epitopes in this group, al	though E clade version	workers (FSW) from Northern Thaila s of previously defined B-clade A2 a of this epitope, which differs from the	nd A24 epitopes were also tested	i.
	This epitope was not cor	nserved in many subtyp	es, and exact matches were very rare		
RT (309–317)	studied in eight HIV-1-in	nfected subjects, two w	HIV-1 infection itopes restricted by HLA class I A are ith acute infection, five with chronic, ividual, A2-restricted CTL response to	and one long-term non-progress	
RT (309–317)	<ul> <li>there is concern protease relevant concentrations of RTV did not alter the protection of the MB1 beta subunit, and destroyed by MB1 in the</li> </ul>	e inhibitors may adverse of RTV when the proteat esentation two RT A2 et and VIYQYMDDL white e constitutive proteason processing and assembly	ely effect CTL epitope processing, but asome is functioning in in an intracell pitopes processed by distinct pathwa the is dependent on IFNgamma induct	at this paper indicates that processular context.  ys: ILKEPVHGV, generated by the context of th	-
RT (309–317)	<ul><li>T-cells, detected by intra</li><li>Ghonorrhea caused the v</li></ul>	cellular cytokine produ veaker HIV-1 specific (	HIV-1 infection  n sex workers caused a functional de- action and tetramer assays, while not CTL responses in 4 HIV-1 exposed pe CTL in 2 HEPS subjects were shown	affecting the total number of epitersistently seronegative (HEPS) v	sope-specific CTLs.  women to become undetectable by
RT (309–317)	than NL-43 with an intac	ct Nef. The effect was s	HIV-1 infection and this study demonstrates directly shown to be specific for class I preser clone 68A62, specific for the class I	ntation of epitopes, and unlike Ne	
RT (309–317)	sensitive to lysis by SLY differences in processing Incubation with a T1-cel while ILKEPVHGV-pre- p17 was preferentially cl In a competition experin	NTVATL-specific CTI g. Il proteolytic extract she cursors were far less fre leaved between Leu85 and the cursors were far less fre	HIV-1 infection pitopes was compared, SLYNTVATL than by ILKEPVHGV-specific CTL owed that by four hours, 25% of a p1 equent (6.8%) even with four times rr and Tyr86, while appropriate Val484 ound TAP 3.7-fold more efficiently th x patients with HLA-A2-restricted re	, because of a higher density of \$7 peptide had a C-term Leu-85 a hore proteolytic extract after 30 h and Tyr485 cleavage was minor an RT peptides.	SLYNTVATL-A2 resulting from nd were SLYNTVATL-precursors, ours.

HXB2 Location	<b>Author's Location</b>	Sequence	Immunogen	Species (HLA)	References
	No significant difference	ce in HLA-A2 binding	of to p17 or RT epitopes was observed		
RT (309–317)	Pol (476–484)  Vaccine Vector/Type: p  • Epitope name: p9	ILKEPVHGV peptide <i>Adjuvant:</i> Fre	Vaccine und's adjuvant	murine (A2)	De Lucca2002
	<ul> <li>BALB/c mice immunia</li> <li>Exposure of lymphocy in human lymphocytes</li> <li>This murine RNA also</li> </ul>	tes from HIV-negative, incubated with RNA ex	ILKEPVHGV, elicited specific lymph HLA-A2 positive people to p9-RNA s stracted from lymphoid organs of p9-v ent protein kinase (PKR) and NFkapp	timulated lymphocyte proliferation vaccinated mice could be more in	
RT (309–317)	period including therap	y with standard treatme			Oxenius2002b  1 infected patients were studied over a rebound rates, plateau viral loads, or
	clearance rates.			<u> </u>	
RT (309–317)	<ul><li>Transgenic mice expre protein (vVK1).</li><li>Compared to vVK1, vo</li></ul>	ssing a HLA-A2/Kb chi G/P-92 induced a signifi	Vaccine Pol Adjuvant: IL-12 (IL-12p35 and I Imeric protein were vaccinated with ei Icant increase in Gag and Pol induced Induced by Elispot and 51Cr-release assays.	ther a p17-p24-p51 fusion protein	-
RT (309–317)	for the A3 supertype) v • Progressors had memo • A positive correlation l observed, which may c	while the effector cells or ry resting CD8+ T-cells between effector CD8+ contribute to the inability	HIV-1 infection g memory resting CD8+ T-cell respons of long-term nonprogressors recognize that recognized far fewer epitopes tha T-cells and plasma viremia and a nega y of LTNPs to clear virus 2 supertypes alleles (A*0201, A*020.)	d far fewer epitopes an LTNPs ative correlation between CD8+ e	es tested, (18 for the A2 supertype, 16 ffector T-cells and CD4+ T-cells was
RT (309–317)	Pol (464–472) • One of the 51 HIV-1 ep HLA alleles	ILKEPVHGV bitopes selected by Ferr	HIV-1 infection ari et al. as good candidate CTL epitop	human (A2, A*0201) best for vaccines by virtue of being	Ferrari2000 g conserved and presented by common
RT (309–317)	<ul> <li>Seroprevalence in this</li> <li>Most isolated HIV stra responses are frequentl</li> <li>This epitope is conserved</li> </ul>	cohort is 90-95% and the cohort is 90-95% and the ins are clade A in Naircely observed using A or lead among B and D clade	HIV-1 exposed seronegat negative prostitutes from Nairobi – the neir HIV-1 exposure is among the high obi, although clades C and D are also for C clade versions of epitopes le viruses was preferentially recognized by CTI	ese CTL may confer protection lest in the world found – B clade epitopes are often	

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
RT (309–317)	RT (309–317)	ILKEPVHGV	Vaccine, in vitro stimulation	human, murine (A2, A2 transgenic)	De Berardinis2000
		HIV-1 peptide in filamento	us bacteriophage major coat protein HI	V component: RT peptides	
	• Epitope name: RT2				
			coupled with T helper epitope KDSWTV		eific CTL responses in vitro in
			rivo in immunization of HLA-A2 transgently used for stimulation of antibodies, and		anitona processing and presentation
	suggests new possibility		ry used for stimulation of antibodies, and	uns novel discovery of C1L	ephope processing and presentation
RT (309–317)	Pol	ILKEPVHGV	Vaccine	SJL/J HLA transgenic	Ishioka1999
111 (30) 317)	1 01	THICH VIIOV	vacenie	mice (A2.1)	ismokuryyy
	Vaccine Vector/Type:	DNA HIV component: po	olyepitope	, ,	
			.1 and 3 HLA A11 restricted CTL epitope	es, the universal Th cell epito	pe PADRE (pan-DR epitope) and an
		l sequence was constructed		• 1	
			on by CTLs during HBV and HIV infection in vivo immunogenicity of DNA vaccines		FI anitonas strong rasponsas wara
			persisted up to four months after a single i		L epitopes – strong responses were
RT (309–317)	RT (476–484 LAI)	ILKEPVHGV	Vaccine	murine (A2.1)	Peter2001
KI (309–317)			<i>Jjuvant:</i> P30, incomplete Freund's adjuvar		
	• Epitope name: LR22	populae Siramii Ziri ria,	yurum 100, meempiete 11eunu o auju vai	(11.1), 1.1011	,, res meropulation
		e binding to HLA-A2.1 wa	s determined for six HLA-A2.1 peptides i	included in this vaccine study	/ – ILKEPVHGV (RT),
			LLWKGEGAV (RT) all bound with high a		
			DYMDDL bound with a lower affinity (rel		
	• The four high-affinity j	peptides formed stable con	nplexes with half-lives ranging between 8	and 32 nours, while the low	affinity peptides had half lives of
		mice were immunized with	the six HIV-1 peptides and P30, as a uni	versal T-helper epitope, with	IFA or Montanide or microspheres
	as adjuvants.		representation of the second		
	All peptides except VI		ng CTL response in Cr-release assays - st	ronger responses were obser	ved when peptides were delivered
	alone, indicating immu	anodominance when the co	ombination was used.		
RT (309-317)	RT (476-484 LAI)	ILKEPVHGV	Vaccine	murine (A2.1)	Peter2002
		peptide Strain: LAI Ad	<i>juvant:</i> P30, incomplete Freund's adjuvar	nt (IFA), IL-12	
	• Epitope name: LR22				
			A-A2.1 transgenic A2-Kb mice, strong red the response to some of the peptides wh		
			so it was given with the multiple epitope v		
			TL responses. This was possibly a consequence		
	in the spleen.	1		,	
RT (309–318)	RT (476–485 LAI)	ILKEPVHGVY	HIV-1 infection	human (B*1501)	Brander2001
(/	• C. Brander notes this i			/	

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References		
RT (309–318)	RT (309–318) • No immunodominant res	IKLEPVHGVY ponses were detected to four B6	HIV-1 infection 52-restricted epitopes tested	human (B62)	Day2001		
RT (309–318)	RT (476–485 LAI)	ILKEPVHGVY	HIV-1 infection	human (Bw62)	McMichael1994, Menendez-Arias1998		
RT (309–318)	<ul> <li>The HIV-1 subtype A for which could direct the property conserved, often immunous Kenya. A DNA and MVA included in the polyepito</li> <li>Multiple CD4+ or CD8+ assays after vaccination on the immunodominant in</li> </ul>	ILKEPVHGVY NA prime with vaccinia MVA becaused vaccine HIVA contains p2 otein to the cell membrane and adominant epitopes that were sell prime-boost vaccination protope string [Hanke2000]. T-cell vaccine-induced response to 5 macaques. The response to	HIV-1 infection, Vaccine boost <i>Strain:</i> subtype A <i>HIV comp</i> 44 and p17, in a reversed order relative inhibit efficient peptide processing a lected to have particularly good cross collusing the HIVA antigen will be used to peptide pools were detected using the Mamu A*01 SIV p27 epitope p1 caques, possibly because of processing the pools where the pools were detected using the Mamu A*01 SIV p27 epitope p1 caques, possibly because of processing the pools where the pools were detected using the mamu A*01 SIV p27 epitope p1 caques, possibly because of processing the pools where the pools were detected using the processing the pools where the pools were detected using the pools where the pools were detected using the pools were detected using the processing the pools were detected using the processing the processing the pools were detected using the processing the pro	we to the Gag polyprotein nd class I presentation, a s-reactive potential for the lased in a phase III clinicating intracellular cytokine 1C (CTPYDINQM), inc	n to prevent myristylation of p17, as well as a polyepitope string of the A-clade epidemic in Nairobi, al trial in Kenya. This epitope is e staining and IFNgamma Elispot cluded in the polyepitope region, was		
RT (328–352)	[Wee2002].  RT (495–515 LAI)  • One of five epitopes defined the second	EIQKQGQGQWTYQIYQEPF- KNLKTG ned for RT-specific CTL clones		human (A11)	Menendez-Arias1998, Walker1989		
RT (340–350)	RT (507–516) • Study of cytokines release	QIYQEPFKNLK ed by HIV-1 specific activated C	HIV-1 infection CTL	human	Menendez-Arias1998, Price199		
RT (340–350)	<ul> <li>Study of cytokines released by HIV-1 specific activated CTL</li> <li>Pol (487–497 93TH253 QIYQEPFKNLK HIV-1 infection, HIV-1 exposed human (A11) Sriwanthana2001 subtype CRF01)</li> <li>Epitope name: P495-505</li> <li>This was a study of HIV-1 exposed persistently seronegative (HEPS) female sex workers in Chiang Mai, northern Thailand</li> <li>HLA-A11 is very common in this population, and was enriched among the HEPS sexworkers – weak CTL responses were detected in 4/7 HEPS wome and CTL responses were found in 8/8 HIV+ controls, and 0/9 HIV- women that were not exposed</li> <li>This epitope was weakly reactive in the HEPS study subject 128 who was HLA A11/A33</li> <li>This epitope was reactive in HIV+ study subjects 053 and 184 who carried HLA-A11</li> </ul>						
RT (340–350)	Thailand, of whom more • 77 possible HLA-A11 epepitopes for CTL response	I subtype E in Bond et al.) epitothan half were HLA-A11 positioners were first defined using Eses from 8 HLA-A11 positive Edicted by the EpiMatrix method en previously defined	EpiMatrix, these were screened for b SWs, six were novel, six were previous	inding to A11 finding an ously identified			

HXB2 Location	<b>Author's Location</b>	Sequence	Immunogen	Species (HLA)	References				
	• This epitope was highly conserved in other subtypes, although exact matches were not very common								
RT (340–352)	RT (507–519 LAI)	QIYQEPFKNLKTG	HIV-1 infection	human (A11)	Johnson1994c, Menendez-Arias1998				
	• This epitope was liste	ed in a review							
RT (340–352)	Pol (495–507)	QIYQEPFKNLKTG	HIV-1 infection	human (A11)	Ferrari2000				
	• One of the 51 HIV-1 HLA alleles	epitopes selected by Ferrari et	al. as good candidate CTL epitopes for	vaccines by virtue of being	g conserved and presented by commo				
RT (341–350)	RT (508–516) • C. Brander notes that	IYQEPFKNLK this is an A*1101 epitope in t	HIV-1 infection he 1999 database	human (A*1101)	Culmann1998				
RT (341–350)	RT (508–517 LAI) • C. Brander notes this	IYQEPFKNLK is an A*1101 epitope	HIV-1 infection	human (A*1101)	Brander2001				
RT (341–350)  RT (341–350)	<ul> <li>individuals treated du</li> <li>The breadth and specindividuals with prim (Group 3), using 259</li> <li>Previously described</li> </ul>	aring chronic infection ificity of the response was det ary infection but post-serocon overlapping peptides spanning and newly defined optimal epi	HIV-1 infection a narrower CTL response, stronger T has ermined using ELISPOT by studying 19 version therapy (Group 2), and 10 indivi g p17, p24, RT, gp41, gp120 and Nef itopes were tested for CTL response response to this epitope broken down by HIV-1 infection, HIV-1 exposed	individuals with pre-sero duals who responded to H	conversion therapy (Group 1), 11 IAART given during chronic infection				
		o study CTL responses to a pa le Nairobi sex workers	seronegative nel of 54 predefined HIV-1 epitopes in 9	1 HIV-1-exposed, persiste	ently seronegative (HEPS) and 87				
RT (356–365)	RMRGAHTNDV HIV-1 infection human (A*3002) Sabbaj2002b  • Epitope name: Pol-RV10  • This study monitored epitope responses in HIV-1 infected minority women living in the United States  • 24 epitopes were described – 8 were novel, 8 used new restricting elements but were previously defined epitopes, and 8 were previously described  • Serial peptide truncations were used to define optimal epitopes for CTL cell lines isolated from 12 individuals, assayed by a Cr-release  • Subject 01RCH50 also recognized the epitope WRFDSRLAF, Nef(183-191), B*1503  • Among HIV+ individuals who carried HLA A30, 5/16 (31%) recognized this epitope								
RT (356–366)	• One individual, AC-0	acutely HIV-infected HLA-A306, was homozygous at all thre	HIV-1 infection  3 (n=7) or -B7 (n=4) or both -A3 and B7 e class I alleles (A3, B7, Cw7), was treat.	ted during acute infection	and had supervised treatment				

• One individual, AC-06, was homozygous at all three class I alleles (A3, B', Cw'), was treated during acute infection and had supervised treatment interruptions (STI). He had only two detectable CTL responses during acute infection, but after STI this broadened to 27 distinct epitopes including 15 restricted by HLA-A3, 11 by HLA-B7, and 1 by HLA-Cw7.

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
			e A3-restricted responses to this epituals began to have detectable respon		y 5/15 of HLA-A3 epitopes tested
RT (364–372)	RT (518–526 U455)	DVKQLTEVV		human (A28, A*6802)	Dong1998a, Menendez-Arias1998
	<ul><li>Predicted on binding m</li><li>Reacts with clade A co</li></ul>		zed the peptide DVKQLAEAV, from th	ne D clade	
RT (364–372)	in East África	individuals with non-class		human (B70) subtype A infections, 1 with subtype	Dorrell1999 pe C – their infections all originated
		patient gave a CTL respon	an A subtype infection onse that could recognize the subtypognize the B clade variant (DVKQL)		substitutions (DVKQLAEAV),
RT (366–385)	<ul><li>each HIV protein.</li><li>Nef and p24 had the hi</li></ul>	nd Elispot data was obtain ghest percentage of reacti	NOTINGK HIV-1 infection ned from 105 HIV-1 positive Botsware peptides, and p24 had the highest clade peptides from among over 350	t magnitude of HIV-1 responses.	Novitsky2002 om between 55 and 64 subjects for
RT (374–383)	RT (LAI)  • Patients studied were fi • CTL epitopes of 3 rapidhem • Epitope recognized by	d progressors were compa	HIV-1 infection  t t t t t t t t t t t t t t t t t t t	human (B*5701)  no differences could be found in th	Menendez-Arias1998, vanderBurg1997 te degree of conservation between
RT (374–383)	RT (LAI) • Recognized by CTL from	KITTESIVIW om a progressor and a lon	HIV-1 infection g-term survivor, PIVLPEKDSW wa	human (B*5701) as also recognized	vanderBurg1997
RT (375–383)	B57 has been associate	d with long-term non-pro CTL responses in HLA B	HIV-1 infection of this epitope, KITTESIVIW [vand gression in the Amsterdam cohort \$5701 LTS were to RT and Gag cognized IVLPEKDSW	human (B*5701 B*5801) erBurg1997]	Klein1998
RT (375–383)	<ul> <li>individuals treated duri</li> <li>The breadth and specifindividuals with primar (Group 3), using 259 o</li> </ul>	ng chronic infection icity of the response was or ry infection but post-seroc verlapping peptides spann	determined using ELISPOT by study	ying 19 individuals with pre-serocor 0 individuals who responded to HA Nef	Altfeld2001b rse viral population than was seen in nversion therapy (Group 1), 11 ART given during chronic infection

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
	• Number of HLA-B57+	individuals that had a C	TL response to this epitope broken d	own by group: 0/0 group 1, 0/0 gr	oup 2, and 1/2 group 3
RT (392–401)			ne epitope is HLA B53/Cw2	human (A*3201)	Harrer1996b, Menendez-Arias1998
	C. Brander notes that the contract of the		in the 1999 database		
RT (392–401)	RT (559–568 LAI) • C. Brander notes this is	PIQKETWETW an A*3201 epitope		human (A*3201)	Brander2001
RT (392–401)	<ul><li>24 epitopes were descr</li><li>Serial peptide truncatio</li><li>Subject 01RCH59 was</li></ul>	pitope responses in HIV bed – 8 were novel, 8 us ns were used to define of Hispanic, was not on H.	HIV-1 infection  -1 infected minority women living in sed new restricting elements but were optimal epitopes for CTL cell lines is AART, viral load 5100, CD4 count 3-62, 1/2 (50%) recognized this epitope	e previou blated 49, and she also recognized QASQ	Sabbaj2002b QEVKNW, p24(176-184), B*5301
RT (392–401)	<ul> <li>individuals treated duri</li> <li>The breadth and specifindividuals with primar (Group 3), using 259 o</li> <li>Previously described at</li> </ul>	ng chronic infection city of the response was y infection but post-sero verlapping peptides span ad newly defined optima	determined using ELISPOT by stud	ying 19 individuals with pre-seroc 0 individuals who responded to H. Nef nse	AART given during chronic infection
RT (392–401)	<ul> <li>CTL epitopes (http://hi</li> <li>60 epitope responses w magnitude of the responses w magnitude of the responses.</li> <li>1 year post-HAART tree in PB, and 13/25 epitope.</li> <li>Treatment interruption become undetectable in Breakdowns of epitope.</li> <li>B7-TL9(p24), and responded to A32-PW1</li> </ul>	and lymph node (LN) CI v-web.lanl.gov/content/here detected in both PB nse was similar in LN ar in the LN. attent in five patients so he responses in the PB be following HAART indu- ted the PB, and the addition responses were shown for the BP-TM9(Nef) at 0(RT) in both PB and Lagreatest response to B2	HIV-1 infection  D8+ T-cell responses were compared niv-db/REVIEWS/brander2001.html) and LN samples of the 15 patients, and PB, but the percentage of CD8+ T tudied, the magnitude of the CD8 T-cecame undetectable, in contrast to 5/2 ced resulted in increased viremia accurated viremia accurated viremia accurate	of for each person's class I HLA allend an additional 8 responses were cells in the LN is lower so the number of the LN. The companied by the restoration of the companied by the restoration of the companied by the greatest response to epitope E yed the greatest response to epitope ainst epitope A32-RW10(gp120) of the companied by the greatest response to epitope ainst epitope A32-RW10(gp120) of the companies of the companies to epitope ainst epitope A32-RW10(gp120) of the companies to epitope A32-RW10(gp120) of the compa	eles. detected only in LN. The total mber of HIV-specific cells per million h LN and PB, but more dramatically e detection of 13 epitopes that had 814-EL9(gp41), a strong response to be B44-AW11(p24) and also was only detected in the LN sample.

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
RT (397–406)	RT (LAI)	TWETWWTEYW	HIV-1 infection	human (B44)	Menendez-Arias1998, vanderBurg1997
	<ul> <li>Recognized by CTL from by the other</li> </ul>	m two progressors, EILK	EPVGHGV and EELRQHLLRW were a	also recognized by one, and	RETKLGKAGY was also recognized
RT (416–424)	Pol (563–571 93TH253 subtype CRF01)		HIV-1 exposed seronegative	human (A11)	Sriwanthana2001
	• Epitope name: P571-579			in China Mai mantham Th	-11 4
	<ul> <li>HLA-A11 is very comm and CTL responses were</li> </ul>	on in this population, and e found in 8/8 HIV+ cont	eronegative (HEPS) female sex workers d was enriched among the HEPS sexwor rols, and 0/9 HIV- women that were not ady subject 128 who was HLA A11/A33	kers – weak CTL responses exposed	
RT (416–424)	Pol (563–571 93TH253 subtype CRF01)	FVNTPPLVK	HIV-1 infection	human (A11)	Bond2001
	<ul> <li>Thailand, of whom more</li> <li>77 possible HLA-A11 epepitopes for CTL respon</li> <li>This is one of the new A</li> </ul>	e than half were HLA-A1 pitopes were first defined uses from 8 HLA-A11 por 11 epitopes identified thr	1.) epitopes were identified that stimulate 1 positive using EpiMatrix, these were screened for sitive FSWs, six were novel, six were prough the streamlined EpiMatrix method not subtype H), but exact matches were results.	or binding to A11 finding ar eviously identified I, and 1/8 tested FSWs recog	nd 26 bound, and 12 of these were
RT (421–429)	patients, respectively)	•	HIV-1 infection ad CTL against pol – RT was more imm	human (A2) unogenic than Integrase and	Haas1998 Protease (81%, 51%, and 24% of 37
	New clusters of epitopes	were defined utilizing di			
RT (432–440)	RT (587–597 SF2)	EPIVGAETF	HIV-1 infection	human (B*3501)	Menendez-Arias1998, Tomiyama1997
		uals had a CTL response t position 1, and V to I at			s region is important for proper viral
RT (432–440)			HIV-1 infection B*3501-epitope tetramers did not expres nd a decrease of CD28+CD45RA+ cells		Tomiyama2000a y HIV-1-infected individuals relative to
	healthy individuals		lls and have high levels of perforin in the		

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References			
RT (432–440)	■ Three individuals with highly focused HIV-specific CTL responses were studied during acute infection using tetramers – high frequencies of HIV-1-specific CD8+ T cells were found prior to seroconversion, and there was a close temporal relationship between the number of circulating HIV-specific T cells and viral load was also found  ■ All three patients were B*2705, with HLA alleles: A1, A30/31, B*2705, B35; A1, A*0301, B7, B2705; and A*0201, A*0301, B2705, B39							
	<ul> <li>subjects showed a dom</li> <li>The subject with A*020</li> <li>Weak responses were o B*2705</li> </ul>	inant response to the Boot 101 had a moderatly strong bserved to A*301-RLR	topes that had been defined earlier and we *2705 epitope KRWIILGGLNK ong response to SLYNTVATL RPGGKKK, A*301-QVPLRPMTYK, and ong epitopes: A*201-ILKEPVHGV, A*30	d B7-TPGPGVRYPL in the sub	ject who was HLA A1, A*0301, B7,			
			PIPVGEIY, B35-NSSKVSQNY, B35-VF					
RT (432–440)	natural attenuated strain	n of HIV-1 which was N	HIV-1 infection 1.3 to 1.5 year period in members of the Nef-defective els of CTL effector and memory cells de		Dyer1999 BBC) who had been infected with a			
RT (432–440)	RT (587–596 SF2) • Binds HLA-B*3501, ar	EPIVGAETF  nd is also presented by	HIV-1 infection B51 – but CTL could not kill RT-vaccini.	human (B35, B51) a virus infected cells that expres	Shiga1996 sed B51			
RT (432–440)	Pol (587–595) • One of the 51 HIV-1 ep HLA alleles	EPIVGAETF itopes selected by Ferr	HIV-1 infection ari et al. as good candidate CTL epitopes	human (B35, B51) s for vaccines by virtue of being	Ferrari2000 conserved and presented by common			
RT (432–441)	<ul> <li>A significant increase in healthy individuals</li> <li>CD28-CD45RA- cells a</li> </ul>	n CD28-CD45RA- cell are likely to be effector	HIV-1 infection fic B*3501-epitope tetramers did not exp s and a decrease of CD28+CD45RA+ ce cells and have high levels of perforin in lls in chronically infected HIV-1-infected	lls was observed in chronically their cytoplasm				
RT (432–441)		note in their review that	HIV-1 infection  I, in contrast to the peptide EPIVGAETF at this epitope is located near the protease Ase) domain		Menendez-Arias1998, Shiga1996 of this region is important for viral			
RT (432–441)	RT (587–597 SF2)  • HLA B35 is associated  • The sequences of 9 pre-		HIV-1 infection gression 1 B35 CTL epitopes were obtained in 10	human (B35) HLA B35+ and 19 HLA B35-	Kawana1999 individuals			

HXB2 Location	<b>Author's Location</b>	Sequence	Immunogen	Species (HLA)	References			
	3/9 CTL epitopes had associated pattern of m		common in B35+ individuals that	an in B35- individuals, but this wa	s one of the six that had no B35			
RT (434–447)	RT (LAI)	IVGAETFYVDGAAS	HIV-1 infection	human (A*6802)	Menendez-Arias1998, vanderBurg1997			
	<ul><li>and KITTESIVIW</li><li>A*6802 is a subset of I</li></ul>			g peptides spanning IVGAETFY	VDGAAS as well as PIVLPEKDSW			
RT (436–445)	RT (591–600 IIIB)  • This epitope spans the	GAETFYVDGA Pol p66 RT – p15 (RNAse) d	HIV-1 infection omain	human (B45)	Menendez-Arias1998			
RT (436–445)	Pol (591–600 IIIB)	GVETFYVDGA	HIV-1 infection	human (B45)	Wilson1999a			
	<ul> <li>This study describes maternal CTL responses in the context of mother-to-infant transmission</li> <li>Detection of CTL escape mutants in the mother was associated with transmission, but the CTL-susceptible forms of the virus tended to be found in infected infants</li> </ul>							
		tope were found in a non-trans Pol p66 RT – p15 (RNAse) d	smitting mother who had a CTL omain	response to it				
RT (437–445)	Epitope name: Pol-AA	AETFYVDGA	HIV-1 infection	human (B*4501)	Sabbaj2002b			
	<ul> <li>24 epitopes were descr</li> <li>Serial peptide truncation</li> <li>Subject 00RCH33 was B*5301; RSLYNTVAT</li> </ul>	ribed – 8 were novel, 8 used nons were used to define optime on HAART had a viral load of the first p17(76-86), HLA A*300	al epitopes for CTL cell lines is	e previously defined epitopes, and olated from 12 individuals, assay and also recognized the epitopes Y 0-318), HLA A*3002				
RT (437–447)	RT (592–602 LAI)	AETFYVDGAAN		human (A28)	Brander1996b, Menendez-Arias1998			
	<ul> <li>P. Johnson, pers. comm.</li> <li>This epitope spans the Pol p66 RT – p15 (RNAse) domain</li> </ul>							
RT (437–447)	Pol (592–602) • One of the 51 HIV-1 ephLA alleles	AETFYVDGAAN pitopes selected by Ferrari et a	HIV-1 infection al. as good candidate CTL epito	human (A28) pes for vaccines by virtue of bein	Ferrari2000 g conserved and presented by common			
RT (438–448)	RT (593–603 IIIB)  • This epitope spans the	ETFYVDGAANR Pol p66 RT – p15 (RNAse) d	HIV-1 infection omain	human (A26)	Menendez-Arias1998			
RT (438–448)	<ul> <li>Detection of CTL esca infants</li> </ul>	pe mutants in the mother was	HIV-1 infection context of mother-to-infant tran associated with transmission, b ough reduced, CTL response: E	out the CTL-susceptible forms of t	Wilson1999a he virus tended to be found in infected			

HXB2 Location	<b>Author's Location</b>	Sequence	Immunogen	Species (HLA)	References
	• This epitope spans the	Pol p66 RT – p15 (RNAse) dom	ain		
RT (448–457)	RT • Patients studied were for	RETKLGKAGY rom the Amsterdam cohort	HIV-1 infection	human (A29)	vanderBurg1997
	<ul><li>CTL epitopes of 3 rapid between them</li><li>Epitope recognized by</li></ul>	d progressors were compared to		) and no differences could be found	in the degree of conservation
RT (449–457)	- This opnope occurs in	ETKLGKAGY	HIV-1 infection	human (A*2601)	Sabbaj2002b
	<ul> <li>24 epitopes were descri</li> <li>Serial peptide truncatio</li> <li>Subject 03RCH40 was Nef(108-115), HLA Cv</li> </ul>	9 pitope responses in HIV-1 infect ibed – 8 were novel, 8 used new ons were used to define optimal e African American, had a viral le	ted minority women living is restricting elements but we epitopes for CTL cell lines is and of 2500, CD4 count of 3	in the United States re previously defined epitopes, and solated from 12 individuals, assaye 372, was not on HAART, and also r	8 were previously described
RT (481–505)		AIYLALQDSGLEVNIVTDS QYALGI ased by HIV-1 specific activated the p15 (RNAse) domain of Pol	CTL	human	Menendez-Arias1998, Price1995
RT (481–505)		AIYLALQDSGLEVNIVTDS QYALGI o study gene usage in HLA-B14 the p15 (RNAse) domain of Pol	response	human (B14)	Kalams1994, Menendez-Arias1998
RT (485–493)	• This CTL epitope (the	ALQDSGLEV antigenic similarity matrix to co HIV-1 LAI fragment with high so r receptor kinase substrate EPS8	imilarity to a human protein	n overlapping this epitope is IYLAI	Maksiutov2002  LQDSGLE) has similarity with the
RT (485–493)				human (A2)	Brander1995a
RT (485–493)	<ul><li> This epitope was used a</li><li> This vaccine failed to it</li></ul>	nized by PBMC from 3/14 HIV-	TSCNTSV and a tetanus to a helper response was evid	human (A2.1)  xin T helper epitope for a synthetic lent	Brander1995a, Brander1996a vaccine

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
RT (485–505)	RT (648–672) • Unpublished, S. Kalams • This epitope occurs in the	ALQDSGLEVVTDSQYALGI ne p15 (RNAse) domain of Pol p	HIV-1 infection	human (B14)	Brander1995b
RT (496–505)	• Epitope name: Pol-VI10		HIV-1 infection	human (B*1503)	Sabbaj2002b
	<ul><li>24 epitopes were describ</li><li>Serial peptide truncation</li><li>Subject 01RCH51 was a</li></ul>		estricting elements but were proitopes for CTL cell lines isolate, viral load 980, CD4 count 81	reviously defined epitopes, and 8 ted from 12 individuals, assayed	
RT (496–505)	<ul> <li>Seroprevalence in this co</li> <li>Most isolated HIV strain responses are frequently</li> </ul>	VTDSQYALGI found in exposed seronegative probort is 90-95% and their HIV-1 as are clade A in Nairobi, althoug observed using A or D clade verd among A, B and D clade virus	exposure is among the highest gh clades C and D are also four rsions of epitopes	CTL may confer protection	Rowland-Jones1998b cross-reactive, however stronger
RT (496–505)	Cw8 molecule instead [I	se in 1995 as B14, but B14 transf		human (Cw8) peptide and it is thought to be properties.	Brander1996b resented by the genetically linked
RT (496–505)	<ul> <li>and D clades – such cros</li> <li>The A and D subtype co</li> <li>Thought to be HLA-Cw</li> </ul>	ss-reactivity could protect agains nsensus are identical to the B cla	t both A and D and confer prot ade epitope y reported (C. Brander, B. Wal		
RT (509–518)	<ul> <li>A subset of the potential epitopes were identified</li> </ul>		ld bind to the appropriate HLA ction in an ELISPOT assay	human (B7) tify conservered regions of HIV A-allele, and 15 predicted B7 sup	De Groot2001 that might serve as epitopes serfamily (HLA B7, B8, and B58)
RT (516–525)	<ul><li>patients, respectively)</li><li>New clusters of epitopes</li></ul>	ELVNQIIEQL ectional analysis, 78% had CTL were defined utilizing different to p15 (RNAse) domain of Pol p	HLA molecules	human (A2) munogenic than Integrase and Pr	Haas1998 rotease (81%, 51%, and 24% of 37

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
RT (520–528)	Pol (520–528 LAI) • C. Brander notes this is	QIIEQLIKK an A*1101 epitope		human (A*1101)	Brander2001, Fukada1999
RT (520–528)	cross-reactive and recognized specific manner. Two of QIIEQLIKK was found was strongly recognized common in the A subty	gnized by clade E infecther HLA A*1101 clade to elicit clade-specific d by CTL from 1/5 B clpe, was also recognized JKK, qiieElikk and qiid	HIV-1 infection f1101 epitopes were generated for clade ted individuals. The clade E and B anal e B defined epitopes were found not to responses in clade B (QIIEQLIKK is n ade infected Japanese subjects, and que in 2/7 E clade infected Thai subjects. eKliEk to HLA A*1101 was similar, bu ted TCR interaction.	ogs to three more HLA A*1101 have stimulated a response in clanost common) and clade E (qiieEeElikk from 3/7 E clade infected	epitopes was recognized in a clade ade E infected individuals. Elikk is most common). QIIEQLIKK Thai subjects. The variant qiieKliEk,
RT (530–538)		HIV-1 LAI fragment wi	HIV-1 infection  trix to compare HIV-1 antigenic determ th high similarity to a human protein over the content of the content		Maksiutov2002  XVYLAWV) has similarity with
RT (530–538)	<ul> <li>24 epitopes were descri</li> <li>Serial peptide truncatio</li> <li>This epitope was newly</li> <li>Patient 04RCH86 was I</li> </ul>	pitope responses in HIV bed – 8 were novel, 8 uns were used to define of defined in this study Hispanic, not on HAAR	HIV-1 infection  7-1 infected minority women living in the sed new restricting elements but were propriated epitopes for CTL cell lines isolated. T, and had a viral load of 7600 and CD *03, 2/21 (10%) recognized this epitopes	oreviously defined epitopes, and ated from 12 individuals, assayed 4 count of i774	
RT (532–540)	for the A3 supertype) w • Progressors had memor • A positive correlation b observed, which may co	while the effector cells of y resting CD8+ T-cells etween effector CD8+ ontribute to the inability	HIV-1 infection g memory resting CD8+ T-cell response of long-term nonprogressors recognized that recognized far fewer epitopes than T-cells and plasma viremia and a negati of LTNPs to clear virus alleles (A*0301, A*1101, A*3101, A*3	far fewer epitopes LTNPs ve correlation between CD8+ ef	s tested, (18 for the A2 supertype, 16
RT (532–540)	patients, respectively)	s were defined utilizing	HIV-1 infection had CTL against pol – RT was more in different HLA molecules n of Pol p66 RT	human (B7) nmunogenic than Integrase and l	Haas 1998 Protease (81%, 51%, and 24% of 37

## II-B-11 Integrase CTL Epitopes

HXB2 Location	<b>Author's Location</b>	Sequence	Immunogen	Species (HLA)	References
Integrase (20–28)	for the A3 supertype) w • Progressors had memore • A positive correlation be observed, which may constitute the superference of the superference o	while the effector cells or ry resting CD8+ T-cells between effector CD8+ To ontribute to the inability	HIV-1 infection memory resting CD8+ T-cell response f long-term nonprogressors recognized that recognized far fewer epitopes than f-cells and plasma viremia and a negati of LTNPs to clear virus supertypes alleles (A*0201, A*020 2,	far fewer epitopes LTNPs ve correlation between CD8+ effe	
Integrase (22–31)	for the A3 supertype) w • Progressors had memor • A positive correlation be observed, which may constitute the superference of	while the effector cells or ry resting CD8+ T-cells between effector CD8+ To ontribute to the inability	HIV-1 infection memory resting CD8+ T-cell response f long-term nonprogressors recognized that recognized far fewer epitopes than f-cells and plasma viremia and a negati of LTNPs to clear virus pes alleles (A*0201, A*0202, A*0203,	far fewer epitopes LTNPs ve correlation between CD8+ effe	
Integrase (28–36)	<ul> <li>Med. 2:405, 1996;Lanc</li> <li>15% of Japanese popul</li> <li>Of the 172 HIV-1 pepti positive individuals, an</li> </ul>	tet 22:1187, 1986;Hum ations carry HLA-B51 v des with HLA-B*5101 a d six were properly proc	HIV-1 infection slow progression to AIDS, while HLA- Immunol 22:73, 1988;Hum Immunol 4 while HLA-B27 and -B57 are detected anchor residues, 33 bound to HLA-B*5 cessed among B subtype sequences – LPPVV	4:156, 1995) in less than 0.3% 5101, seven of these peptides were	
Integrase (82–89)	Phe, Leu or Ile at the C  This peptide induced C	term) – 53 of the 59 per TL in 1/4 HIV-1+ people			
Integrase (89–98)	• This CTL epitope (the		HIV-1 infection  rix to compare HIV-1 antigenic determ th high similarity to a human protein ov AETNGEITAY.		Maksiutov2002  QETAY) has similarity with Integrin
Integrase (89–98)	<ul> <li>A subset of the potential epitopes could stimulat</li> </ul>	al epitopes was identified to IFN $\gamma$ production in an	n with the program Conservatrix to ide d that could bind to the appropriate HL ELISPOT assay  A-B56 epitope in this study		

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
Integrase (96–104)	Integrase (823–831) • Epitope found in clade	ETAYFILKL A, B, and D – Pers. Cor	nm. S. Rowland-Jones and T. Dong	human (A*6802)	Dong1998b
Integrase (96–104)	<ul><li>CD8+ T cell responses</li><li>Low risk individuals di</li><li>CD8+ T cell epitopes: 1</li></ul>	tended to be to the same d not have such CD8+ c	uals), SLYNVATL (4 individuals), LSPRTL	cervical CD8+ T cell response	onses
Integrase (96–104)	<ul><li>sex workers eventually</li><li>The epidemiological fa working for a period or</li></ul>	seroconverted, and for sector associated with sero	HIV-1 infection cosed, persistently seronegative individuals, in these HIV CTL reactive epitopes had beconversion was stopping sex work and HIV-worker controls (ML1671)	een defined while seroneg	gative
Integrase (96–104)	<ul> <li>HIV-1-infected female</li> <li>Responses in HEPS wo reduced risk of infection women</li> <li>43/91 HEPS women ha</li> <li>Among HLA-A*6802 vertended to respond to D'</li> <li>The dominant response epitope</li> <li>Differences in epitope seassociated with resistant</li> <li>Subject ML 1203 started acquired additional responder of the subject ML 1707 started RDYVDRFFKTL post-</li> </ul>	study CTL responses to Nairobi sex workers omen tended to be lower, in, and there was a shift of CD8+ responses and of women, 3/12 HEPS and TVLEDINL, while infect to this HLA allele was specificity were only see acceptated with CTL responses to ponses to A*6802 ETAY and with a CTL response to seroconversion	a panel of 54 predefined HIV-1 epitopes in 9 and focused on different epitopes with HLA in the response in the HEPS women upon lat detection of HIV-1-specific CTL in HEPS wo 9/11 HIV-1 infected women recognized this sted women to ETAYFYILKL to this epitope in 2 of the 3/12 HEPS cases a on for responses restricted by class I HLA allern for responses re	presenting molecules that e seroconversion to epitopomen increased with the depitope likelihood ratio 7 and in all 9/11 HIV-1 infecteles A2, A24, A*6802, BOVPLR prior to seroconversion, and switched to A*6	thave previously been associated with the previously been associated with the previously the HIV-1 infected uration of viral exposure 1.9, p value 0.01, and HEPS women ted women that responded to the 1.4, and B18, previously shown to be 1.4, and upon seroconversion QGL, and B7 SPRTLNAWV 5802 ETAYFILKL and A24
Integrase (96–104)	Pol (744–752)  • This epitope is newly d	ETAYFILKL efined in this study	HIV-1 infection	human (A*6802)	Appay2000

- Combined tetramer and intracellular cytokine staining was used to study the function of circulating CD8+ T cells specific for HIV and CMV
- HIV-specific CD8+ T cells expressed lower levels of perforin than CMV-specific CD8+ T cells from the same donor, and this was associated with persistent CD27 expression on HIV-specific cells, suggesting impaired maturation

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
	• In most donors, betwee produce TNF-α	n 50% and 95% of the a	activated virus-specific CD8+ T cells p	roduced IFN- $\gamma$ and MIP-1 $\beta$ with	a distinct subset that failed to
•	for the A3 supertype) w Progressors had memor A positive correlation b observed, which may co	while the effector cells of y resting CD8+ T-cells etween effector CD8+ Tontribute to the inability	HIV-1 infection memory resting CD8+ T-cell response f long-term nonprogressors recognized that recognized far fewer epitopes that r-cells and plasma viremia and a negat of LTNPs to clear virus supertypes alleles (A*0201, A*0202,	I far fewer epitopes n LTNPs ive correlation between CD8+ ef	s tested, (18 for the A2 supertype, 16
•	Pol (888–896)  C. Brander notes this is  Epitope is motif based,  Subtype of B57 not dete	personal communicatio	n from C. Hay	human (B*5701)	Brander2001
Integrase (173–181)	Pol (888–896) • Epitope is motif based,	KTAVQMAVF personal communicatio	n from C. Hay	human (B57)	Hay1999a
•	for the A3 supertype) w Progressors had memor A positive correlation b observed, which may co	while the effector cells of y resting CD8+ T-cells etween effector CD8+ Tontribute to the inability	HIV-1 infection memory resting CD8+ T-cell response f long-term nonprogressors recognized that recognized far fewer epitopes that r-cells and plasma viremia and a negat of LTNPs to clear virus lleles (A*0301, A*1101, A*3101, A*	I far fewer epitopes 1 LTNPs ive correlation between CD8+ ef	s tested, (18 for the A2 supertype, 16
•	for the A3 supertype) w • Progressors had memor • A positive correlation b observed, which may co	while the effector cells of y resting CD8+ T-cells etween effector CD8+ Tontribute to the inability	HIV-1 infection memory resting CD8+ T-cell response f long-term nonprogressors recognized that recognized far fewer epitopes that r-cells and plasma viremia and a negat of LTNPs to clear virus dleles (A*0301, A*1101, A*3101, A*	I far fewer epitopes n LTNPs ive correlation between CD8+ ef	s tested, (18 for the A2 supertype, 16
•	for the A3 supertype) w • Progressors had memor • A positive correlation b observed, which may co	while the effector cells of y resting CD8+ T-cells etween effector CD8+ Tontribute to the inability	HIV-1 infection memory resting CD8+ T-cell response f long-term nonprogressors recognized that recognized far fewer epitopes that F-cells and plasma viremia and a negat of LTNPs to clear virus lleles (A*0301, A*1101, A*3101, A*	I far fewer epitopes n LTNPs ive correlation between CD8+ ef	s tested, (18 for the A2 supertype, 16
Integrase (179–188)	Integrase (179–188 LA)  C. Brander notes this is			human (A*1101)	Brander2001, Fukada1999

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
	cross-reactive and recogn specific manner. Two oth	nized by clade E infected individuely HLA A*1101 clade B define	HIV-1 infection opes were generated for clade E (CR luals. The clade E and B analogs to d epitopes were found not to have st ng subtypes A-E. It was strongly rec	three more HLA A*1101 epimulated a response in clad	pitopes was recognized in a clade e E infected individuals.
	<ul> <li>HLA-A11 is very common and CTL responses were</li> <li>This epitope was weakly</li> </ul>	1 exposed persistently seronega on in this population, and was en found in 8/8 HIV+ controls, and	HIV-1 exposed seronegative tive (HEPS) female sex workers in Carriched among the HEPS sexworkers d 0/9 HIV- women that were not expects 265 who was HLA A2/A11 and	s – weak CTL responses wo	ere detected in 4/7 HEPS women,
	<ul> <li>One individual, AC-06, v interruptions (STI). He h restricted by HLA-A3, 1</li> <li>0/14 HLA-A3 positive in</li> </ul>	tely HIV-infected HLA-A3 (n=7) was homozygous at all three class and only two detectable CTL responders and 1 by HLA-C adividuals had detectable A3-responders.	HIV-1 infection  7) or -B7 (n=4) or both -A3 and B7 (as I alleles (A3, B7, Cw7), was treated ponses during acute infection, but af w7.  tricted responses to this epitope during an to have detectable responses to the	ed during acute infection and ter STI this broadened to 2' and acute infection, but only	d had supervised treatment 7 distinct epitopes including 15
	<ul><li>each HIV protein.</li><li>Nef and p24 had the high</li></ul>	nest percentage of reactive peption	HIV-1 infection n 105 HIV-1 positive Botswanans; E des, and p24 had the highest magnitudes from among over 350 tested s	ude of HIV-1 responses.	Novitsky2002 om between 55 and 64 subjects for
	<ul><li>each HIV protein.</li><li>Nef and p24 had the high</li></ul>	nest percentage of reactive peption	HIV-1 infection n 105 HIV-1 positive Botswanans; E des, and p24 had the highest magnitu ptides from among over 350 tested s	ude of HIV-1 responses.	Novitsky2002 om between 55 and 64 subjects for
Integrase (219–227)	• Epitope name: Pol-KY9	KIQNFRVYY	HIV-1 infection	human (A*3002)	Sabbaj2002b

- This study monitored epitope responses in HIV-1 infected minority women living in the United States
- 24 epitopes were described 8 were novel, 8 used new restricting elements but were previously defined epitopes, and 8 were previously described
- Serial peptide truncations were used to define optimal epitopes for CTL cell lines isolated from 12 individuals, assayed by a Cr-release
- Patient 00RCH28 was African American, not on HAART, had a viral load of 5900 and CD4 count of 889, and she also recognized RIRQGLERA, gp160(846-854), A\*0205

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
	Among HIV+ individual	ls who carried HLA A3	0, 6/16 (38%) recognized this epitope		
	<ul> <li>for the A3 supertype) wl</li> <li>Progressors had memory</li> <li>A positive correlation be observed, which may co</li> </ul>	hile the effector cells of resting CD8+ T-cells to tween effector CD8+ T ntribute to the inability	HIV-1 infection memory resting CD8+ T-cell responses long-term nonprogressors recognized that recognized far fewer epitopes than c-cells and plasma viremia and a negativ of LTNPs to clear virus lleles (A*0301, A*1101, A*3101, A*3	far fewer epitopes LTNPs ve correlation between CD8+ 6	es tested, (18 for the A2 supertype, 16
			in vitro stimulation genicity in transgenic HLA-A*0201/K C derived from uninfected individual	human (A*0201) <sup>b</sup> mice	vanderBurg1996
	monthly into six HIV-int  1/6 showed increased Er no change – pulsed DCs	fected patients nv-specific CTL and inc were well tolerated served HLA-A2 epitope	HIV-1 infection from HLA-identical siblings, pulsed we reased lymphoproliferative responses, a included in this study – 6/6 patients has	2/6 showed increase only in pr	oliferative responses, and 3/6 showed
Integrase (241–249)	Pol (956–964 HXB2R)  • Studied in the context of	LLWKGEGAV HLA-A2 peptide bind	Peptide-HLA interaction ing	human (A2)	Parker1992, Parker1994
Integrase (241–249)	Pol (956–964 HXB2R)  No CTL activity found i	LLWKGEGAV n HIV-infected subjects	Peptide-HLA interaction s, epitope studied in the context of inclu	human (A2) usion in a synthetic vaccine	Brander1995a
Integrase (241–249)	Pol (956–964) • One of the 51 HIV-1 epi HLA alleles	LLWKGEGAW topes selected by Ferrar	HIV-1 infection ri et al. as good candidate CTL epitope	human (A2, A*0201) s for vaccines by virtue of bein	
	<ul> <li>Epitope name: LR28</li> <li>The stability of peptide I SLYNTVATL (p17), SLI (GILGFVFTL), while R</li> <li>The four high-affinity peless than an hour.</li> <li>HLA-A2.1 transgenic m as adjuvants.</li> </ul>	binding to HLA-A2.1 w LNATDIAV (gp41) and GPGRAFVTI and VIY eptides formed stable co- ice were immunized wi QYMDDL induced a st	Vaccine Adjuvant: P30, incomplete Freund's adjuvant: P30, incomplete Freund's adjuvant as determined for six HLA-A2.1 peptil LLWKGEGAV (RT) all bound with half QYMDDL bound with a lower affinity omplexes with half-lives ranging between the six HIV-1 peptides and P30, as a stong CTL response in Cr-release assays	des included in this vaccine stuigh affinity comparable to a information (relative binding activity = 0.0 en 8 and 32 hours, while the long universal T-helper epitope, with	ady – ILKEPVHGV (RT), fluenza epitope reference fluenza epitope refere

HXB2 Location	<b>Author's Location</b>	Sequence	Immunogen	Species (HLA)	References
Integrase (241–249)	RT (956–964 HXB2R)	LLWKGEGAV	Vaccine	murine (A2.1)	Peter2002
_	Vaccine Vector/Type: pe	ptide Strain: LAI	Adjuvant: P30, incomplete Freund's ad	ljuvant (IFA), IL-12	
•	<ul> <li>Epitope name: LR28</li> </ul>				
•	<ul> <li>When HIV-1 peptides we</li> </ul>	ere used to vaccinate	HLA-A2.1 transgenic A2-Kb mice, stro	ng responses to five peptides were	observed when the peptides were
	given individually, but in	nmunodominance lim	nited the response to some of the peptide	es when they were given in combin	nation [Peter2001]. IL-12 can
	counteract immunodomi	nance in BALB/c mid	ce, so it was given with the multiple epit	ope vaccination, and was instead f	found to specifically eliminate the
	HLA-A2.1-epitope CTL	responses, but not Kl	b CTL responses. This was possibly a co	onsequence of transient depletion of	of T-cells, B cells and macropahges
	in the spleen.				

## II-B-12 Pol CTL Epitopes

<b>HXB2</b> Location	<b>Author's Location</b>	Sequence	Immunogen	Species (HLA)	References
Pol		orrelation between stror CD4 and CD8 cells, an		human se in 7-12 month old infants, and	Buseyne1998a d remaining AIDS-free for the first year
Pol	<ul><li>delivery of protein alor</li><li>Chloroquine administr</li></ul>	ne	HIV-1 infection 24 NY5) to human dendritic cells (DC) presentation, and brefeldin A and peptime pathway	-	
Pol	infants • No HIV+ infants had r disease, and not in rap	no demonstrable CTL at	HIV-1 infection had lower Th1 responses and decrease birth, but Th1 responses accompanied g dilution using autologous B cells infe	by CTL responses developed in	n children with slowly progressive
Pol	<ul><li>The vaccine used was</li><li>Twenty HIV negatives</li><li>Immunization with vC</li></ul>	a rec canarypox with H subjects were vaccinated P205 induced HIV-1-sp	Vaccine I, MN HIV component: gp41, Gag, F IV-1 gp120 MN, tm/gag/protease LAI ( d in phase I trial with combinations of vecific ABs to gp120, V3, and p24 antig s against Env, Gag and Pol, but the CL	(vCP205), alone or with p24E-V vCP205 and CLTB-36 gens, and CTL immune response	es against vCP205 were detected after
Pol	<ul><li>The vaccine used was :</li><li>In vitro inducible CTL</li></ul>	canarypox prime with rarec canarypox expressir activity against HIV-1	Vaccine gp120 boost Strain: LAI and SF2 H gg HIV-1 env, gag, pol, nef and protease Env, Gag, Pol, and Nef antigens was obther resulted in an overall increase in C	e (vCP300) with or without admoserved in 79% (15 of 19) of vac	ninistration of HIV-1 SF-2 rgp120 ccine recipients
Pol			HIV-1 infection  n between HIV Type I plasma viral load term survivors (LTS) of HIV-1 infection		Betts1999 inst HIV-1 Pol, and stronger combined
Pol			HIV-1 infection release assay in bulk culture showed no , CD4 and time to death	human correlation between CTL-activ	Aladdin1999 ity (gp120, Gag, Pol and Nef) and
Pol	RT (LAI) • In infants with positive subtypes	e CTL responses, most r	HIV-1 infection responses showed cross-clade reactivity	human with somewhat diminished rec	Buseyne1998b ognition of epitopes from different

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
Pol	<ul> <li>A gag/pol, vif or gp16 dramatic increase in b</li> </ul>	60 DNA vaccine, when both the cytotoxic and p	Vaccine  at: Gag, Pol, Vif, Env Adjuvant: B7, II delivered in conjunction with the plasm proliferative responses in mice d be detected even without in vitro stim	id encoding the co-stimulatory	Kim1997c molecules B7 and IL-12, gave a
Pol			HIV-1 infection sed with their own lymphocytes, cryopre re seen in 7/12, and an increase in the C		
Pol	<ul> <li>Reactivity against Gaş autologous EBV trans</li> <li>The child who progres</li> <li>The long-term non-progression</li> </ul>	g, Pol, Env and Tat prot formed B cells ssed consistently had C	detectable CTL, but was heterozygous f	cells reacting with protein exp	
Pol	Env proteins		HIV-1 infection clade virus had CTL that were able to r	-	-
Pol	• Anti-NKR IgM MAb	masked this inhibitory	HIV-1 infection Il receptor (NKR+) can exhibit down reg function and increased HIV-1 specific C e other case anti-NKR MAb brought HI	CTL activity in phytohemagglut	
Pol	CTL activity was corr	elated with a CCR5 wi	ldtype genotype	IV-1 specific CTL against Env,	Goh1999 Gag, Pol, or a combination of proteins – our individuals had responses to multiple
Pol	<ul> <li>A Canarypox vaccine</li> </ul>	expressing gp120, gp4	Vaccine  conent: gp120, gp41, Gag, Pro, Nef, RT 1, Gag, Protease, Nef and Pol CTL epite ected 3-6 months after the last vaccination	opes gave rise to CTL that coul-	Evans1999 d be detected in 61% of the volunteers –
Pol	The study explores the	e use of co-stimulatory	Vaccine  nt: Env, Gag, Pol Adjuvant: CD86, CD  molecules co-expressed with an HIV-1  atically increased both HIV Env and Ga	immunogen in a DNA vaccine	-

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
Pol	Pol (IIIB)  CTL precursor frequent non-transmitting mother		HIV-1 infection in HIV-1 infected pregnant women, and a mothers;	human significantly higher CTLp freq	Jin1998a uencies to Pol and Nef were found in
Pol	<ul><li>tested increased lysis b</li><li>2/10 individuals with &lt;</li></ul>	y > 5%) if the culture (200 CD4 cells/ul, and	HIV-1 infection IL12) to cultures increased HIV-specific was derived from HIV+ individuals who 3/10 individuals with 200-500 CD4cells CD8 cells that maintained responsivenes	had CD4 cells/ul > 500 s/ul, had an increase of >5% up	-
Pol	cross-reactive CTL res HIV-1 clades A, B, and • Proteins corresponding	ponses in HIV infected ID. g to the subtype of the i	HIV-1 infection lan epidemic, and a vaccine trial using B I Ugandans to A, D, and B clade recomb infecting strains tended to trigger higher with B clade proteins and the co-circulati	inant vaccinia viruses expressi levels of CTL response measu	ng Gag, Env, Pol, RT or Nef from
Pol	Pol  HIV-specific CTL active could be identified in t	•	HIV-1 infection e female reproductive tract of only 1/3 H women	human IV-infected women who under	White2001 went a hysterectomy, although CTL
Pol		and Pol expressed in va	HIV-1 infection red in long term non-progressors (LTNP) accinia in autologous targets low viral load	human with low viral load using limi	Jin2000a ting dilution analysis and measuring
Pol	<ul> <li>The CTL responses assorted of a lower magnitude to CD8+ CTL responses to clear if there is a stable.</li> <li>CD8+ CTL responses and ELISPOT, and the individuals relative to the HIV-1 specific CD8+ CD8+ CD8+ CD8+ CD8+ CD8+ CD8+ CD8+</li></ul>	sayed by ELISPOT and han in chronic HIV-1 it tend to be detectable in tend to be detectable in the HEPS population authors consider the pHIV-1 infected individuantly responses in HIV-	HIV-1 exposed seronegatives about HIV-specific CTL found in the Help by CTL precursor frequencies by limiting fections – the responses in HEPS cases a HEPS subjects only if they are recently in HEPS cases in are associated with HIV-1 specific CD cossibility that HIV-1-specific T-help responses, who tend to have a poor HIV-1-specific infected individuals show reduced leve EPS individuals this is considered as a possibility that HIV-1 specific T-help responses to the tendence of the tendence	IIV-1 exposed persistently seroing dilution analysis indicate the are below the level of detection exposed, and the response dim 4+ T cell responses, assayed by conses improve the "quality" of cific T-help response els of perforin, and the T cells in	nat CTL in HEPS individuals tend to be on by tetramer assays innishes if exposure is reduced – it is not by proliferation assays, IL-2 secretion, f the CD8+ response in HEPS may not mature properly, and although
Pol		. •	HIV-1 exposed seronegative this) born to HIV+ mothers had HIV-1 sp		De Maria1994, Kuhn2002 nia-expressed Nef, Gag/Pol, Env.

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
Pol	<ul><li>remained very low in 3</li><li>The two infants with hi</li><li>Stronger responses were</li></ul>	infants with a rapidly igh levels of Env peptic re detected after initiation infected though bornatly in PBMC after birth	HIV-1 infection ponses were not detectable in icord blooprogressive disease. For those who progle-stimulated IL-2 responses had the higher on of the antiretroviral therapy. In to HIV+ mothers had detectable though.	gressed more slowly, the HIV-sphest CTLp frequencies.	pecific CTL activity varied.
Pol			HIV-1 infection	human	Aldhous1994, Kuhn2002
	responses were detecte	d at all time points.  that were not infected the	HIV-1 specific CTL responses to vacciough born to HIV+ mothers had detecta		
Pol			HIV-1 infection	human	Yusim2002
	invariant, most highly of	p24, and Pol proteins R conserved regions of R' egions, as functional co	T and Protease, epitopes are more even f and Protease. This might be due to the onstraints for enzyme function would no	e virus evolving conserved feat	ures that disallow the CTL responses in
Pol	• Therapeutic RT inhibit analogs to CTL epitope		HIV-1 infection in vitro for resistance mutations in subt I for the B subtype,	human type C viruses. Many of the res	Loemba2002 istance mutations were located within
Pol	CD8 T-cell activity as a	measured by Elispot SF	HIV-1 infection fection showed a correlation between the FC per million PBMC summed across P than those treated later (N = 23), and a	ol, Env, Nef and Gag. The subj	ects treated early after infection had
	episodes.				
Pol	<ul><li>Nef and/or Pol CTL res</li><li>The magnitude and bre</li><li>Pol and Int CTL response</li></ul>	sponses were detected it eadth of Gag and p24 Tenses correlated positive	HIV-1 infection ted patients elicited gamma-IFN CD8+ n 86% of the subjects cell responses correlated with absolute ly with absolute CD4+ T-cell count either CD4 counts or viral load		Edwards2002 related with viral load
Pol	patients on successful I	HAART treatment, rela	HIV-1 infection ccinia expressing Gag, Pol, Nef and En- tive to autologous monocytes. Some we etection of low frequency memory cells	eak responses could only be det	

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
Pol		ns were obtained in 14 da	HIV-1 infection ion of CD8+ and CD4+ T-cells with the tys with optimized concentrations of II		
Pol	was measured in an El proteins.  • All 22 patients targeted recognized Nef. Robus  • Despite high HCV vira strong anti-HCV response.	d at least one protein. 20 st CTL activity was indeal loads, very few HCV conses were mounted.	HIV-1 and HCV co-infected in 22 individuals who were co-inferenced using targets expressing either Ga 1/22 patients recognized RT, 17/22 patientenced of disease progression or vira CD8+ T-cell Elispot responses were detected in 9/17 coinfected patients, but the content of the coinfected patients, but the content of the coinfected patients, but the coinfected patients are coinfected patients.	cted with HIV-1 and hepatitis C vg, RT, Env and Nef in a vaccinia ents recognized Gag, 13/22 subject load.  etected. In a control HCV infected.	construct, or one of seven HCV exts recognized Env and 11/22 patients d person who did not have HIV-1,
Pol	<ul> <li>Before ART 2/13 infar became undetectable a</li> <li>One older infant, at 23 group. 3/4 infants older</li> </ul>	nts <6 months of age sho after successful therapy— 3 months, had CTL respo er than 6 months of age r	HIV-1 infection RT were studied in 13 HIV-1 vertically owed IFNgamma Elispot CD8+ T-cell 3 infants were coinfected with CMV a conses against all for proteins tested, Ga responded to either Nef or Pol. and the HIV-1-specific CTL response in	responses, one to Nef and one to and all 3 had CMV-specific CD8-g, Pol, Nef and Env, and had the	Env and Nef, and these responses + T-cell responses. lowest plasma viremia of the study
Pol	DC cells could stimula	ate CD4+ and CD8+ T-ce	HIV-1 infection gens derived from dead, apoptotic cells ells resulting in IFNgamma production aspect of the initial immune respons	n in an Elispot assay. Both HLA	Class I and class II molecules were
Pol	boosted HIV-1 specific rebound to pretreatmen	c CTL responses and ele	HIV-1 infection infected patients undergoing HAART wated CTL responses were maintained count decline was observed. CD8 responses was contact and the count decline was observed.	up to 22 weeks after the last trea	tment interruption, but viral load
Pol			HIV-1 infection		
Pol	Computational method HLA-A*0201 and HL	ds (artificial neural netwo A-B*3501 HIV T-cell ep	computer prediction computer prediction orks, hidden Markov models, binding a bitope candidates from 533 Gag, Env a isons to known epitopes and between o	(A*0201, B*3501) matrices based on HLA associati and Pol sequences of which 374 v	Schönbach2002 on rates) were used to identify

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
Pol	Cohort Study. 64 sign -B15. Fifteen of these particular HLA molec • 25 negative associatio presented by common	ificant associations betw were in positions with I ules flanked known epit ns were also found betw	HIV-1 infection xamined relation to HLA alleles found reen polymorphisms at particular position to the polymorphism and particular position and may relate to processing. The polymorphism and HLA alleles. The in the population, and give examples of A-A2.	ons and HLA alleles were detect 1 in other positions. Six addition he authors propose this is due to	ed, for HLA-B7, -B12, -B35 and all polymorphic sites associated with escape mutations in epitopes
Pol	<ul> <li>Of 32 patients with HI 69% to Gag, 50% to N</li> <li>The overall magnitude in those that had lower</li> </ul>	LA-B*35 alleles CD8+ 0 Nef, and 41% to Env. to of CTL responses did to the RNA levels that carried	HIV-1 infection (3503, B*3504, and B*5301 tend to pro CTL responses were quantified using an anot differ between those bearing B*350 d B*3501, and there was a negative assorptotection in B*3501 individuals, but	n intracellular cytokine staining and the others. A higher percentiation with viral load and CTL	assay – 75% had responses to Pol, ntage of Gag responses was observed activity. The data is consistent with
Pol	Mice were immunized construct	I with four humanized D	Vaccine 32, pol NL43 HIV component: Gag, F NA constructs: GagPol, that would for fusion construct all elicited strong anti-	m a pseudoparticle carrying Gag	

# II-B-13 Vif CTL Epitopes

<b>HXB2</b> Location	<b>Author's Location</b>	Sequence	Immunogen	Species (HLA)	References
Vif (17–26)	variable regions found  While the uneven distrused to probe the immeto not be found in C-te virus where variation is and turn regions in the  In the more conserved  What was learned from	in Nef, Env and p17. ibution of epitopes may une response and autolorminal positions of epit is best tolerated traces of proteins. p24, and Pol proteins Far proteins where many dized in Rev, Tat, Vif, a	HIV-1 infection ture and included in this database tend to be in part due to a limited cross-recogn agous strains, regions with a paucity of topes, and had lower cleavage prediction of immune escape have left an imprint of all the protease, epitopes are more even epitopes have been defined (Gag, Pol, Eund Vpr. Predictions were made blinded diregions.	nition of specific responses beca defined epitopes also had higher n scores for epitope processing. n the viral population. Epitopes ally distributed. Env and Nef) was used to develop	use of differences between peptides frequencies of amino acids that tend. This suggests that in the regions of the also were concentrated in alpha-helix p an algorithm to predict where
Vif (17–26)	Vif (17–26 SF2)  • Epitope name: RK10  • CTL responses against  • 10/29 (35%) individua  • This epitope was recog  • HIV+ individual AC-0 from 7 proteins, sugge	RIRTWKSLVK  HIV-1 Vpr, Vpu, and Vals tested responded to Value by 3/15 individu 6 was tested for reactive sting that the breadth of	HIV-1 infection  Vif were analyzed in multiple HIV-1-inf	V-1 proteins in an ELISPOT and accessory proteins are not includ	ed in the study
Vif (17–26)	• 28% targeted one or m	ore overlapping Tat per	HIV-1 infection bry proteins in 70 HIV-1 infected patient otides; 36%, Rev peptides; 33%, Vif per numarized for the five proteins.		e i i
Vif (17–26)	<ul><li>Epitope name: Vif-RK</li><li>Among HIV+ individu</li></ul>		HIV-1 infection A03, 3/21 (14%) recognized this epitope	human (A03)	Sabbaj2002b
Vif (17–26)	(LAI)	RIRTWKSLVK		(A3)	Altfeld2000a, Brander2001
Vif (17–26)	• One individual, AC-06	cutely HIV-infected HI , was homozygous at a had only two detectab	HIV-1 infection  A-A3 (n=7) or -B7 (n=4) or both -A3 a  Il three class I alleles (A3, B7, Cw7), was  le CTL responses during acute infection by HLA-Cw7.	as treated during acute infection	and had supervised treatment

HIV CTL Epitope Tables

Vif CTL Epitopes

HXB2 Location	<b>Author's Location</b>	Sequence	Immunogen	Species (HLA)	References		
			A3-restricted responses to this epials had detectable responses to this		nly 5/15 of HLA-A3 epitopes tested		
Vif (27–41)	<ul><li>targeted one or more V</li><li>The regulatory proteins</li></ul>	if peptides, and this peptides s Rev and Tat combined con		ed epitope in Vif (25%). proteins Vif, Vpr and Vpu to 7%	Addo2002b g peptides and Elispot – 33% (23/70) , of the total magnitude of HIV-1		
Vif (28–36)	• 28% targeted one or m	ore overlapping Tat peptide	HIV-1 infection proteins in 70 HIV-1 infected patients; 36%, Rev peptides; 33%, Vif particles for the five proteins.				
Vif (28–36)	<ul> <li>One individual, AC-06 interruptions (STI). He restricted by HLA-A3,</li> <li>0/14 HLA-A3 positive</li> </ul>	cutely HIV-infected HLA-A, was homozygous at all the had only two detectable C 11 by HLA-B7, and 1 by Hindividuals had detectable	A3-restricted responses to this epi	was treated during acute infection on, but after STI this broadened to tope during acute infection, but o	and had supervised treatment		
Vif (31–39)	ISKKAKGWF HIV-1 infection human Yusim2002  • Epitopes that have been described in the literature and included in this database tend to cluster in conserved regions and be absent or rarely found highly variable regions found in Nef, Env and p17.  • While the uneven distribution of epitopes may be in part due to a limited cross-recognition of specific responses because of differences between peptides used to probe the immune response and autologous strains, regions with a paucity of defined epitopes also had higher frequencies of amino acids that tend to not be found in C-terminal positions of epitopes, and had lower cleavage prediction scores for epitope processing. This suggests that in the regions of the virus where variation is best tolerated traces of immune escape have left an imprint on the viral population. Epitopes also were concentrated in alpha-helix and turn regions in the proteins.  • In the more conserved p24, and Pol proteins RT and Protease, epitopes are more evenly distributed.  • What was learned from proteins where many epitopes have been defined (Gag, Pol, Env and Nef) was used to develop an algorithm to predict where epitopes would be localized in Rev, Tat, Vif, and Vpr. Predictions were made blinded, and then compared to the first 15 epitopes defined in these proteins; the epitopes were concentrated in the predicted regions.						
Vif (31–39)	• 10/29 (35%) individua	ISKKAKGWF HIV-1 Vpr, Vpu, and Vif v is tested responded to Vif nized by 2/6 individuals ex	HIV-1 infection were analyzed in multiple HIV-1-in pressing B*5701 allele	human (B*5701) fected individuals	Altfeld2001a		
Vif (31–39)			HIV-1 infection proteins in 70 HIV-1 infected patients; 36%, Rev peptides; 33%, Vif pe				

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
	All known optimally dependent of the second of the se	efined epitopes were sun	nmarized for the five proteins.		
Vif (48–57)	<ul> <li>Epitopes that have been variable regions found</li> <li>While the uneven distriused to probe the immute to not be found in C-te virus where variation is and turn regions in the</li> <li>In the more conserved</li> <li>What was learned from</li> </ul>	HPRVSSEVHI n described in the literate in Nef, Env and p17. ibution of epitopes may une response and autolog rminal positions of epito s best tolerated traces of proteins. p24, and Pol proteins R1 n proteins where many ep	HIV-1 infection ure and included in this database tend be in part due to a limited cross-recog gous strains, regions with a paucity of spes, and had lower cleavage prediction	gnition of specific responses becan defined epitopes also had higher on scores for epitope processing. on the viral population. Epitopes nly distributed. Env and Nef) was used to develop	use of differences between peptides frequencies of amino acids that tend This suggests that in the regions of the also were concentrated in alpha-helix p an algorithm to predict where
Vif (48–57)	the epitopes were conc Vif (48–57 SF2) • Epitope name: HI10 • CTL responses against • 10/29 (35%) individual • This epitope was recog • HIV+ individual AC-0 from 7 proteins, sugges	HPRVSSEVHI  HIV-1 Vpr, Vpu, and Visits tested responded to Visitized by 3/8 individuals 6 was tested for reactive sting that the breadth of	regions.  HIV-1 infection  if were analyzed in multiple HIV-1-in f expressing B*0702 allele overlapping peptides spanning all HI CTL responses are underestimated if	human (B*0702)  Ifected individuals  V-1 proteins in an ELISPOT and accessory proteins are not include	Altfeld2001a  was found to react with 12 peptides ed in the study
Vif (48–57)	Vif (48–57) • CTL responses against • 28% targeted one or m	HPRVSSVHI regulatory and accessor ore overlapping Tat pept	WH and THPRVSSEVHIPLG both resemble.  HIV-1 infection y proteins in 70 HIV-1 infected patier ides; 36%, Rev peptides; 33%, Vif penmarized for the five proteins.	human (B*0702) nts were studied using overlappin	Addo2002b g peptides and Elispot.
Vif (48–57)	Vif (48–57) • Epitope name: B7-HI1 • CTL responses in 18 ac • One individual, AC-06 interruptions (STI). He restricted by HLA-A3, • 0/11 HLA-B7 individu	HPRVSSEVHI  0 cutely HIV-infected HLA , was homozygous at all had only two detectable 11 by HLA-B7, and 1 b als had detectable B7-re	HIV-1 infection  A-A3 (n=7) or -B7 (n=4) or both -A3 three class I alleles (A3, B7, Cw7), we CTL responses during acute infection y HLA-Cw7.	was treated during acute infection on, but after STI this broadened to a cute infection – 10/15 of HL	and had supervised treatment
Vif (61–80)	Vif (61–80)  HLA, viral sequence, a each HIV protein.  Nef and p24 had the hi	EARLVIKTYWGLOT and Elispot data was obta ghest percentage of reac	TGERDWH HIV-1 infection ained from 105 HIV-1 positive Botswattive peptides, and p24 had the highest clade peptides from among over 350	human anans; Elispot data was obtained t magnitude of HIV-1 responses.	•

HIV CTL Epitope Tables

Vif CTL Epitopes

HXB2 Location	<b>Author's Location</b>	Sequence	Immunogen	Species (HLA)	References
Vif (71–90)	<ul><li>each HIV protein.</li><li>Nef and p24 had the high</li></ul>	ghest percentage of reactive peptic	105 HIV-1 positive Botsv les, and p24 had the higher	human wanans; Elispot data was obtained from st magnitude of HIV-1 responses. O tested spanning all HIV proteins.	Novitsky2002 om between 55 and 64 subjects for
Vif (102–111)	<ul> <li>variable regions found</li> <li>While the uneven distriused to probe the immuto not be found in C-tervirus where variation is and turn regions in the</li> <li>In the more conserved</li> <li>What was learned from epitopes would be local</li> </ul>	in Nef, Env and p17. bution of epitopes may be in part of the response and autologous strain reminal positions of epitopes, and has best tolerated traces of immune eproteins.  224, and Pol proteins RT and Proteins where many epitopes has	due to a limited cross-reco is, regions with a paucity of ad lower cleavage predicti scape have left an imprint ease, epitopes are more ev- ve been defined (Gag, Pol,	on the viral population. Epitopes als	e of differences between peptides requencies of amino acids that tend his suggests that in the regions of the so were concentrated in alpha-helix an algorithm to predict where
Vif (102–111)	• 10/29 (35%) individual	LADQLIHLHY HIV-1 Vpr, Vpu, and Vif were and stested responded to Vif nized by 2/5 individuals expressin		human (B*1801) nfected individuals	Altfeld2001a
Vif (102–111)	• 28% targeted one or mo		, Rev peptides; 33%, Vif p	human (B*1801) ents were studied using overlapping eptides; 40%, Vpr peptides; and 2%	
Vif (158–168)	• 28% targeted one or mo		, Rev peptides; 33%, Vif p	human (A*0301) ents were studied using overlapping eptides; 40%, Vpr peptides; and 2%	
Vif (158–168)	<ul> <li>One individual, AC-06, interruptions (STI). He restricted by HLA-A3,</li> <li>0/14 HLA-A3 positive</li> </ul>	utely HIV-infected HLA-A3 (n=7 was homozygous at all three clas had only two detectable CTL resp 11 by HLA-B7, and 1 by HLA-Cv	s I alleles (A3, B7, Cw7), conses during acute infecti w7. rricted responses to this ep	human (A3)  B and B7 (n=7) positive individuals was treated during acute infection at on, but after STI this broadened to 2 itope during acute infection, but only is epitope after STI.	nd had supervised treatment 7 distinct epitopes including 15

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
Vif (160–169)	<ul> <li>A subset of the potenti epitopes could stimula</li> </ul>	al epitopes was identified te IFN $\gamma$ production in an	11 1		De Groot2001 V that might serve as epitopes uperfamily (HLA B7, B8, and B58)
Vif	<ul> <li>A gag/pol, vif or env D increase in both the cy</li> </ul>	NA vaccine, when delive totoxic and proliferative		l encoding the co-stimulatory mol	Kim1997c ecules B7 and IL-12, gave a dramatic
Vif	<ul> <li>Splenocytes from BAL IFN-gamma levels</li> <li>Antigen stimulation in</li> <li>IL-4 production was no</li> <li>Cross-clade CTL activ</li> </ul>	creased IFN-gamma proot significantly changed a ity was also observed: A	h pVVN-P DNA were incubated winduction in pVVN-P immunized mice after antigen stimulation compared to	e, indicating a Th1 response o control levels is could serve as targets for the B of	clade immunization-stimulated CTL -
Vif	<ul> <li>Splenocytes from BAL IFN-gamma levels</li> <li>Antigen stimulation in</li> <li>IL-4 production was no</li> <li>Cross-clade CTL activ</li> </ul>	creased IFN-gamma proc ot significantly changed a ity was also observed: A	h pVVN-P DNA were incubated winduction in pVVN-P immunized mice after antigen stimulation compared to	e, indicating a Th1 response o control levels as could serve as targets for the B of	clade immunization-stimulated CTL -

HIV CTL Epitope Tables

Vpr CTL Epitopes

## **II-B-14** Vpr CTL Epitopes

HXB2 Location	<b>Author's Location</b>	Sequence	Immunogen	Species (HLA)	References
Vpr (12–20)	variable regions found  While the uneven distrused to probe the immuto not be found in C-te virus where variation is and turn regions in the  In the more conserved  What was learned from	in Nef, Env and p17. Ibution of epitopes may me response and autolograminal positions of epitors best tolerated traces of proteins. p24, and Pol proteins Raproteins where many elized in Rev, Tat, Vif, a	HIV-1 infection ture and included in this database tend to be in part due to a limited cross-recogn gous strains, regions with a paucity of copes, and had lower cleavage prediction f immune escape have left an imprint or T and Protease, epitopes are more even epitopes have been defined (Gag, Pol, E and Vpr. Predictions were made blinded d regions.	nition of specific responses beca defined epitopes also had higher a scores for epitope processing. In the viral population. Epitopes by distributed. In and Nef) was used to develop	use of differences between peptides frequencies of amino acids that tend This suggests that in the regions of the also were concentrated in alpha-helix of an algorithm to predict where
Vpr (12–20)	<ul><li>Individuals with long-t</li><li>Only one B*4002+ ind</li></ul>	erm nonprogressive and ividual was tested, and of HIV-1 specific CD8	HIV-1 infection  /if were analyzed in multiple HIV-1-inf- d treated chronic HIV-1 infection targete had a CTL response against REPHNEV + T-cells – a response was detected in 4 ells	ed Vpr more frequently than ind WTL	
Vpr (12–20)	• 28% targeted one or m	ore overlapping Tat pep	HIV-1 infection ry proteins in 70 HIV-1 infected patient tides; 36%, Rev peptides; 33%, Vif pep mmarized for the five proteins.		
Vpr (30–38)	variable regions found  While the uneven distrused to probe the immuto not be found in C-te virus where variation is and turn regions in the  In the more conserved  What was learned from	in Nef, Env and p17. Ibution of epitopes may me response and autolograminal positions of epitopes best tolerated traces of proteins. p24, and Pol proteins Raproteins where many elized in Rev, Tat, Vif, a	HIV-1 infection ture and included in this database tend to be in part due to a limited cross-recogn gous strains, regions with a paucity of copes, and had lower cleavage prediction f immune escape have left an imprint or T and Protease, epitopes are more even epitopes have been defined (Gag, Pol, E and Vpr. Predictions were made blinded, d regions.	nition of specific responses beca defined epitopes also had higher a scores for epitope processing. In the viral population. Epitopes by distributed. In and Nef) was used to develop	use of differences between peptides frequencies of amino acids that tend This suggests that in the regions of the also were concentrated in alpha-helix of an algorithm to predict where
Vpr (30–38)			HIV-1 infection /if were analyzed in multiple HIV-1-infe s expressing B*5701 allele	human (B*5701) ected individuals	Altfeld2001a

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
	<ul> <li>Vpr is a frequent target</li> </ul>			argeted Vpr more frequently than individuals tested and Vpr	
Vpr (30–38)	• 28% targeted one or me		, Rev peptides; 33%, V	human (B*5701) atients were studied using overlapping f peptides; 40%, Vpr peptides; and 2%	
Vpr (30–38)	<ul><li>Epitope name: Vpr-AW</li><li>Among HIV+ individu</li></ul>	AVRHFPRIW 79 als who carried HLA B57, 1/7 (14	HIV-1 infection %) recognized this epit	human (B57)	Sabbaj2002b
Vpr (31–50)	<ul><li>each HIV protein.</li><li>Nef and p24 had the hij</li></ul>	ghest percentage of reactive peptic	105 HIV-1 positive Bolles, and p24 had the hig	human tswanans; Elispot data was obtained fr hest magnitude of HIV-1 responses. 50 tested spanning all HIV proteins.	Novitsky2002 rom between 55 and 64 subjects for
Vpr (34–42)	variable regions found  While the uneven distriused to probe the immuto not be found in C-tervirus where variation is and turn regions in the  In the more conserved  What was learned from epitopes would be loca	in Nef, Env and p17. bution of epitopes may be in part of the response and autologous strain reminal positions of epitopes, and his best tolerated traces of immune eproteins. p24, and Pol proteins RT and Protein proteins where many epitopes have	due to a limited cross-re, regions with a paucit ad lower cleavage pred scape have left an impresse, epitopes are more we been defined (Gag, F	human end to cluster in conserved regions and ecognition of specific responses because y of defined epitopes also had higher f iction scores for epitope processing. The int on the viral population. Epitopes al evenly distributed. fol, Env and Nef) was used to develop a inded, and then compared to the first 15	se of differences between peptides requencies of amino acids that tend his suggests that in the regions of the so were concentrated in alpha-helix an algorithm to predict where
Vpr (34–42)	<ul> <li>Vpr (34–42 SF2)</li> <li>Epitope name: FL9</li> <li>CTL responses against</li> <li>This epitope was recog</li> <li>Individuals with long-to</li> <li>Vpr is a frequent target targeted proteins per ur</li> <li>HIV+ individual AC-00 from 7 proteins, suggest</li> </ul>	FPRIWLHGL  HIV-1 Vpr, Vpu, and Vif were and nized by 2/2 individuals expressing erm nonprogressive and treated chof HIV-1 specific CD8+ T-cells—nit length by CD8+ T-cells was tested for reactive overlapping.	g B*8101 allele and 4/8 ronic HIV-1 infection to a response was detected and peptides spanning all onses are underestimate	human (B*0702)  1-infected individuals B individuals expressing B*0702 allele argeted Vpr more frequently than individ in 45% of individuals tested and Vpr  I HIV-1 proteins in an ELISPOT and we diff accessory proteins are not included	viduals with treated acute infection and p17 were the most preferentially vas found to react with 12 peptides
Vpr (34–42)	Vpr (34–42)	FPRIWLHGL	HIV-1 infection	human (B*0702)	Addo2002b peptides and Elispot.

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References		
	<ul> <li>28% targeted one or more overlapping Tat peptides; 36%, Rev peptides; 33%, Vif peptides; 40%, Vpr peptides; and 2%, Vpu peptides.</li> <li>All known optimally defined epitopes were summarized for the five proteins.</li> </ul>						
Vpr (34–42)	Vpr (34–42 SF2) • Epitope name: FL9	FPRIWLHGL	HIV-1 infection	human (B*8101)	Altfeld2001a		
	<ul><li> This epitope was recog</li><li> Individuals with long-t</li><li> Vpr is a frequent target</li></ul>	nized by 2/2 individuals erm nonprogressive and	If were analyzed in multiple HIV-1-informs expressing B*8101 allele and 4/8 ind I treated chronic HIV-1 infection target + T-cells – a response was detected in 4 ells	ividuals expressing B*0702 alleled Vpr more frequently than indi	ividuals with treated acute infection		
Vpr (34–42)	• 28% targeted one or m	ore overlapping Tat pep	HIV-1 infection ry proteins in 70 HIV-1 infected patien tides; 36%, Rev peptides; 33%, Vif pep mmarized for the five proteins.				
Vpr (34–42)	<ul> <li>One individual, AC-06 interruptions (STI). He restricted by HLA-A3,</li> <li>1/11 HLA-B7 individu</li> </ul>	cutely HIV-infected HL, was homozygous at all had only two detectable 11 by HLA-B7, and 1 tals had detectable B7-ref	HIV-1 infection  A-A3 (n=7) or -B7 (n=4) or both -A3 a I three class I alleles (A3, B7, Cw7), w e CTL responses during acute infection by HLA-Cw7. estricted responses to this epitope durin individuals had detectable responses to	ras treated during acute infection n, but after STI this broadened to ng acute infection – 10/15 of HLA	and had supervised treatment 27 distinct epitopes including 15		
Vpr (55–70)	<ul><li>targeted one or more V</li><li>The regulatory proteins</li></ul>	pr peptides, and this person of the services Rev and Tat combined	LFI HIV-1 infection ry proteins in 70 HIV-1 infected patien ptide was the most frequently recogniz contributed to 3%, and the accessory processed individuals in whom all HIV	ted epitope in Vpr (41%).  proteins Vif, Vpr and Vpu to 7%,			
Vpr (59–67)	variable regions found  While the uneven distrused to probe the immuto not be found in C-te virus where variation is and turn regions in the  In the more conserved  What was learned from epitopes would be local	in Nef, Env and p17. ibution of epitopes may une response and autolorminal positions of epitos best tolerated traces of proteins. p24, and Pol proteins R a proteins where many e	HIV-1 infection ture and included in this database tend be in part due to a limited cross-recognous strains, regions with a paucity of opes, and had lower cleavage prediction immune escape have left an imprint of and Protease, epitopes are more even epitopes have been defined (Gag, Pol, End Vpr. Predictions were made blinded diregions.	nition of specific responses becau defined epitopes also had higher n scores for epitope processing. In the viral population. Epitopes and ally distributed. Env and Nef) was used to develop	use of differences between peptides frequencies of amino acids that tend This suggests that in the regions of the also were concentrated in alpha-helix of an algorithm to predict where		

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
Vpr (59–67)	Vpr (58–66 LAI) • C. Brander notes this is	AIIRILQQL an A*0201 epitope		human (A*0201)	Altfeld2001c, Brander2001
Vpr (59–67)	<ul> <li>This epitope was recog</li> <li>Epitope is located with</li> <li>Individuals with long-to</li> <li>Vpr is a frequent target targeted proteins per ur</li> </ul>	nized by 8/24 individua in a highly conserved al erm nonprogressive and of HIV-1 specific CD8- tit length by CD8+ T-ce	treated chronic HIV-1 infection targeted + T-cells – a response was detected in 45	d Vpr more frequently than indi 5% of individuals tested and Vpr	and p17 were the most preferentially
Vpr (59–67)	<ul> <li>criteria, and 30 of these</li> <li>Three additional previor recognized at least one maximum of 2)</li> <li>AIIRILQQL binds to fee</li> <li>5/22 individuals with cee</li> <li>2/12 HLA-A2 patients immunodominant while</li> <li>One of the the acutely in the second content of the</li></ul>	AIIRILQQL  Il peptides which carried bound to HLA-A*020 busly described HLA-A2 of the 23 peptides (medium HLA-A2 supertype thronic HIV-1 infection with acute HIV-1 infect to Vpr-59 was weak and infected individuals, AC	HIV-1 infection  If the A2-supermotif pattern conserved is 1 – 20/30 bound to at least 3/5 of HLA-20 epitopes were added to the set of 20, a lian of 2 and maximum of 6), while 6/12 alleles: A*0203, A*0201, A*0206 and recognized this epitope, but with low maximum of this peptide, but sub-dominant 13, was HLA A*0201/68 B44/14 and a led and presented in TAP-competent B-0	A2 supertype alleles tested and 18/22 chronically infected H 2 acute infected individuals reco A*6802 (highest affinity), but no agnitude responses in ELISPOT but during chronic infection SL9 also had a strong acute response	LA-A2 individuals had CTL that gnized at least 1 (median of 1 and of A*0202) and Gag-386 tended to be
Vpr (59–67)	• 28% targeted one or me	ore overlapping Tat pept	HIV-1 infection ry proteins in 70 HIV-1 infected patients iides; 36%, Rev peptides; 33%, Vif pept marized for the five proteins.		
Vpr (59–67)	<ul><li>Epitope name: Vpr-AL</li><li>Among HIV+ individu</li></ul>		HIV-1 infection 02, 4/35 (11%) recognized this epitope	human (A02)	Sabbaj2002b
Vpr (59–67)	recognized during the i	nitial decline in viremia	HIV-1 infection epitope in initial control of viremia in a ot evident until 18 months post-presenta		Goulder2001a reral subdominant CTL epitopes

HIV CTL Epitope Tables

Vpr CTL Epitopes

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
Vpr (59–67)	<ul> <li>individuals treated duri</li> <li>The breadth and specification individuals with primar (Group 3), using 259 or</li> <li>Previously described an</li> </ul>	ng chronic infection icity of the response was ry infection but post-sero verlapping peptides span nd newly defined optima	determined using ELISPOT by study	ying 19 individuals with pre-seroe 0 individuals who responded to E Nef nse	IAART given during chronic infection
Vpr (59–67)	for the A3 supertype) v • Progressors had memore • A positive correlation be observed, which may c	while the effector cells of ry resting CD8+ T-cells of between effector CD8+ To ontribute to the inability	HIV-1 infection memory resting CD8+ T-cell response f long-term nonprogressors recognize that recognized far fewer epitopes tha f-cells and plasma viremia and a negator of LTNPs to clear virus supertypes alleles (A*0201, A*020 2	d far fewer epitopes an LTNPs ative correlation between CD8+ e	es tested, (18 for the A2 supertype, 16
Vpr (62–70)	<ul> <li>criteria, and 30 of these</li> <li>Three additional previor recognized at least one maximum of 2)</li> <li>This epitope binds to the 3/22 chronically infector</li> </ul>	e bound to HLA-A*0201 busly described HLA-A2 of the 23 peptides (med arree HLA-A2 supertype ed patients had a weak E	HIV-1 infection  I the A2-supermotif pattern conserved 1 – 20/30 bound to at least 3/5 of HLA 2 epitopes were added to the set of 20, ian of 2 and maximum of 6), while 6/ alleles: A*0202, A*6802 (strongest a LISPOT response to this epitope ion responded to this peptide	A-A2 supertype alleles tested , and 18/22 chronically infected F /12 acute infected individuals reco	ILA-A2 individuals had CTL that
Vpr (62–70)	• 28% targeted one or me	ore overlapping Tat pept	HIV-1 infection y proteins in 70 HIV-1 infected patier ides; 36%, Rev peptides; 33%, Vif pen marized for the five proteins.		
Vpr (62–70)	for the A3 supertype) v • Progressors had memore • A positive correlation be observed, which may c	while the effector cells of ry resting CD8+ T-cells between effector CD8+ To ontribute to the inability	HIV-1 infection memory resting CD8+ T-cell response flong-term nonprogressors recognize that recognized far fewer epitopes that recolls and plasma viremia and a negation of LTNPs to clear virus a supertypes alleles (A*0201, A*0202)	d far fewer epitopes an LTNPs ative correlation between CD8+ e	es tested, (18 for the A2 supertype, 16
Vpr	Vaccine Vector/Type: a	ndenovirus HIV compo	Vaccine nent: Vpr, Nef, Gag/Pol	murine	Muthumani2002

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References		
	<ul> <li>Vpr can cause cells to go into G2 arrest, and it surpresses immune cell activation and inflammatory cytokine production, so co-immunization of BALB/c mice with recombinant adenovirus expressing Vpr and HIV-1 antigens Nef or Gag/Pol was tested to see if Vpr reduced the immune response to the other HIV antigens.</li> </ul>						
			s and T-helper proliferative responses i on of IL-12 and TNFalpha, indicative o	-	<del>-</del>		

# II-B-15 Tat CTL Epitopes

<b>HXB2</b> Location	<b>Author's Location</b>	Sequence	Immunogen	Species (HLA)	References
Tat (2–11)	<ul> <li>Epitopes that have been variable regions found</li> <li>While the uneven distrused to probe the immuto not be found in C-te virus where variation is and turn regions in the</li> <li>In the more conserved</li> <li>What was learned from epitopes would be local</li> </ul>	WPVDPRLEPW  In described in the literature in Nef, Env and p17. ibution of epitopes may be une response and autologor rminal positions of epitopes s best tolerated traces of in proteins. p24, and Pol proteins RT proteins where many epitopes	HIV-1 infection re and included in this database tend e in part due to a limited cross-recognous strains, regions with a paucity of ses, and had lower cleavage prediction mmune escape have left an imprint of and Protease, epitopes are more ever itopes have been defined (Gag, Pol, El Vpr. Predictions were made blinded	human to cluster in conserved regions a nition of specific responses beca defined epitopes also had higher n scores for epitope processing. n the viral population. Epitopes ally distributed. Env and Nef) was used to develo	Yusim2002  nd be absent or rarely found highly  use of differences between peptides frequencies of amino acids that tend This suggests that in the regions of the also were concentrated in alpha-helix
Tat (2–11)	<ul><li>Epitope name: Tat-EW</li><li>Among HIV+ individu</li></ul>		HIV-1 infection 5301, 3/15 (20%) recognized this epit	human (B*5301)	Sabbaj2002b
Tat (2–11)	(LAI)	EPVDPRLEPW		(B53)	Addo2001, Brander2001
Tat (2–11)	CTL responses against • 11/57 (19.3%) HIV-1+	Tat and Rev were screene individuals recognized at	HIV-1 infection  cycle and thus may be important targed using overlapping peptides t least 1 Tat peptide, and 21/57 (37%) uals, but only two were B53, thus thi	responded to at least 1 Rev pep	
Tat (2–11)	• 28% targeted one or m	ore overlapping Tat peption	HIV-1 infection proteins in 70 HIV-1 infected patien dles; 36%, Rev peptides; 33%, Vif pep marized for the five proteins.		
Tat (16–30)	<ul><li>each HIV protein.</li><li>Nef and p24 had the hi</li></ul>	ghest percentage of reacti		magnitude of HIV-1 responses.	Novitsky2002 from between 55 and 64 subjects for s.
Tat (17–26)	Epitopes that have beer variable regions found		HIV-1 infection re and included in this database tend	human to cluster in conserved regions a	Yusim2002 nd be absent or rarely found highly

HXB2 Location	<b>Author's Location</b>	Sequence	Immunogen	Species (HLA)	References
	used to probe the imm to not be found in C-to virus where variation is and turn regions in the In the more conserved What was learned fror epitopes would be loca	nune response and autologerminal positions of epitoris best tolerated traces of eproteins.  I p24, and Pol proteins R7 m proteins where many epitoris where many epitoris R7 m.	ppes, and had lower cleavage predictimmune escape have left an imprint Γ and Protease, epitopes are more evpitopes have been defined (Gag, Pol. d Vpr. Predictions were made blinder.)	of defined epitopes also had higher ion scores for epitope processing. To on the viral population. Epitopes a enly distributed.  Env and Nef) was used to develop	frequencies of amino acids that tend This suggests that in the regions of the also were concentrated in alpha-helix
Tat (17–26)	• 28% targeted one or m	nore overlapping Tat pept	HIV-1 infection y proteins in 70 HIV-1 infected patie ides; 36%, Rev peptides; 33%, Vif p nmarized for the five proteins.		
Tat (36–50)	<ul><li>17 of 46 patient reacte</li><li>Most of the CTL response</li></ul>	ed with Tat immunodomin onses occurred despite a	ses and full length HIV-1 genome section and peptide VCFQTKGLGISYGRF	Tal sequence and peptide – comple	te matches were seen only in 4 of 19
Tat (36–50)	<ul><li>each HIV protein.</li><li>Nef and p24 had the h</li></ul>	ighest percentage of reac		st magnitude of HIV-1 responses.	Novitsky2002 from between 55 and 64 subjects for
Tat (36–52)	<ul><li>targeted one or more ?</li><li>The regulatory protein</li></ul>	Tat peptides, and this peptins Rev and Tat combined		zed epitope in Tat (27%). y proteins Vif, Vpr and Vpu to 7%.	Addo2002b g peptides and Elispot – 28% (19/70) of the total magnitude of HIV-1
Tat (38–47)	• 17 of 46 patient reacte	a survey of CTL responsed with Tat immunodomin	ses and full length HIV-1 genome senant peptide VCFQTKGLGISYGRF peptide VCFQTKGLGISYGRK am	Ž	Novitsky2001 Botswanan cohort
Tat (39–49)		A-A*6801 presenting mol	HIV-1 infection ecule were rapidly defined using a n epitopes tolerate length variation.	human (A*6801) nodified Elispot assay.	Oxenius2002a

**HIV CTL Epitope Tables Tat CTL Epitopes** 

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
Tat (39–49)	• 28% targeted one or m	nore overlapping Tat peption	HIV-1 infection proteins in 70 HIV-1 infected patie des; 36%, Rev peptides; 33%, Vif pomarized for the five proteins.		
Tat (40–49)	variable regions found  While the uneven distrused to probe the imm to not be found in C-te virus where variation i and turn regions in the  In the more conserved  What was learned from epitopes would be local	in Nef, Env and p17. ribution of epitopes may be une response and autologorminal positions of epitopes best tolerated traces of it proteins. p24, and Pol proteins RT in proteins where many ep	ous strains, regions with a paucity of the paucity	gnition of specific responses beca f defined epitopes also had higher on scores for epitope processing. on the viral population. Epitopes enly distributed. Env and Nef) was used to develop	use of differences between peptides frequencies of amino acids that tend This suggests that in the regions of the also were concentrated in alpha-helix
Tat (49–57)	The system was demon	nstrated by vaccinating m	d to a protein can cause that protein ce with an OVA-Tat peptide conjug peptide SIINFEKL was stimulated		
Tat (49–57)	<ul> <li>DNA vaccinated BALL immunization</li> <li>Strong but non-lasting protein boost</li> <li>Immunization with eith</li> </ul>	B/c mice primed and boos HIV-specific CTL respon her the multiepitopic DNA	Vaccine NA with recombinant protein boost ted with the multiepitopic vaccine vaces were detected by a Cr-release as A or with the mixed DNA vaccine in onses but decreased anti-HIV antibo	with IL18 showed lymphoprolifers ssay and DNA prime/DNA boost of the book of t	was more effective than DNA prime
Tat (83–92)	<ul> <li>A subset of the potenti epitopes could stimula</li> </ul>	ial epitopes was identified te IFN $\gamma$ production in an			De Groot2001 V that might serve as epitopes uperfamily (HLA B7, B8, and B58)
Tat			Vaccine Nef, Rev Tat A vaccinations for nef, rev or tat, an	•	Calarota1999 sponses were generated

- The nef DNA immunization induced the highest and most consistent CTLp activity, IFN-gamma production, and IL-6 and IgG responses

HXB2 Location	<b>Author's Location</b>	Sequence	Immunogen	Species (HLA)	References
			T) did not induce new HIV-specific CTL al load – thus this is a potentially comple		
Tat	<ul> <li>Reactivity against Gag autologous EBV trans:</li> <li>The child who progress</li> <li>The long-term non-pro</li> </ul>	g, Pol, Env and Tat proto formed B cells seed consistently had C	detectable CTL, but was heterozygous for	ells reacting with protein exp	ressed in vaccinia constructs in
Tat	• This review discusses		HIV-1 infection, Vaccine t: Nef, Rev, Tat Adjuvant: CpG motifs sponse, and comments on the stimulatory tic HIV+ individuals	human role of CpG motifs and how	Calarota2001  HIV-1 DNA vaccines can boost the CTI
Tat	<ul><li> Macaques (macaca fas unmethylated</li><li> The vaccinated animal</li></ul>	scicularis) were immuni	Vaccine  HIV component: Tat Adjuvant: CpG, ized with HIV-1 Tat on an adenovirus man an adenovirus man adenoviru	jor late promotor in a plasmic	
Tat	responses were detected	ed at all time points. that were not infected the	HIV-1 infection d HIV-1 specific CTL responses to vaccir nough born to HIV+ mothers had detectal		<u>-</u>
Tat	<ul> <li>CTL against Tat and R</li> <li>Tat/Rev vaccinations of CTL having lower vire</li> </ul>	tev were found preferent of macaques provided premia, while Gag/Pol vac	HIV-1 infection, Vaccine sing Tat and Rev as part of a vaccine strantially in long term non-progressors. rotection or reduction in viremia, with his ccinations with did not result in decreased in the enhanced benefit of a CTL response.	gh levels of CTL providing produced of the contract of the con	
Tat	<ul><li>An AAV vector expres</li><li>A single injection stim</li></ul>	ssing HIV-1 env, tat, and nulated and long lasting	Vaccine (AAV) HIV component: Env, Tat, Rev d rev genes (AAV-HIV vector) was used t serum IgG, fecal IgA, and HIV-specific of IL2 enhanced T-cell immunity.	to vaccinate BALB/c mice	Xin2001

# II-B-16 Rev CTL Epitopes

<b>HXB2</b> Location	<b>Author's Location</b>	Sequence	Immunogen	Species (HLA)	References
Rev (9–23)	Rev (9–23 HXB2) • Induces both Th and CT	DEELIRTVRLIKLLY L activities, no HLA restric	HIV-1 infection tion analysis performed	human	Blazevic1995
Rev (11–23)	• 28% targeted one or mor		36%, Rev peptides; 33%, Vif pe	human (B*5701) nts were studied using overlapping eptides; 40%, Vpr peptides; and 29	
Rev (11–23)	• 28% targeted one or mor		36%, Rev peptides; 33%, Vif po	human (B*5801) nts were studied using overlapping eptides; 40%, Vpr peptides; and 29	
Rev (12–31)	Only one subject had C7	LLKAVRLIKFLYQSNPP CTL specific for more than IL that could recognize vacc response to this peptide, and	n 1 HIV-1 protein	human	Lieberman1997a
Rev (14–23)	variable regions found in  While the uneven distribused to probe the immunto not be found in C-terrivirus where variation is and turn regions in the p  In the more conserved p  What was learned from epitopes would be locali	n Nef, Env and p17.  nution of epitopes may be in the response and autologous minal positions of epitopes, the tolerated traces of imm roteins.  24, and Pol proteins RT and proteins where many epitop	part due to a limited cross-recognistrains, regions with a paucity of and had lower cleavage prediction escape have left an imprint a Protease, epitopes are more every escape have been defined (Gag, Pol, or. Predictions were made blinde	gnition of specific responses becau f defined epitopes also had higher on scores for epitope processing. To on the viral population. Epitopes a enly distributed. Env and Nef) was used to develop	Yusim2002 and be absent or rarely found highly use of differences between peptides frequencies of amino acids that tend This suggests that in the regions of the also were concentrated in alpha-helix an algorithm to predict where 5 epitopes defined in these proteins;
Rev (14–23)	Rev (14–23 subtype B) • C. Brander notes this is	KAVRLIKFLY a B*5701 epitope		human (B*5701)	Addo2001, Brander2001
Rev (14–23)	CTL responses against 7 • 11/57 (19.3%) HIV-1+ i	Cat and Rev were screened undividuals recognized at leacognized by another individuals	using overlapping peptides list 1 Tat peptide, and 21/57 (37%)	human (B*5701)  rgets for CTL against HIV early in  b) responded to at least 1 Rev pept HLA*B5801, an allele closely re	

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
Rev (14–23)	Rev (14–23 subtype B) • C. Brander notes this is	KAVRLIKFLY a B*5801 epitope		human (B*5801)	Addo2001, Brander2001
Rev (14–23)	CTL responses against 7 • 11/57 (19.3%) HIV-1+ i	Tat and Rev were screened and individuals recognized at leacognized by another individuals.		responded to at least 1 Rev pept	
Rev (25–39)	Rev (25–39 HXB2) • Induces both Th and CT	SNPPPNPEGTRQARR L activities, no HLA restric	HIV-1 infection ction analysis performed	human	Blazevic1995
Rev (33–48)	Rev (33–48 HXB2) • Induces both Th and CT	GTRQARRNRRRRWRER L activities, no HLA restric	HIV-1 infection ction analysis performed	human	Blazevic1995
Rev (41–56)	Rev (41–56 HXB2) • Induces both Th and CT	RRRRWRERQRQIHSIS L activities	HIV-1 infection	human	Blazevic1995
Rev (55–63)	<ul><li>Both forms LSGWL(L of An HLA-A1 individual)</li><li>3/7 long-term non-program</li></ul>	who did not make a Rev resessors and 0/5 progressors	HIV-1 infection or residues 2S and 9Y rs, were found in an HLA-A1+ indi sponse had lost the C-term anchor, were positive for HLA-B57 (associ rrelated with rapid progression to A	ISGWILS(T or N)S atted with prolonged survival)	vanBaalen1997 L
Rev (55–63)	Rev (55–63)  • ELISPOT was used to st HIV-1-infected female N		HIV-1 infection, HIV-1 exp seronegative nel of 54 predefined HIV-1 epitope		Kaul2001a ntly seronegative (HEPS) and 87
Rev (57–66)	variable regions found in  While the uneven distribused to probe the immunto not be found in C-terr virus where variation is and turn regions in the p  In the more conserved p  What was learned from epitopes would be locali	n Nef, Env and p17.  pution of epitopes may be in the response and autologous minal positions of epitopes, best tolerated traces of immorateins.  24, and Pol proteins RT and proteins where many epitopes.	strains, regions with a paucity of d and had lower cleavage prediction nune escape have left an imprint on d Protease, epitopes are more evenl- pes have been defined (Gag, Pol, En or, Predictions were made blinded,	ition of specific responses becau efined epitopes also had higher scores for epitope processing. The the viral population. Epitopes and y distributed.	use of differences between peptides frequencies of amino acids that tend This suggests that in the regions of the also were concentrated in alpha-helix

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
Rev (57–66)	Rev (57–66) • Epitope name: A3-ER	ERILSTYLGR	HIV-1 infection	human (A3)	Yu2002a
	<ul> <li>One individual, AC-00 interruptions (STI). H restricted by HLA-A3</li> <li>0/14 HLA-A3 positive</li> </ul>	6, was homozygous at all the had only two detectable C , 11 by HLA-B7, and 1 by I e individuals had detectable		vas treated during acute infection n, but after STI this broadened to ope during acute infection, but or	and had supervised treatment
Rev (58–66)	• 28% targeted one or n		HIV-1 infection proteins in 70 HIV-1 infected patients; 36%, Rev peptides; 33%, Vif penarized for the five proteins.		
Rev (66–81)	<ul><li>targeted one or more I</li><li>The regulatory protein</li></ul>	Rev peptides, and this peptions Rev and Tat combined co		zed epitope in Rev (32%). proteins Vif, Vpr and Vpu to 7%	Addo2002b g peptides and Elispot – 36% (25/70) , of the total magnitude of HIV-1
Rev (67–75)	<ul> <li>variable regions found</li> <li>While the uneven dist used to probe the immediate to not be found in C-to virus where variation and turn regions in the</li> </ul>	I in Nef, Env and p17. ribution of epitopes may be nune response and autologou erminal positions of epitope is best tolerated traces of im- e proteins.	in part due to a limited cross-recog as strains, regions with a paucity of s, and had lower cleavage predictio	nition of specific responses becar defined epitopes also had higher n scores for epitope processing.	Yusim2002 nd be absent or rarely found highly use of differences between peptides frequencies of amino acids that tend This suggests that in the regions of the also were concentrated in alpha-helix
	<ul> <li>What was learned from epitopes would be loc</li> </ul>	m proteins where many epit		Env and Nef) was used to develor	o an algorithm to predict where 15 epitopes defined in these proteins;
Rev (67–75)	<ul> <li>What was learned from the epitopes would be located the epitopes were considered.</li> <li>Rev (65–77 BH10, LA</li> <li>This study employs are this CTL epitope (the transforming growth for the transforming growth grow</li></ul>	m proteins where many epitalized in Rev, Tat, Vif, and centrated in the predicted real. SAEPVPLQL an antigenic similarity matrix HIV-1 LAI fragment with factor beta binding protein p	opes have been defined (Gag, Pol, I Vpr. Predictions were made blinded gions.  HIV-1 infection to compare HIV-1 antigenic determined in the similarity to a human protein of the rotein I, fragment ARSAEPEVATA high similarity to a human protein of the similarity to a huma	Env and Nef) was used to develop I, and then compared to the first human minants with human proteins. overlapping this epitope is GRSA IPP.	15 epitopes defined in these proteins;  Maksiutov2002

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
Rev (67–75)	use to infect irradiated outgrowth of macropha  • The CTL clone TCC10 the mice to apply speci  • The macrophage-tropic latter isolate was suppr allow additional replica  • Specific HIV-1 variants	XID mice that had been age tropic strains 08 specific for SAEPVPI ific CTL pressure at HIV-1 strain #2.1 escapessed in 13/14 animals ation to assist with acqui	LQL, previously described by van Baal ped CTL pressure more efficiently (7/1 - macrophage may serve as a CTL sand sition of escape TCC108 were for strain 1.2: SEEPVP	n B14+ seronegative donors – red den 1997, and van Baalen 1998, 4 animals) than its non-macrople ctuary and reduced pressure on a	sults indicate CTL may favor selective was stimulated in vitro and given to mage-tropic counterpart #1.2(SI) – the
Rev (67–75)	B14-restricted Rev-SA co-incubated with CD4 in ten days of culture.	EPVPLQL specific CD8 4+ cultures innoculated v When the RT epitope wa	HIV-1 infection ressed upon acute infection of T-cells ( B T-cell clone TCC108, and the B57-re with HIV-1 at low MOI. Co-incubation as cloned into the Nef gene of the infect A mathematical model of CTL-target i	stricted RT-IVLPEKDSW speci with the Rev-specific CTL resu string strain, another early expres	fic CD8 T-cell clone TCL1C11 were lited in two logs less HIV-1 production sed protein, it proved as effective as
Rev (67–75)	• 28% targeted one or me	ore overlapping Tat pept	HIV-1 infection y proteins in 70 HIV-1 infected patient ides; 36%, Rev peptides; 33%, Vif per numarized for the five proteins.	0 11	
Rev (67–75)	<ul> <li>Tat are expressed early</li> <li>The CTL clone TCC10</li> <li>CTLs added immediate lysis occurred after the</li> <li>Rapid selection of a E6</li> </ul>	and CTL activity agains 98 specific for this epitor ely after infection suppre onset of progeny viral r 69K mutation, which abo	HIV-1 infection as from an individual infected with HI at these proteins has been correlated w be was studied in vitro assed viral production, indicative of CT allelease, but prior to peak viral production blished CTL, recognition was observed w8 and B14 are in linkage disequilibri	ith long-term survival  TL interference with viral produ  on  I	ction prior to lysis – CTL-mediated
Rev (67–75)	(LAI)	SAEPVPLQL		human (Cw5)	Addo2001, Brander2001
Rev (67–75)	recognized during the i	initial decline in viremia	HIV-1 infection epitope in initial control of viremia in t evident until 18 months post-present		Goulder2001a everal subdominant CTL epitopes
Rev (67–75)	Rev (67–75 SF2)  Therapy provided during individuals treated during individuals.		HIV-1 infection ed in a narrower CTL response, strong	human (Cw5) er T help response, and a less di	Altfeld2001b verse viral population than was seen in

HIV CTL Epitope Tables Rev CTL Epitopes

HXB2 Location	<b>Author's Location</b>	Sequence	Immunogen	Species (HLA)	References	
	individuals with prima (Group 3), using 259 o • Previously described a	ry infection but post-sero verlapping peptides spar nd newly defined optima	determined using ELISPOT by study oconversion therapy (Group 2), and 10 uning p17, p24, RT, gp41, gp120 and all epitopes were tested for CTL respon CTL response to this epitope broken d	0 individuals who responded to H Nef nse	AART given during chronic infection	
Rev (67–75)	• 28% targeted one or m	ore overlapping Tat pept	HIV-1 infection y proteins in 70 HIV-1 infected patier ides; 36%, Rev peptides; 33%, Vif pen nmarized for the five proteins.			
Rev (67–75)	Rev (69–77 BRU) SAEPVPLQL HIV-1 infection human (Cw8) Addo2001  • Epitope name: Rev SL9  • Rev and Tat are expressed early in the virus life cycle and thus may be important targets for CTL against HIV early in infection and for vaccines – therefore CTL responses against Tat and Rev were screened using overlapping peptides  • 11/57 (19.3%) HIV-1+ individuals recognized at least 1 Tat peptide, and 21/57 (37%) responded to at least 1 Rev peptide  • This epitope is the first HIV-specific CTL epitope resticted by HLA-Cw5  • This epitope was recognized by 2/5 individuals expressing HLA-Cw8 and by 5/11 individuals expressing Cw5 allele, which differs from Cw8 by 4 amino acids, suggesting promiscuous presentation of the epitope between those HLA molecules  • Longitudinal data was available for 6 Rev-SL9 responders, who were treated during acute infection, and the response was stable 2 and 12 months after initiaion of HAART, measurements by ELISPOT and flow-based intracellular cytokine staining (ICS) were concordant – in two subjects the response was					
Rev (75–83)	LPPLERLTL HIV-1 infection human Yusim2002  • Epitopes that have been described in the literature and included in this database tend to cluster in conserved regions and be absent or rarely found highly variable regions found in Nef, Env and p17.  • While the uneven distribution of epitopes may be in part due to a limited cross-recognition of specific responses because of differences between peptides used to probe the immune response and autologous strains, regions with a paucity of defined epitopes also had higher frequencies of amino acids that tend to not be found in C-terminal positions of epitopes, and had lower cleavage prediction scores for epitope processing. This suggests that in the regions of the virus where variation is best tolerated traces of immune escape have left an imprint on the viral population. Epitopes also were concentrated in alpha-helix and turn regions in the proteins.  • In the more conserved p24, and Pol proteins RT and Protease, epitopes are more evenly distributed.  • What was learned from proteins where many epitopes have been defined (Gag, Pol, Env and Nef) was used to develop an algorithm to predict where epitopes would be localized in Rev, Tat, Vif, and Vpr. Predictions were made blinded, and then compared to the first 15 epitopes defined in these proteins; the epitopes were concentrated in the predicted regions.					
Rev	<ul><li>9/9 HIV-1+ subjects w</li><li>The nef DNA immuniz</li><li>Highly active antiretro</li></ul>	zation induced the highest viral treatment (HAART	Vaccine Nef, Rev Tat NA vaccinations for nef, rev or tat, an st and most consistent CTLp activity, ) did not induce new HIV-specific CT load – thus this is a potentially comp	IFN-gamma production, and IL-6 IL responses but reduced viral loa	and IgG responses d, while DNA vaccination induced	

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
Rev		ses were distributed the	onses and full length HIV-1 genome sequence roughout the protein and 27 of 47 subjects (5)		
Rev		the cellular immune re	HIV-1 infection, Vaccine at: Nef, Rev, Tat Adjuvant: CpG motifs sponse, and comments on the stimulatory rolutic HIV+ individuals	human e of CpG motifs and how I	Calarota2001 HIV-1 DNA vaccines can boost the CTL
Rev	<ul> <li>CTL against Tat and R</li> <li>Tat/Rev vaccinations of CTL having lower vire</li> </ul>	Rev were found prefere of macaques provided p emia, while Gag/Pol va	HIV-1 infection, Vaccine using Tat and Rev as part of a vaccine strategratially in long term non-progressors. Protection or reduction in viremia, with high accinations with did not result in decreased viain the enhanced benefit of a CTL response of	levels of CTL providing priremia.	
Rev	• pCMV160/Rev is a DI	NA vaccine candidate	Vaccine otor with cationic liposome HIV component carrying gp160 and Rev linked to a cytomega ationic liposome gave enhanced DTH, Ab ar	alovirus (CMV promotor)	Ishii1997
Rev			Vaccine  at: rev Adjuvant: CD40 e induced Th1, Th2 and IgG responses, and e	murine $(H-2^d)$ enhanced the CTL response	Ihata1999 to Rev, but did not induce mucosal IgA
Rev	<ul><li>An AAV vector expres</li><li>A single injection stim</li></ul>	ssing HIV-1 env, tat, ar nulated and long lasting	Vaccine (AAV) HIV component: Env, Tat, Rev A d rev genes (AAV-HIV vector) was used to v g serum IgG, fecal IgA, and HIV-specific CT d IL2 enhanced T-cell immunity	vaccinate BALB/c mice	Xin2001

# II-B-17 Vpu CTL Epitopes

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
Vpu (4–13)	<ul> <li>A subset of the potential epitopes could stimulate</li> </ul>	al epitopes was identified the IFN $\gamma$ production in an	on with the program Conservatrix to ided that could bind to the appropriate HIn ELISPOT assay  A-B7 epitope in this study using ELISP	LA-allele, and 15 predicted B7 st	uperfamily (HLA B7, B8, and B58)
Vpu (25–40)	<ul><li>(2/70) targeted one or r</li><li>The regulatory proteins</li></ul>	nore Vpu peptides, incl s Rev and Tat combined	ry proteins in 70 HIV-1 infected patien	proteins Vif, Vpr and Vpu to 7%	
Vpu (29–37)	• 28% targeted one or me	ore overlapping Tat pep	HIV-1 infection ry proteins in 70 HIV-1 infected patien tides; 36%, Rev peptides; 33%, Vif per mmarized for the five proteins.		
Vpu (29–37)		s first detected in a long	HIV-1 infection, and this is the first optimally defined term non-progressor, and 3/6 HLA A*Asia.		Addo2002a  Sound to have a CTL response to this
Vpu	<ul> <li>Splenocytes from BAL IFN-gamma levels</li> <li>Antigen stimulation inc</li> <li>IL-4 production was no</li> <li>Cross-clade CTL activity</li> </ul>	creased IFN-gamma pro ot significantly changed ity was also observed: A	Vaccine Vif, Vpu, Nef ith pVVN-P DNA were incubated with oduction in pVVN-P immunized mice, after antigen stimulation compared to A, B clade, CRF01(AE) clade antigens imulate a CTL response, but was expression	indicating a Th1 response control levels could serve as targets for the B c	lade immunization-stimulated CTL –

# II-B-18 gp160 CTL Epitopes

HXB2 Location	<b>Author's Location</b>	Sequence	Immunogen	Species (HLA)	References
gp160 (2–10)	gp160 (2–10 IIIB) • C. Brander notes this is	RVKEKYQHL a B*0801 epitope	HIV-1 infection	human (B*0801)	Brander2001
gp160 (2–10)	• Type-specific epitope, u	inique to the LAI and IIIB variant found in JRCSF, wa	HIV-1 infection CTL epitopes recognized by 3 lab w because of a deletion of three amino s not recognized		
gp160 (2–10)	gp120 (2–10)  • B8-restricted CTL acco	RVKEKYQHL unted for about 1/3 of the t	HIV-1 infection otal CTL response in one individual	human (B8)	Day2001
gp160 (6-12)	<ul> <li>HLA-A11 is very command CTL responses were</li> </ul>	non in this population, and re found in 8/8 HIV+ contro	HIV-1 exposed seronegative conegative (HEPS) female sex worked was enriched among the HEPS sexwells, and 0/9 HIV- women that were not be a weak response in HEPS study su	rs in Chiang Mai, northern Tha orkers – weak CTL responses ot exposed	were detected in 4/7 HEPS women,
gp160 (6–12)	Thailand, of whom mor  • 77 possible HLA-A11 e epitopes for CTL respon  • This is one of the new A	re than half were HLA-A11 epitopes were first defined unses from 8 HLA-A11 posi A11 epitopes identified thro	HIV-1 infection  ) epitopes were identified that stimular positive using EpiMatrix, these were screened tive FSWs, six were novel, six were ough the streamlined EpiMatrix method exact matches were rare	I for binding to A11 finding an previously identified	d 26 bound, and 12 of these were
gp160 (30–49)	contribution of CD8+C be similarly distributed • HIV CTL responses to • The clonal composition	t all CD8+ T cells are CD2: D28- cells to CTL memory in the CD28 depleted cell p 3 Env and 2 Gag peptides v	vere studied es was studied and was found to be h	o persistent human viruses, Cl	MV and HIV – clones were found to
gp160 (31–39)	gp120 (30–38 SF2)  • Therapy provided durin individuals treated durin		HIV-1 infection n a narrower CTL response, stronger	human (B44) T help response, and a less div	Altfeld2001b verse viral population than was seen i

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
	individuals with prima (Group 3), using 259 co. • Previously described a	ry infection but post-seroc overlapping peptides spann and newly defined optimal	determined using ELISPOT by study onversion therapy (Group 2), and 10 ing p17, p24, RT, gp41, gp120 and 10 epitopes were tested for CTL respont to this epitope broken do	) individuals who responded to F Nef ise	IAART given during chronic infection
gp160 (31–39)	gp120 (30-38)	AENLWVTVY	HIV-1 infection	human (B44)	Day2001
gp160 (31–39)	<ul> <li>CTL could be activated exogenous protein and</li> </ul>	allows processing through	HIV-1 infection es AENLWVTVY. HIV protein and anthrax lethal facto the MHC class I pathway. This stra- sing live viral vectors carrying a prot	ategy for CTL detection could al	low antigen presentation without
gp160 (31–40)	gp160 (30–39 WEAU) • C. Brander notes this i		HIV-1 infection	human (B*4402)	Brander2001
gp160 (31–40)	responded equally wel Rapidly post-infection The naturally occurring wild type AENLWVT The glutamic acid in the	ne patient WEAU were stull with one or two N-term A, a strong immunodominal g forms of the peptide fou VY – but the forms AKNI he second position is a B4-	nt response was observed against this and in WEAU were tested as targets for WVTVY, AGNLWVTVY, AANLW	s epitope or early WEAU CTLs – the forn VTVY did not serve as targets	n TENLWVTVY was as reactive as the
gp160 (31–55)		TEKLWVTVYYGVPVV TTLFCA vaccinia HIV component esponse to epitope in HIV-	: gp160	human (B18)	Johnson1994a
gp160 (31–55)		TEKLWVTVYYGVPVV TTLFCA vaccinia HIV component ocessed for HLA-B18 pres		human (B18) ent and dependent pathways	Ferris1999, Hammond1995
gp160 (33–42)		KLWVTVYYGV recombinant protein <i>Stro</i> sitive subject react with the	Vaccine  iin: MN HIV component: gp160  iis peptide	human (A2)	Dupuis1995
gp160 (33–42)	<ul><li>Ten HIV-1+ HLA A2 a</li><li>Two hundred and fifty</li></ul>	recombinant protein <i>Stro</i> asymptomatic individuals			Kundu1998a period Val at the C terminus) were identified

HXB2 Location	<b>Author's Location</b>	Sequence	Immunogen	Species (HLA)	References
		mmunization may include recall r	ding affinity – a CTL response wa responses – only individuals with		in at least 1 individual uences prior to vaccination showed
gp160 (34–55)	gp120 (25–46 BRU)	LWVTVYYGVPVWKEATTTL- FCA		human (A2)	Dadaglio1991
	Defined through peptide	blocking of CTL activity, and E	nv deletions		
gp160 (36–46)	gp120 (36–46 CM243 subtype CRF01) • Epitope name: E36-4	VTVYYGVPVWR	HIV-1 exposed seronegative	human (A11)	Sriwanthana2001
	<ul> <li>HLA-A11 is very command CTL responses were</li> </ul>	non in this population, and was en e found in 8/8 HIV+ controls, and	tive (HEPS) female sex workers in nriched among the HEPS sexwork d 0/9 HIV- women that were not e eak response in HEPS study subject	ers – weak CTL responses exposed	were detected in 4/7 HEPS women,
gp160 (36–46)	Thailand, of whom mor  77 possible HLA-A11 e epitopes for CTL respor  This epitope was not pre A11 epitopes that had b  1/8 tested FSWs recogn	e than half were HLA-A11 positive pitopes were first defined using Enses from 8 HLA-A11 positive FS edicted by the EpiMatrix method een previously defined ized this epitope	ve EpiMatrix, these were screened for SWs, six were novel, six were pre	r binding to A11 finding an viously identified h it served as an epitope in	Bond2001 sex workers (FSW) from Northern and 26 bound, and 12 of these were the FSWs, and it was one of the six
gp160 (36–46)	<ul><li>The A3 super-type is ch</li><li>While most lines were s</li></ul>	aracterized as a hydrophobic or h	HIV-1 infection  pe epitope (the A3-super-type include and another residue)  FL line was derived from an HIV-1	e at position 2, and a posit	
gp160 (37–46)	Multiple CTL clones ob	TVYYGVPVWK accinia HIV component: gp160 tained from two vaccinees is is an A*0301 epitope in the 19		human (A*0301)	Johnson1994b
gp160 (37–46)	gp120 (37–46 LAI)  Vaccine Vector/Type: va  C. Brander notes this is	TVYYGVPVWK accinia HIV component: gp160 an A*0301 epitope	Vaccine	human (A*0301)	Brander2001
gp160 (37–46)	gp120  Vaccine Vector/Type: D	TVYYGVPVWK NA prime with vaccinia MVA bo	HIV-1 infection, Vaccine oost Strain: subtype A HIV con	human (A*0301) mponent: p17, p24, polyep	Hanke2000, Wee2002

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
	which could direct the conserved, often immu Kenya. A DNA and M included in the polyepi  • Multiple CD4+ or CD8 assays after vaccination	protein to the cell membrandominant epitopes that VA prime-boost vaccination tope string [Hanke2000]. He T-cell vaccine-induced to of 5 macaques. The responsible to the contract of the tresponsible to the tresponsible tresponsible to the tresponsible tresponsib	ntains p24 and p17, in a reversed order and inhibit efficient peptide proof twere selected to have particularly gion protocol using the HIVA antigen I responses to peptide pools were det ponse to the Mamu A*01 SIV p27 epated macaques, possibly because of	cessing and class I presentation, as cood cross-reactive potential for the will be used in a phase III clinical ected using intracellular cytokine solitope p11C (CTPYDINQM), inclu	well as a polyepitope string of A-clade epidemic in Nairobi, trial in Kenya. This epitope is taining and IFNgamma Elispot ded in the polyepitope region, was
gp160 (37–46)	- Enitone nemer Env VI	TVYYGVPVWK	HIV-1 infection	human (A03)	Sabbaj2002b
	<ul><li>Epitope name: Env-Vk</li><li>Among HIV+ individu</li></ul>		3, 0/20 (0%) recognized this epitope		
gp160 (37–46)	Env	TVYYGVPVWK	Vaccine	SJL/J HLA transgenic mice (A11)	Ishioka1999
	<ul><li>A minigene vaccine co ER translocating signal</li><li>The epitopes were chosen</li></ul>	sequence was constructed sen for dominant recognite	2.1 and 3 HLA A11 restricted CTL e	infections in humans	
gp160 (37–46)	<ul> <li>The vaccine used was a Gag, HIV-1 LAI protea</li> <li>CD4+ and CD8+ Gag a</li> <li>CTL responses to epitor</li> </ul>	a live recombinant canary use) and Env specific CTL res opes SLYNTVATL and To y vaccinees were non-res	Vaccine LAI HIV component: gp120, gp41 pox (CP) virus vaccine containing m ponses were detected in only 1/5 vac VYYGVPVWK from HIV+ control sponsive – non-response was not due	nultiple HIV-1 genes (HIV-1 MN gracinated volunteers, and were not dopatients were used as positive contract.)	etectable 1 year after vaccination rols
gp160 (37–46)	<ul> <li>One had a response to</li> </ul>	this epitope, the other did	HIV-1 infection  Infected with the same batch of factor  I not  that summarizes this study	human (A3) · VIII	Goulder1997e, Goulder1997a
gp160 (37–46)	gp120 (36–45) • One of the 51 HIV-1 ep HLA alleles	TVYYGVPVWK pitopes selected by Ferrar	HIV-1 infection i et al. as good candidate CTL epitop	human (A3) bes for vaccines by virtue of being of	Ferrari2000 conserved and presented by common
gp160 (37–46)	studied in eight HIV-1-	infected subjects, two wi ecognized in a given indi	HIV-1 infection itopes restricted by HLA class I A ar th acute infection, five with chronic, vidual, A2-restricted CTL response t	and one long-term non-progressor	(LTNP)

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
	All patients recognized	at least 1 A3 epitope, up	to 8 A3 epitopes, but none was clear	ly dominant	
gp160 (37–46)	for the A3 supertype) v • Progressors had memore • A positive correlation be observed, which may c	while the effector cells of lary resting CD8+ T-cells the petween effector CD8+ T-contribute to the inability of	long-term nonprogressors recognized nat recognized far fewer epitopes tha cells and plasma viremia and a nega	d far fewer epitopes n LTNPs tive correlation between CD8+ e	Propato2001 es tested, (18 for the A2 supertype, 16 ffector T-cells and CD4+ T-cells was
gp160 (37–46)	* *	TVYYGVPVWK raccinia HIV component per recognized by multiple	Vaccine :: gp160 e CTL clones from vaccinee	human (A3.1)	Johnson1994a
gp160 (37–46)	* *	TVYYGVPVWK raccinia HIV component occessed for HLA-A3.1 pro	Vaccine :: gp160 :sentation by TAP-1/2 independent a	human (A3.1) nd dependent pathways	Ferris1999, Hammond1995
gp160 (37–46)	<ul> <li>CD8+ T cells were fou viral load was also four</li> <li>All three patients were</li> <li>ELISPOT was used to a subjects showed a dom</li> <li>The subject with A*020</li> <li>Weak responses were of B*2705</li> <li>No acute response was</li> </ul>	nd prior to seroconversion and B*2705, with HLA allele test a panel of CTL epitor inant response to the B*2 01 had a moderatly strong observed to A*301-RLRP detected to the following	n, and there was a close temporal relates: A1, A30/31, B*2705, B35; A1, A pes that had been defined earlier and 705 epitope KRWIILGGLNK gresponse to SLYNTVATL GGKKK, A*301-QVPLRPMTYK, a	ationship between the number of *0301, B7, B2705; and A*0201 were appropriate for the HLA hand B7-TPGPGVRYPL in the sum 301-KIRLRPGGK, A*301-AIFG	plotypes of the study subjects – 3/3 bject who was HLA A1, A*0301, B7, QSSMTK, A*301-TVYYGVPVWK,
gp160 (38–48)	CTLs – Cw7 specific C	TL were found against th	HIV-1 infection tomatic HIV+ individual were studiouree peptides, including this one		Nehete1998a I C-restricted CD8+ Env-specific
	HLA-C confers protect	ion against lysis by natura		icted effector T cells and Cw7 di	
gp160 (42–51)	<ul> <li>HLA-C confers protect the authors hypothesize</li> </ul>	ion against lysis by natura that pathogens that inhib	al killer cells and by non-MHC-restr	icted effector T cells and Cw7 di	rectly governs this resistance to lysis - gulate Cw7, thus triggering non-MHC Brander2001

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
gp160 (42–51)	gp120 (41–55) • One of the 51 HIV-1 ep HLA alleles	VPVWKEATTT itopes selected by Ferrari et al.	HIV-1 infection as good candidate CTL epitop	human (B55) pes for vaccines by virtue of being c	Ferrari2000 onserved and presented by common
gp160 (42–52)	• This CTL epitope (the	antigenic similarity matrix to c	similarity to a human protein	overlapping this peptide is PVWKE	Maksiutov2002 (ATTTL) has similarity with the
gp160 (42–52)	gp120 (42–52) • C. Brander notes this is	VPVWKEATTTL a B*3501 epitope	HIV-1 infection	human (B*3501)	Brander2001
gp160 (42–52)	<ul><li> VPVWKDAETTL is th</li><li> VPVWKEADTTL is th</li></ul>	VPVWKEATTTL  e consensus sequence for clade ne consensus sequence for clade ne consensus sequence for clade ne consensus sequence for clade	e A and it is cross-reactive e C and it is cross-reactive	human (B35)	Cao1997a ivity
gp160 (42–52)	gp120 (41–51) • One of the 51 HIV-1 ep HLA alleles	VPVWKEATTTL it al.	HIV-1 infection as good candidate CTL epitop	human (B35) pes for vaccines by virtue of being c	Ferrari2000 onserved and presented by common
gp160 (42–61)	gp120 (49–68) • HIV-specific CTL lines	VPVWKEATTTLFCASDAKA developed by ex vivo stimulat		human	Lieberman1995
gp160 (42–61)	<ul><li> Eleven subjects had CT</li><li> Three of these 11 had C</li></ul>	VPVWKEATTTLFCASDAK, d CTL specific for more than 1 L that could recognize vaccinis TL response to this peptide s were HLA-A2, A3, B8, B62;	HIV-1 protein a-expressed LAI gp160	human	Lieberman1997a
gp160 (42–61)	gp120 (49–68 SF2) • CTL expanded ex vivo	VPVWKEATTTLFCASDAK were later infused into HIV-1 i		human	Lieberman1997b
gp160 (50–59)	for the A3 supertype) w • Progressors had memor • A positive correlation be observed, which may co	while the effector cells of long-try resting CD8+ T-cells that rec	erm nonprogressors recognize cognized far fewer epitopes that and plasma viremia and a nega NPs to clear virus	an LTNPs ative correlation between CD8+ effe	
gp160 (51–59)	for the A3 supertype) v	TLFCASDAK sors (LTNPs) had strong memo while the effector cells of long-t ry resting CD8+ T-cells that rec	erm nonprogressors recognize	ed far fewer epitopes	Propato2001 tested, (18 for the A2 supertype, 16

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
	observed, which may co	ontribute to the inability of LTNPs	I plasma viremia and a negative corr s to clear virus 0301, A*1101, A*3101, A*3301 an		ctor T-cells and CD4+ T-cells was
gp160 (52–61)		LFCASDAKAY T cell line and peptide mapping is is an A*2402 epitope in the 19	HIV-1 infection  99 database	human (A*2402)	Lieberman1992
gp160 (52–61)	gp120 (53–62 LAI) • C. Brander notes this is	LFCASDAKAY an A*2402 epitope	HIV-1 infection	human (A*2402)	Brander2001
gp160 (52–61)	gp120 (53-62)	LFCASDAKAY	HIV-1 infection, HIV-1 exposed seronegative	human (A24)	Kaul2001a
	• ELISPOT was used to s HIV-1-infected female		54 predefined HIV-1 epitopes in 91	HIV-1-exposed, persistently	y seronegative (HEPS) and 87
gp160 (52–61)	gp120 (53–62 LAI) • Uncertain whether opting	LFCASCAKAY mal, binds A24 as well	HIV-1 infection	human (B38)	Shankar1996
gp160 (52–71)	gp120 (59–78)	LFCASDAKAYDTEVHINVW- AT	HIV-1 infection	human	Lieberman1995
	<ul> <li>HIV-specific CTL lines</li> </ul>	developed by ex vivo stimulation	with peptide		
gp160 (52–71)		LFCASDAKAYDTEVHINVW- AT d CTL specific for more than 1 H	IV-1 protein	human	Lieberman1997a
	<ul><li> Eleven subjects had CT</li><li> One of these 11 had CT</li><li> The responding subject</li></ul>		xpressed LAI gp160		
gp160 (62–80)				human	Lieberman1997a
gp160 (78–86)	gp120 (77–85)  • This epitope was included low viral load	DPNPQEVVL led to illustrate the specificity of H	HIV-1 infection HIV-tetrameric staining, in a cross-se	human (B*3501) ectional study correlating H	Ogg1998b LA A*0201 CTL effector cells and
gp160 (78–86)	gp120 (77–85 SF2) • C. Brander notes this is	DPNPQEVVL a B*3501 epitope	HIV-1 infection	human (B*3501)	Brander2001
gp160 (78–86)		DPNPQEVVL e to this epitope was obtained duals have a CTL response to this ariable	HIV-1 infection epitope	human (B*3501)	Tomiyama1997

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
	<ul><li>The substitutions: 1N, 3</li><li>The substitution 8V to 8</li></ul>		I, 8K all abrogate specific CTL lysis, vific CTL activity	while only 8K reduces binding t	o B*3501
gp160 (78–86)	<ul><li>in seven patients, and the</li><li>Levels of CTL effectors</li></ul>	ne B*3501 epitope DPN stypically decline for 5-	HIV-1 infection ARV therapy using HLA-tetramer con PQEVVL in one additional patient days and then rebound, fluctuating of exponential decay with a median half-li	luring the first two weeks of the	
gp160 (78–86)	natural attenuated strair	of HIV-1 which was N	HIV-1 infection 1.3 to 1.5 year period in members of the ef-defective els of CTL effector and memory cells described.		Dyer1999 SBBC) who had been infected with a
gp160 (78–86)	<ul> <li>CD8+ T cells were four viral load was also four</li> <li>All three patients were</li> <li>ELISPOT was used to t subjects showed a domi</li> <li>The subject with A*020</li> <li>Weak responses were o B*2705</li> <li>No acute response was</li> </ul>	nd prior to seroconversion d B*2705, with HLA alle est a panel of CTL epito mant response to the B* 01 had a moderatly stror bserved to A*301-RLR detected to the followin	les: A1, A30/31, B*2705, B35; A1, A opes that had been defined earlier and v2705 epitope KRWIILGGLNK ng response to SLYNTVATL	*0301, B7, B2705; and A*0201 were appropriate for the HLA hand B7-TPGPGVRYPL in the su	, A*0301, B2705, B39 aplotypes of the study subjects – 3/3 abject who was HLA A1, A*0301, B7, QSSMTK, A*301-TVYYGVPVWK,
gp160 (78–86)		viously described HIV-1 ubstitutions that were m	HIV-1 infection ression B35 CTL epitopes were obtained in 1 fore common in B35+ individuals than		
gp160 (78–86)	<ul> <li>individuals treated durin</li> <li>The breadth and specification individuals with primar (Group 3), using 259 ox</li> <li>Previously described an</li> </ul>	ng chronic infection city of the response was y infection but post-sero rerlapping peptides spar d newly defined optima	s determined using ELISPOT by study	ing 19 individuals with pre-sero individuals who responded to F Vef se	IAART given during chronic infection
gp160 (78–86)	• Epitope name: Env-DL	DPNPQEVVL 9	HIV-1 infection	human (B35)	Sabbaj2002b

HXB2 Location	<b>Author's Location</b>	Sequence	Immunogen	Species (HLA)	References
	Among HIV+ individual	s who carried HLA B35, 3/20 (	(15%) recognized this epitope		
gp160 (78–86)	gp120 (77–85 SF2) • Binds HLA-B*3501 and	DPNPQEVVL B*5101 – binds and kills gp12	HIV-1 infection 20-vaccinia virus infected cells carrying	human (B35, B51) g B35 or B51	Shiga1996
gp160 (78–86)	gp120 (77–85)	DPNPQEVVL	HIV-1 infection, HIV-1 exposed seronegative	human (B51)	Kaul2001a
	<ul> <li>ELISPOT was used to st HIV-1-infected female N</li> </ul>		of 54 predefined HIV-1 epitopes in 91	HIV-1-exposed, persistently	seronegative (HEPS) and 87
gp160 (103–111)	Env (102–110) • CTL responses in six pathave A2 anchor residues		HIV-1 infection e studied: D2: LLNATAIAV, 5.3: RLR	human (A*0201) DLLLIV, D1: KLTPLCVT	Kmieciak1998a L, and 4.3: QMHEDIISL – all
	N-terminal epitopes, were Peptides 4.3 and D1 bou		•		L response, while D1 and 4.3,
gp160 (104–119)	gp120 (111–126 IIIB) • Primary CTL response w	MQEDIISLWDQSLKPC vith cells from non-infected dor	in vitro stimulation nors stimulated by the peptide	human	Macatonia1991
gp160 (105–117)	T1	HEDIISLWDQSLK  were detected in chimpanzees cells have been found to be stim	HIV-1 infection immunized with adenovirus-HIV-1 M nulated by this peptide (T2)	chimpanzee IN gp160 recombinant desp	Lubeck1997 ite a response to peptides P18 and
gp160 (105–117)	gp120 (112–124 IIIB) • CTL and T helper cell re	HEDIISLWDQSLK eactivity in healthcare workers	HIV-1 exposed seronegative exposed to HIV	human	Pinto1995
gp160 (105–117)	gp120 (112–124 IIIB)  • Helper and cytotoxic T c	HEDIISLWDQSLK cells can be stimulated by this p	HIV-1 infection peptide (T2)	human (A2)	Clerici1991a
gp160 (108–116)	Env (107–115 subtype B) Vaccine Vector/Type: rec	IISLWDQSL  combinant protein Strain: MI	Vaccine  N HIV component: gp160	human (A2.1)	Kundu1998a
	<ul> <li>Ten HIV-1+ HLA A2 as</li> <li>Two hundred and fifty th in gp160, of which 25 ha</li> <li>Eleven peptides were stu</li> </ul>	ymptomatic individuals were givee HIV-1 peptides of 9 or 10 and a high or intermediate bindiridied that had high HLA-A2 bindinguization may include recall	iven two courses of HIV-1 MN rgp160 na possessing the HLA-A2.1 binding m	notif (Leu at position 2, Val etected to 9/11 peptides in a	at the C terminus) were identified at least 1 individual
gp160 (109–117)	Env (109–117 CM243 subtype CRF01) • Epitope name: E109-117 • This was a study of HIV-		HIV-1 exposed seronegative gative (HEPS) female sex workers in C	human (A11) hiang Mai, northern Thaila	Bond2001

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
	and CTL responses wer	re found in 8/8 HIV+ c	and was enriched among the HEPS sex controls, and 0/9 HIV- women that were S study subject 265 who was HLA A2/A	not exposed	
gp160 (112–130)	<ul> <li>gp120 (119–139 SF2)</li> <li>Of 25 patients, most ha</li> <li>Eleven subjects had CT</li> <li>One of these 11 had CT</li> <li>The responding subject</li> </ul>	L that could recognize LL response to this pep	re than 1 HIV-1 protein e vaccinia-expressed LAI gp160 tide	human	Lieberman1997a
gp160 (117–126)	• A dominant B7 epitope	was defined using coregy, EpiMatrix, to iden	HIV-1 infection CTL responses detected in a long-term reportional methods, and three additional tify 2078 possible epitopes in the autological process.	l sub-dominant HLA B7 epitope	
gp160 (121–129)	<ul> <li>have A2 anchor residue</li> <li>The C terminal epitopes</li> <li>N-terminal epitopes, we</li> <li>Peptides 4.3 and D1 bo</li> <li>Peptides 4.3 and D1 sti</li> </ul>	es (D2 and 5.3) were hi ere much more conserund HLA-A*0201 mo mulated CTL with a re	HIV-1 infection topes were studied: D2: LLNATAIAV, 5 ghly variable and the variability was conved and gave evidence of high levels of lecules with high affinity elatively limited TCR V $\beta$ repertoire the variable D2 epitope diminished over	nsidered responsible for limited CTL response in vitro	CTL response, while D1 and 4.3,
gp160 (121–129)	<ul> <li>criteria, and 30 of these</li> <li>Three additional previor recognized at least one maximum of 2)</li> <li>2/22 individuals with cl</li> <li>0/12 acutely infected in</li> </ul>	Il peptides which carrie bound to HLA-A*020 busly described HLA-A of the 23 peptides (me hronic HIV-1 infection dividuals recognized t	HIV-1 infection  ed the A2-supermotif pattern conserved 01 – 20/30 bound to at least 3/5 of HLA 22 epitopes were added to the set of 20, idian of 2 and maximum of 6), while 6/3 recognized this epitope in ELISPOT his epitope be alleles: A*0201, A*0202, A*0203 ar	and 18/22 chronically infected F and 18/22 chronically infected F 12 acute infected individuals reco	HLA-A2 individuals had CTL that
gp160 (121–129)	gp120 (120–128 LAI)  Vaccine Vector/Type: r  CTL from HLA-A2 po		Vaccine Strain: MN HIV component: gp160 h this peptide	human (A2)	Dupuis1995
gp160 (121–129)	gp120 (120–128)  Vaccine Vector/Type: v  • A polyepitope vaccine		Vaccine ent: polyepitope cinia construct that contiguously encode	human (A2) ed seven epitopes, all presented	Woodberry1999 by HLA A-2

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
	<ul> <li>expressed in the mice</li> <li>CTL responses to Gag observed in HIV polyto</li> <li>No CTL immune responses to CTL im</li></ul>	(77-85) SLYNTVATL ope HHD-vaccinated nonses were generated a FDSRL) ents were tested for the vidual recognized all stretchan one epitope, but	Property of the transmembrane and cytotoxic of the property of	20-128) KLTPLCVTL, and Nef d with vaccinia boost Nef 157-166 (PLTFGWCYKL) ptide restimulation in culture wi TL cultures able to recognize at	f (190-198) AFHHVAREL were p, Pol 346-354 (VIYQYMDDL), and th the epitopes selected for inclusion in the least one of the epitopes, and 6 of
gp160 (121–129)	monthly into six HIV-i  1/6 showed increased e no change – pulsed DC  KLTPLCVTL is a cons response	nfected patients env-specific CTL and i es were well tolerated served HLA-A2 epitop	HIV-1 infection ed from HLA-identical siblings, pulsed ncreased lymphoproliferative responses e included in this study – all six patient get, epitope is naturally processed and e	, 2/6 showed increase only in prossing the shad this sequence as their HIV	oliferative responses, and 3/6 showed
gp160 (121–129)	gp120 (120–128) • Increased CTL respons	KLTPLCVTL se to cells expressing a	HIV-1 infection VV construct Δv3 mutant compared with	human (A2) ith a full-length env gene produc	Kmieciak1998b
gp160 (121–129)	<ul> <li>HIV-uninfected donors</li> <li>Strong CTL responses macrophages were not</li> <li>A weak response to KI</li> </ul>	using peptide-pulsed were elicited by the ep able to prime a CTL r TPLCVSL was stimu	in vitro stimulation ges and dendritic cells to stimulate prim APC – the dendritic cells performed bet pitopes DRFYKTLRA and GEIYKRWI esponse against DRFYKTLRA lated using macrophages as the APC following previously-defined HIV epito	tter as APC for the stimulation of I when presented by either imma	f primary responses ature or mature dendritic cells –
gp160 (121–129)	gp120 (120–128) • One of the 51 HIV-1 ep HLA alleles	KTLPLCVTL bitopes selected by Fer	HIV-1 infection rari et al. as good candidate CTL epitop	human (A2) bes for vaccines by virtue of bein	Ferrari2000 ag conserved and presented by common
gp160 (121–129)	<ul> <li>IL-12p40)</li> <li>Epitope name: D1</li> <li>Transgenic mice express Mice given gp160delta region of gp120, KLTF</li> <li>Greater resistance was</li> </ul>	ssing a HLA-A2/Kb cl V3 had a broader imm LCVTL, and the C-ter conferred by the gp16	Vaccine Inbinant protein boost Strain: IIIB H Inimeric protein were vaccinated with a strain response than those given gp160, was region of gp41, SLLNATAIAV. IndeltaV3 than the gp160 vaccine to a chavas conferred by CD8+ T-cells.	full length gp160 or with gp1600 vith increased responses to conse	deltaV3, with the V3 loop deleted. erved HLA-A2 epitopes in the C1

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
gp160 (121–129)	for the A3 supertype) w • Progressors had memor • A positive correlation b observed, which may co	thile the effector cells of y resting CD8+ T-cells etween effector CD8+ contribute to the inability	HIV-1 infection g memory resting CD8+ T-cell response of long-term nonprogressors recognized s that recognized far fewer epitopes thar T-cells and plasma viremia and a negat y of LTNPs to clear virus 2 supertypes alleles (A*0201, A*020 2,	far fewer epitopes a LTNPs ive correlation between CD8+ effo	
gp160 (121–129)	Env	KLTPLCVTL	Vaccine	SJL/J HLA transgenic mice (A2.1)	Ishioka1999
	<ul><li>ER translocating signal</li><li>The epitopes were chos</li><li>HLA transgenic mice w</li></ul>	astruct encoding 6 HL. sequence was construent for dominant recognere used for quantitati	A 2.1 and 3 HLA A11 restricted CTL ep	nfections in humans crines encoding HLA-restricted C	
gp160 (121–129)	<ul> <li>Ten HIV-1+ HLA A2 at</li> <li>Two hundred and fifty t in gp160, of which 25 h</li> <li>Eleven peptides were st</li> </ul>	symptomatic individua hree HIV-1 peptides o lad a high or intermedi udied that had high HI mmunization may incl	Vaccine  Strain: MN HIV component: gp160 als were given two courses of HIV-1 MN f 9 or 10 aa possessing the HLA-A2.1 b ate binding affinity  LA-A2 binding affinity – a CTL responsed ude recall responses – only individuals	inding motif (Leu at position 2, Voice was detected to 9/11 peptides in	al at the C terminus) were identified at least 1 individual
gp160 (156–165)	• This CTL epitope (the I	HIV-1 LAI fragment w	HIV-1 infection  attrix to compare HIV-1 antigenic determining the high similarity to a human protein of the fragment SISIRLKVQK.		Maksiutov2002  GKVQK) has similarity with the
gp160 (156–165)	<ul> <li>The processing of this e</li> <li>Only peptide that has be critical, position 1 could</li> <li>This peptide also contained</li> <li>The HIV-1 Env epitope glycosylation, export be</li> </ul>	epitope is TAP1/2-depe een deglycosylated, a p d be either D or N ins a Cys involved in a s are typically processor ack into the cytosol, an	HIV-1 infection from a lab worker exposed to HIV-1 in 15 endent, as are most Env epitopes, and it process that changes asparagine (N) to a disulfide linkage but reducing condition ed by a TAP1/2 dependent mechanism, d deglycosylation for processing, and re pe may have an impact on the presentation	contains two N-linked glycosylatic spartic acid (D) was recognized: the spartic acid (D) was recognized: the spartic acid (D) was recognition by Combined the sparting sparting the sparting sparting sparting the sparting	TL clone LWF A5 nslocation into the ER, ciation with class I molecules

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
gp160 (156–165)	<ul> <li>NCSFNITTSI, a variant</li> </ul>	found in HIV-1 MN, was not rec	HIV-1 infection epitopes recognized by 3 lab worke cognized, thus this epitope was type tion sites and cysteine residue, poss	-specific	
gp160 (188–207)	gp120 (193–212 BRU) • Defined through blockin	TTSYTLTSCNTSVITQACPK g CTL activity, and Env deletion		human (A2)	Dadaglio1991
gp160 (191–200)	HLA-A11 is very comm and CTL responses were	) -1 exposed persistently seronega on in this population, and was er	HIV-1 infection  tive (HEPS) female sex workers in arriched among the HEPS sexworked 0/9 HIV- women that were not ex 144 who carried HLA-A2	rs – weak CTL responses v	
gp160 (191–200)	<ul><li>epitopes in this group, al</li><li>1/4 tested FSWs recogni KLTSCNTSV</li></ul>	ort of HIV+ female sex workers (though E clade versions of previ	HIV-1 infection (FSW) from Northern Thailand wer lously defined B-clade A2 and A24 pitope, which differs from the previous (EKF01 (E), B, C, and D	epitopes were also tested.	•
gp160 (192–200)	gp120 (192–199)  • Epitope name: SL9  • Administration of triple-responses in patients with	KLTSCNTSV  drug antiretroviral therapy (IDV,	HIV-1 infection , 3TC and ZDV) sometimes showed re is a stable population of tetramer		
gp160 (192–200)	gp120 (192–199 HXB2R) • Epitope predicted on HL	KLTSCNTSV  A binding motif, and studied in	HIV-1 infection the context of inclusion in a synthe	human (A2)	Brander1995a
gp160 (192–200)	_		HIV-1 infection y specific, and found to work well e erved in response to anti-retroviral to		
gp160 (192–200)	gp120 (197–205) • Crystallization of HLA-	TLTSCNTSV A2 molecules complexed with ar	Peptide-HLA interaction ntigenic peptides – refers to Dadagl	human (A2) io et al 1991	Garboczi1992
gp160 (192–200)	1 1	TLTSCNTSV ized by PBMC from 6/14 HIV+ ong with pol CTL epitope ALQI	HIV-1 infection asymptomatic patients DSGLEV and a tetanus toxin T help	human (A2.1) per epitope for a synthetic	Brander1996a vaccine

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
	• This vaccine failed to inc	duce a CTL response, although a	helper response was evident		
gp160 (192–211)			IV-1 protein	human	Lieberman1997a
gp160 (199–207)	cross-reactive and recog specific manner. Two oth SVITQACPK was found D) and clade E (saiKqac from 0/7 E clade infecte	nized by clade E infected individual inter HLA A*1101 clade B defined to elicit clade-specific response pk is most common). SVITQAC d Thai subjects, so this seems to	HIV-1 infection opes were generated for clade E (CR. luals. The clade E and B analogs to the d epitopes were found not to have stills in clade B (SVITQACPK is most compared by CTL from 3/5 be a B clade exclusive epitope. I was comparable, implicating TCR in	hree more HLA A*1101 ep mulated a response in clade common, sAitqacpk is most 5 B clade infected Japanese	itopes was recognized in a clade E infected individuals. common variant in clade A, C and
gp160 (201–225)		ITQACPKVSFEPIPHYCAP- AGFAI ccinia HIV component: gp160 n LAI IIIB gp160 vaccinees		human (CD4+ CTL)	Johnson1994b, Johnson1994a
gp160 (202–221)	gp120 (209–228) • HIV-specific CTL lines of	TQACPKVSFEPIPIHYCAPA developed by ex vivo stimulation		human	Lieberman1995
gp160 (202–221)	contribution of CD8+CI be similarly distributed t • HIV CTL responses to 3 • The clonal composition	028- cells to CTL memory pools he CD28 depleted cell populatio Env and 2 Gag peptides were st	oirth, and the proportion of CD28-CD for CTL clones specific for two pers n udied e studied and was found to be highly	istent human viruses, CMV	and HIV – clones were found to
gp160 (202–221)	gp120 • Peptide 740.18: Memory	TQACPKVSFEPIPIHYCAPA CTL specific for HIV-1 may co	HIV-1 infection intribute to oligoclonal expansions w	human ithin the CD57+ CD28- CD	Weekes 1999a 08+ CTLp populations
gp160 (202–221)		TQACPKVSFEPIPIHYCAPA CTL specific for more than 1 H that could recognize vaccinia-e response to this peptide	IV-1 protein	human	Lieberman1997a
gp160 (202–221)	gp120 (209–228 SF2) • CTL expanded ex vivo v	TQACPKVSFEPIPIHYCAPA vere later infused into HIV-1 infe		human	Lieberman1997b

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
gp160 (207–216)	cross-reactive CTL res and D • Proteins corresponding was extensive inter-sub • CTL derived from subt	ponses in Ugandans to A  to the subtype of the in otype cross-reactivity wi type A clade infection (p  B clade version of the p	fecting strains tended to trigger higher th B clade proteins and the co-circulat patient SP 528), recognized the subtyp peptide (KVSFEPIPIH), and no lysis u	a viruses expressing Gag, Env, F r levels of CTL response measur- ting subtype e A version of the peptide (KMS)	Pol, RT or Nef from HIV-1 clades A, B, ed by percent specific lysis, but there SFEPIPIH), had a slightly reduced
gp160 (208–217)	<ul><li>CD8+ T cell responses</li><li>Low risk individuals d</li><li>CD8+ T cell epitopes:</li></ul>	tended to be to the sam	duals), SLYNVATL (4 individuals), LS	HIV-specific CD8 gamma-IFN is than cervical CD8+ T cell resp	onses
gp160 (208–217)	gp120 (263–272)  • ELISPOT was used to HIV-1-infected female	•	HIV-1 infection, HIV-1 ex seronegative a panel of 54 predefined HIV-1 epitop		Kaul2001a ently seronegative (HEPS) and 87
gp160 (208–219)	<ul> <li>CTL could be activated exogenous protein and</li> </ul>	d by a fusion protein of a allows processing throu	HIV-1 infection d from a Ugandan subject that recogni an HIV protein and anthrax lethal factor gh the MHC class I pathway. This stra using live viral vectors carrying a prot	or (LFn-HIV) that promotes anti ategy for CTL detection could al	low antigen presentation without
gp160 (209–217)	(LAI)	SFEPIPIHY		(A29)	Altfeld2000a, Brander2001
gp160 (209–217)	<ul> <li>individuals treated dur</li> <li>The breadth and specifindividuals with prima (Group 3), using 259 o</li> <li>Previously described a</li> </ul>	ing chronic infection ficity of the response wary infection but post-serverlapping peptides spand nd newly defined optima	s determined using ELISPOT by study	ving 19 individuals with pre-sero ) individuals who responded to I Nef nse	HAART given during chronic infection
gp160 (212–231)	gp120 • Peptide 740.19: Memo		ILKCNNK HIV-1 infection  7-1 may contribute to oligoclonal expa	human nsions within the CD57+ CD28-	Weekes1999a - CD8+ CTLp populations
gp160 (212–231)	gp120 (219–238 HXB) • CTL epitope defined b		ILKCNNK HIV-1 infection mapping	human	Lieberman 1992

HXB2 Location	<b>Author's Location</b>	Sequence	Immunogen	Species (HLA)	References
gp160 (212–231)	gp120 (219–238) • HIV-specific CTL lines	PIPIHYCAPAGFAILKCNNK developed by ex vivo stimulation		human	Lieberman1995
gp160 (212–231)	contribution of CD8+C be similarly distributed • HIV CTL responses to • The clonal composition	PIPIHYCAPAGFAILKCNNK at all CD8+ T cells are CD28+ at b D28- cells to CTL memory pools in the CD28 depleted cell popula 3 Env and 2 Gag peptides were st of the TCR Vbeta responses was pecific response – clones to this ep	oirth, and the proportion of CE for CTL clones specific for twation tudied studied and was found to be leading to the control of the control	vo persistent human viruses, Cl	MV and HIV – clones were found to
gp160 (212–231)	patients – this observati		ated decreased the IL-2-expanction and impaired function of	f T helper cells, CTL exhaustion	
gp160 (237–246)	<ul> <li>A subset of the potential epitopes were identified</li> </ul>	GPCKNVSTVQ was used in conjunction with the all epitopes was identified that could that could stimulate IFNγ production with the could be sufficient to the could be su	ld bind to the appropriate HLA ction in an ELISPOT assay	A-allele, and 15 predicted B7 st	perfamily (HLA B7, B8, and B58)
gp160 (239–247)		CTNVSTVQC used to define the range of CTL s a potential N-linked glycosylation			Sipsas1997 ith HIV-1 IIIB t for a high sensitizing dose of peptide
gp160 (242–261)	gp120 (249–268) • HIV-specific CTL lines	VSTVQCTHGIRPVVSTQLLL developed by ex vivo stimulation		human	Lieberman1995
gp160 (242–261)	<ul> <li>Eleven subjects had CT</li> </ul>	VSTVQCTHGIRPVVSTQLLL d CTL specific for more than 1 H L that could recognize vaccinia-e L response to this peptide was HLA-2, -B21	IV-1 protein	human	Lieberman1997a
gp160 (242–261)	gp120 (249–268) • CTL expanded ex vivo	VSTVQCTHGIRPVVSTQLLL were later infused into HIV-1 info		human	Lieberman1997b
gp160 (252–260)	<ul><li>Only 1/7 B35-positive i</li><li>An I to V substitution a</li></ul>	RPIVSTQLL e to this epitope was obtained ndividuals had a CTL response to t position 3 reduces specific lysis t position 7 abrogates specific lys	, but not binding to B*3501	human (B*3501)	Tomiyama1997

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
gp160 (252–260)	gp120 (255–263 SF2) • Binds HLA-B*3501	RPIVSTQLL	HIV-1 infection	human (B35)	Shiga1996
gp160 (252–260)	• The sequences of 9 prev	ubstitutions that were more cor	TL epitopes were obtained in	human (B35) n 10 HLA B35+ and 19 HLA B35- nan in B35- individuals, but this was	
gp160 (252–261)	<ul> <li>A subset of the potential B58) epitopes were iden</li> </ul>	l epitopes was identified that contified that could stimulate IFN	ould bind to the appropriate $\gamma$ production in an ELISPOT		B7 superfamily (HLA B7, B8, and
gp160 (252–271)	• This CTL epitope (the H	•	ompare HIV-1 antigenic dete similarity to a human protein		Maksiutov2002 LLNGSLAEE) has similarity with th
gp160 (252–271)	gp120 (256–275 LAI)	RPVVSTQLLLNGSLAEEEV	VV HIV-1 infection	human (B7)	Shankar1996
gp160 (291–307)	• This CTL epitope (the H	HIV-1 LAI fragment with high	similarity to a human protein	human erminants with human proteins. n overlapping this epitope is VEINO 5 antigen) fragment VEINCTRQN	Maksiutov2002  CTRPNN) has similarity with the Fast.
gp160 (291–307)	gp120 (295–312 BRU) • Defined through blocking	SVEINCTRPNNNTRKSI ng CTL activity, and Env deleti	HIV-1 infection	human (A2)	Dadaglio1991
gp160 (291–307)	<ul> <li>Transgenic mice express Mice given gp160delta\tagenty region of gp120, KLTPI</li> <li>Greater resistance was c isolates (VI-06 and 89.6</li> </ul>	sing a HLA-A2/Kb chimeric p. 3 had a broader immune respondence. CVTL, and the C-term region	rotein were vaccinated with a conse than those given gp160, of gp41, SLLNATAIAV. than the gp160 vaccine to a corred by CD8+ T-cells.	murine (A2)  HIV component: gp160 Adjuvant a full length gp160 or with gp160de with increased responses to conser challenge of vaccinia expressing he V3 peptides.	eltaV3, with the V3 loop deleted. ved HLA-A2 epitopes in the C1
gp160 (297–322)		TRPNNNTRKRIRIQRGPGH AFVTIGK eptide Strain: IIIB HIV con	nponent: V3 Adjuvant: lip	murine (H-2D $^d$ ) osome	Chang1999

• Induction of peptide-specific CTLs in BALB/c mice was dependent on immunization with peptide encapsulated liposomes containing MPL as adjuvant

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
	• T26K (26mer) elicited a	a stronger AB and CTL response	than R15K (a V3 15me	, RIQRGPGRAFVTIGK)	
gp160 (297–330)	<ul> <li>Anti-HIV lipopeptide va administered in a phase</li> <li>A CD4+ T cell prolifera</li> <li>9/12 tested mounted a C peptide was particularly</li> <li>None of the 12 tested has</li> </ul>	I trial tive response to at least one of the TL response to at least one of the immunogenic, eliciting a CTL re	peptides no acid peptides derived ne six peptides was obse e six peptides; each of the esponse in five vaccinee p160 and vaccinees cou	human  from Nef, Gag and Env HIV-1 protein  rved in 9/10 vaccinees – 6/10 reacted to the six peptides elicited a CTL responses  d be differentiated from HIV-1 seropo	to this peptide e in at least one individual – this
gp160 (298–307)	gp120 (298–307)  • The processing of this e • Peptide that had been do efficiently than either gl • Position 5 is not involve • HIV-1 Env epitopes are export back into the cyto-	RPNNNTRKSI pitope is TAP1/2-dependent, as a eglycosylated, a process that char ycosylated or non-glycosylated F ed with HLA B*07 binding, so is typically processed by a TAP1/2 osol, and deglycosylation for pro-	HIV-1 infection are most Env epitopes, a nges asparagine (N) to a RPNNNTRKSI probably important for dependent mechanism, cessing, and retransport	human (B*07)  nd it contains an N-linked glycosylation spartic acid (D) (RPNDNTRKSI) was  FCR recognition which involves cotranslational translocation the ER for the association with cleantation of that epitope, quantitatively	recognized a 100-fold more cation into the ER, glycosylation, lass I molecules
gp160 (298–307)	gp120 (302–312 HXB2 • C. Brander notes this is		HIV-1 infection	human (B*0702)	Brander2001
gp160 (298–307)	gp120 (302–312 HXB2) • CTL from two acute ser	•	HIV-1 infection	human (B7)	Safrit1994b
gp160 (298–307)	<ul><li>gp120 (302–312 HXB2</li><li>Peptide processed by a of the CTL from an acute sero</li></ul>	TAP-1/2-dependent pathway only	HIV-1 infection	human (B7)	Hammond1995
gp160 (298–307)	gp120 (302–312 HXB2 • Longitudinal study of ep		HIV-1 infection	human (B7)	Wolinsky1996
gp160 (298–307)	<ul><li>cross-reactivity was obs</li><li>Two HLA B7 individua note that the B7 epitope</li></ul>	clade cross-reactivity from CTL erved ls had CTL response to B_LAI, A RPNNNTRKSI is immunodomi	A_92UG037 and C_92E nant, conserved betwee	human (B7) s newly infected with B clade virus w R025 gp160, but were B clade strain I the LAI and clade A and C strains, b e response in the HLA B7 individuals	MN non-responders – the authors ut is very divergent in MN
gp160 (298–307)	gp120 (303–312 SF2) • Therapy provided durin individuals treated durin		HIV-1 infection rrower CTL response, st	human (B7) ronger T help response, and a less div	Altfeld2001b erse viral population than was seen in

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
	individuals with prima (Group 3), using 259 o • Previously described a	ry infection but post-seroe verlapping peptides spanr nd newly defined optimal	determined using ELISPOT by stude conversion therapy (Group 2), and 1 using p17, p24, RT, gp41, gp120 and epitopes were tested for CTL response to this epitope broken do	0 individuals who responded to I Nef onse	HAART given during chronic infection
gp160 (298–307)	<ul> <li>studied in eight HIV-1</li> <li>2 to 17 epitopes were repitopes were targeted</li> <li>Subjects with chronic l</li> <li>An acute seroconvertor</li> <li>The other acute seroco</li> </ul>	infected subjects, two wire ecognized in a given indi- by at least one person HIV-1 infection recognize r homozygous for the B7 anvertor failed to recognize	HIV-1 infection topes restricted by HLA class I A a th acute infection, five with chronic vidual, A2-restricted CTL response d between 2-8 out of 11 B7-restrict allele recognized five B7-restricted e any of the 11 B7-restricted epitop able and there was no clearly domin	, and one long-term non-progress tended to be narrow and never do red epitopes epitopes es tested	
gp160 (298–307)	<ul> <li>One individual, AC-06 interruptions (STI). He restricted by HLA-A3,</li> <li>4/11 HLA-B7 individual</li> </ul>	cutely HIV-infected HLA, was homozygous at all to had only two detectable 11 by HLA-B7, and 1 by als had detectable B7-rest		was treated during acute infection on, but after STI this broadened to ing acute infection – 10/15 of HL	and had supervised treatment
gp160 (298–307)	<ul><li>specific T-cell response</li><li>Nef epitope recognition</li></ul>	es by Elispot and Tetrame n was detected in all 4 sub	HIV-1 infection cessful anti-viral therapy but with o r staining, maintained for 2-4 years pjects, gp120, Pol and Gag-specific ate maturation phenotype character	after initiation of HAART. in 1 or 2 subjects.	Appay2002 d Nef mRNA transcription, showed d high levels of CD27 expression.
gp160 (298–307)			HIV-1 infection IDS Foundation ARIEL Project, a recurring variants, were found in no		Wilson1996 tudy o recognize these variants has not yet
gp160 (299–319)	<ul><li>each HIV protein.</li><li>Nef and p24 had the hi</li></ul>	ghest percentage of reacti		st magnitude of HIV-1 responses.	
gp160 (303–322)	gp120 Vaccine Vector/Type:	TRKSIHIGPGRAFY: virus-like particle Strain	TTGE Vaccine : B subtype consensus HIV comp	murine BALB/c	Luo1998

HXB2 Location	<b>Author's Location</b>	Sequence	Immunogen	Species (HLA)	References				
	• Intramuscular injection of chimeric gag-env virus-like particles (VLPs) containing V3 loop sequences into BALB/c mice induce V3 specific CTL – TRKSIHIGPGRAFYTTGE is a B subtype consensus that stimulated a cross-reactive CTL response								
gp160 (304–318)	<ul> <li>Virus-like particles coul critical to VLP formatic</li> <li>CTL responses in BALI (KRIHIGPGRAFYTTK</li> </ul>	d be formed from HIV-2 g on B/c mice were induced by G X), RF (SITKGPGRVIYATO	chimeric gag-V3 particles again GQ), and SF2 (SIYIGPGRAFI	ds at the C-terminal end – a proling st the V3 region of HIV-1 clade B	Kang 1999 e rich region in positions 373-377 was isolates IIIB (SIRIQRGRAFVTI), MN				
gp160 (306–322)	gp160 (LAI)  Vaccine Vector/Type: re  Addition of CpG oligod	SIRIQGPGRAFVTIGI	Vaccine a: LAI HIV component: gp16 //alum vaccine given to BALB/	murine (H-2D <sup>d</sup> )  0 Adjuvant: CpG oligodeoxynuc  e mice shifted the response to Th0/	Deml1999 Eleotide, alum				
gp160 (308–321)	<ul> <li>Epitope name: P18IIIB</li> <li>BALB/c and A.AL were KQIINMWQEVGKAN</li> <li>Substitution of Glu (wt) responding Th cells, and and enhanced CTL respondences</li> </ul>	IYA.  to Ala in T1, kqiinmwqAvd shifting the response towonses to P18.	peptide vaccine construct contary gkamya, caused increased affi ards Th1. Increased Th respons	es stimulated DCs to produce high	Ahlers2001 If the T helper epitope T1, In the upregulation of CD40L in the ner levels of IL-12, and B7-1 and B7-2, Dressing HIV-1 IIIB gp120 compared to				
gp160 (308–322)	gp160 (MN) RIHIGPGRAFYTTKN Vaccine human Pinto1999  Vaccine Vector/Type: peptide Strain: MN HIV component: V3 Adjuvant: Montanide ISA 51  Peptide P18: Eight HIV+ individuals were vaccinated with peptides containing specific T helper, CTL and Ab epitopes in Montanide ISA 51 in a Phase trial  Four displayed a 4-fold increase in PCLUS 3-18 MN-specific T helper responses  One patient developed a new, sustained P18MN-peptide-specific CTL response – the patient's HLA haplotype was A2,30; B53,7; Cw2,4, and anti-HLA antibody did not inhibit the response, suggesting it was not A2  Patients with low baseline Ab levels developed an increase of neutralizing Ab titers  No significant change was observed in plasma HIV viral loads and CD4 cell counts								
gp160 (308–322)			HIV-1 infection munized with adenovirus-HIV- subsequent HIV-1 SF2 challen	chimpanzee  1 MN gp160 recombinant e in a chimpanzee lacking neutrali	Lubeck1997				
gp160 (308–322)	gp120 (315–329 IIIB)	RIQRGPGRAFVTIGK eactivity in healthcare work	HIV-1 exposed serone		Pinto1995				

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
gp160 (308–322)	gp120 (313–327 MN) • CTL and T helper cell re	RIHIGPGRAFYTTKN activity in healthcare workers	HIV-1 exposed seronegative exposed to HIV	human	Pinto1995
gp160 (308–322)	<ul> <li>Intramuscular immunizaresponses – gp160 induceresponses and IFN-responses and IFN-responses that were enhanced immunistration of GM.</li> <li>Repeated immunization responses.</li> </ul>	tion of BALB/c mice with DN ed strong gp160-specific CTL passes but little CTL activity. Issuids encoding cytokines and anced quantitatively, but not all MCSF most strongly enhanced with pNGVL-Nef failed to income the strong transfer of the strong tran	Vaccine IL-2, IL-12, IL-15, GMCSF, FLt3 li IA vaccines carrying either gp160 or and IFN-responses and low-titer hund/or hematopoietic growth factors, IL tered qualitatively. I CTL and IFN-responses against pNoduce CTL responses. Co-administration	Nef in the expression vect moral responses, and Nef § .2, IL-12, IL-15, Flt3 ligan GVL-gp160. ion of IL-12 most strongly	generated humoral (IgG1, IgG2a) d (FL), and GMCSF tended to give enhanced humoral and IFNgamma
gp160 (308–322)	Env (315–329)  Vaccine Vector/Type: Di  Epitope name: P18  C3H (H-2k) transgenic repidermal gene gun with the proteasome.  A single immunization vector immunodominant epitop responses and stimulated.  The presence of multiple	RIQRGPGRAFVTIGK NA HIV component: HIV-1 nice carrying a fused HLA-A <sup>2</sup> n an ubiquitin expression librar with the UB-HIV-1 library vac tes SLYNTVATL (Gag), ILKE I CTL that were functional in the plasmids HLA-A*0201-restr	Vaccine divided into a 32 plasmids in a ubiqu *0201 alpha1 and alpha2 and H-2Dk	murine (A*0201) aitin expression library alpha3 hybrid class I mole IV-1 genome. Ubiquitin ta ivalent CTL responses agai GK(P18) and AFHHVARE ype antigen. CTL immunogenicity, and	Singh2002, Sykes1999  Eccule were immunized using an regets the expressed HIV-1 peptides to first all library members.  K (Nef) elicited strong CD8+/IFN-
gp160 (308–322)		RIQRGPGRAFVTIGK ccinia Strain: IIIB HIV coictions associated with this pe		human (A11)	Achour1994
gp160 (308–322)	gp120 (315–329 BRU)  • Defined through blockin	RIQRGPGRAFVTIGK g CTL activity, and Env deleti	HIV-1 infection ions	human (A2)	Dadaglio1991
gp160 (308–322)	gp120 (315–329 IIIB)  • Helper and cytotoxic T of	RIQRGPGRAFVTIGK rells can be stimulated by this	HIV-1 infection peptide (P18)	human (A2)	Clerici1991a
gp160 (308–322)	<ul> <li>Transgenic mice express Mice given gp160deltaV region of gp120, KLTPL</li> <li>Greater resistance was c</li> </ul>	ing a HLA-A2/Kb chimeric p 3 had a broader immune responder CVTL, and the C-term region	than the gp160 vaccine to a challeng	ngth gp160 or with gp160d creased responses to conse	eltaV3, with the V3 loop deleted. rved HLA-A2 epitopes in the C1

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
	• The most intense CTL re	esponses to the intact gp160 vac	ccine were directed at three V3 pept	ides.	
gp160 (308–322)		RIQRGPGRAFVTIGK ccinia HIV component: gp160 cictions associated with this pep		human (A2, A3)	Achour1993
gp160 (308–322)		RIQRGPGRAFVTIGK ptide Strain: IIIB HIV comp are important for MHC/peptide		murine $(D^d)$	Takahashi1989a
gp160 (308–322)		RIQRGPGRAFVTIGK ptide Strain: IIIB HIV comp o the footpad of a mouse could		murine $(D^d)$	Sastry1992
gp160 (308–322)	<ul><li>PCLUS 3-18MN synthe</li><li>A substitution in the T1</li></ul>	* *	ntained T1 helper epitope covalently. Th response and class II binding sp	-	
gp160 (308–322)		RIHIGPGRAFYTTKN ccinia <i>Strain:</i> MN, IIIB <i>HI</i> V h V(11 IIIB) interchanges speci		murine $(D^d)$	Takahashi1989b
gp160 (308–322)		SITKGPGRVIYATGQ  ccinia Strain: RF HIV comp  B, and RF specificities, position		murine $(D^d)$	Takahashi1992
gp160 (308–322)	Dd-restricted P18 peptid	e. The RT-1 TCR alpha chain we ported the observation that a sir	in vitro stimulation  Igh analyzing the spectrum of TCR- was able to react with 1/3 of the teste Igle TCR alpha chain would confer	ed TCR beta chains to create	a specific response. Experiments in
gp160 (308–322)		RIQRGPGRAFVTIGK combinant protein HIV comports munization elicited V3 CTL r		murine (H-2 <sup>d</sup> )	Griffiths1993
gp160 (308–322)		RIQRGPGRAFVTIGK rus-like particle HIV compone particles (VLPs) can elicit a CT	Vaccine ent: Gag, Env L response that is dependent on the	murine $(H-2^d)$ amount of Env presented on	Deml1997 the VLP
gp160 (308–322)	gp120 (313–327 MN) Vaccine Vector/Type: Di	RIHIGPGRAFYTTKN NA <i>Strain:</i> MN <i>HIV compo</i>	Vaccine nent: gp160, V3	murine BALB/c (H-2 <sup>d</sup> )	Fomsgaard1998a

HXB2 Location	<b>Author's Location</b>	Sequence	Immunogen	Species (HLA)	References
		esponses to the V3 region of to a gp160 plasmid vaccino		nization by gene gun with a chimer	ic DNA vaccine of V3-hepatitis B
gp160 (308–322)	<ul><li> Vaccine constructs cont</li><li> The peptide CTL response</li></ul>	raining helper, antibody and notes was as cross-reactive as	Vaccine Y component: V3 Adjuvant: GM CTL peptide epitopes induce st s one elicited by a vaccinia const effective for inducing and boostin	rong Th1, CTL and NAb responses ruct expressing rgp160 MN	Ahlers1996, Ahlers1997a against the autologous HIV-1 virus
gp160 (308–322)			Vaccine IIIB HIV component: V3, Gag c CTL in mice in the absence of		Layton1993
gp160 (308–322)	• A discistronic IL-2 gp1 Il-2/IgG fusion protein administration.	20 expression vector gave a enhanced the immune resp	onse and administration of a Il-2.	murine (H-2 <sup>d</sup> ) L-2 or IL-2/Ig 20 alone in the expression vector, heading of the expression vector is a suppression vector of the expression vector is a suppression vector of the expression vector of the expres	epended on the timing of
gp160 (308–322)	<ul> <li>Epitope name: P18</li> <li>Peptide immunization u electric pulsing was trie</li> <li>BALB/c immunized wi</li> <li>The CTL response was AGCGCT, AACGCT, s proliferation</li> </ul>	asually doesn't elicit a good ed (i.m. injection followed) th HIV P18 or hepatitis C I enhanced by addition of in equences common in proka	d CTL response because epitopes by 8 electric pulses), to enhance P17 peptides with an electric puls immunostimulatory sequences ISS aryotic genomes but rare in eukar	peptide uptake through electropora se elicited a CTL response, those the s in the plasmid pCMV-LacZ, that of	and presented, so vaccination with tion at did not receive the pulse did not contains hexamers GACGTC, kines and result in B cell and T-cell
gp160 (308–322)	gp160 (MN)  Vaccine Vector/Type:   • CTL responses to a prin				Fomsgaard1998b ) bivacaine pretreatment, cardiotoxin
gp160 (308–322)	gp120 (315–329 IIIB)  Vaccine Vector/Type: v  In a murine system mul  The MHC class I molec	RIQRGPGRAFVTIGK accinia <i>Strain:</i> IIIB <i>HI</i> tiple class I molecules can cule $D^d$ as well as $H-2^{u,p,q}$ ,	Vaccine V component: gp160 present this peptide, called P18, were found to present peptides l	murine (H- $2^{d,p,u,q}$ ) to CTL, including H- $2D^d$ , H- $2D^p$ ,	

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
gp160 (308–322)				murine (H-2D <sup>d</sup> )  ent: gp160 Adjuvant: mucosal adjuct CTL activity and Th1 and Th2 cyto	
gp160 (308–322)	<ul><li>A intranasal peptide va</li><li>IIIB peptide referred to</li><li>Peptide-specific CTLs</li></ul>	ccine with cholera toxin as as R15K were induced after in vitro inducing CTL compared to	Vaccine 'component: V3 Adjuvant: c a mucosal adjuvant was given. restimulation with peptide-puls the RGPGRAFVTI, in contrast	•	Porgador1997
gp160 (308–322)			Vaccine HA gene cassette Strain: IIIB TL in BALB/c mice, but could	(H-2D <sup>d</sup> )  HIV component: P18 I not induce a P18IIIB-specific antibo	Chiba1999 ody response
gp160 (308–322)		RIHIGPGRAFYTTKN peptide Strain: MN, SC and SC induce murine CTL	Vaccine HIV component: V3 that are cross-reactive with div	murine (H-2D $^d$ ) werse strains	Casement1995
gp160 (308–322)			Vaccine n: MN HIV component: gp12 and RF vaccinia-expressed Env		Newman1997
gp160 (308–322)			Vaccine  n: IIIB HIV component: gp12 s peptide (P18), and an addition	murine (H-2D <sup>d</sup> ) 20 Adjuvant: QS-21 adjuvant nal Env CTL response that was cross	Newman1997 -reactive
gp160 (308–322)		RIQRGPGRAFVTIGK raccinia Strain: IIIB HI in mice vaccinated with gp	1 61	murine (H-2D <sup>d</sup> )	Takahashi1988
gp160 (308–322)	<ul><li>The peptide RIQRGPG response in mice</li><li>Liposomes coated with</li></ul>	RAFVTIGK was incorporate oligomannose show no tox		s a subcutaneous injection, which inc L response upon a single subcutaneous	
gp160 (308–322)	Vaccine Vector/Type: fi • Epitope name: P18	RIQRGPGRAFVTIGK usion protein with anthrax of	Vaccine delivery domain HIV compon	murine (H-2D <sup>d</sup> ) nent: V3 Adjuvant: B. anthracia let	Lu2000a hal toxin LF component

HXB2 Location	<b>Author's Location</b>	Sequence	Immunogen	Species (HLA)	References
	cells in BALBc mice. L	Fn causes exogenous pro	tein to be taken up and processed		region fusion proteins induce CD8 T teins from Gag p24 and nef fragments lonor PBMCs in vitro.
gp160 (308–322)	<ul> <li>Cholera toxin (CT) is a BALB/c mice V3 peptide.</li> <li>Peptide vaccine induced activity than any single.</li> <li>Combinations of cytoki immunization was obse.</li> <li>Nasal immunization with</li> </ul>	potent adjuvant used in a des to attempt to replace of CTL activity was significated cytokine.  In could be more potent to the present of the present the present the present the present was associated with	W component: V3 Adjuvant: chenimal studies that is not safe in hucT as a potent adjuvant. cantly increased by IL-1alpha, IL hat CT as an adjuvant. The highes IL-18 as adjuvant. sence of IL-1alpha, IL-12 and GM upregulation of MHC class II and		were used in nasal immunization of juvant, but CT gave more potent CTL e-specific PBMC after nasal ng cells in the cervical lymph node,
gp160 (308–322)	Dd-restricted P18 peption	de. The RT-1 TCR alpha pported the observation the	d through analyzing the spectrum chain was able to react with 1/3 of		Yokosuka2002  to reconstitute a reaction to the H-2 te a specific response. Experiments in nse and could interact with a large
gp160 (308–322)		RIQRGPGRAFVTIGK accinia HIV component can cross-present this epi		murine (H-2D $^{d,p,q}$ , H-2 $^{u}$ )  QGAYRAIR, to specific CTL	Shirai1996b
gp160 (309–317)	Phe, Leu or Ile at the C  This peptide induced C	term) – 53 of the 59 pept TL in 1/4 HIV-1+ people	ides bound A*2402 tested	human (A*2402) predicted by searching for A*2402 and construct and presented – no speci	Ikeda-Moore1997 Inchors in HIV proteins (Tyr at 2, and fic CTL clones were obtained
gp160 (309–318)	<ul> <li>HLA-A11 is very command CTL responses wer</li> </ul>	8 7-1 exposed persistently sonon in this population, an e found in 8/8 HIV+ cont		-	

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
gp160 (309–318)	gp120 (314–323 CM243 subtype CRF01)	ITVGPGQVFY	HIV-1 infection	human (A11)	Bond2001
	Thailand, of whom more	than half were HLA-A1	•		
	<ul><li>epitopes for CTL respons</li><li>This is one of the new A</li></ul>	ses from 8 HLA-A11 pos 11 epitopes identified thro	using EpiMatrix, these were screen itive FSWs, six were novel, six were ough the streamlined EpiMatrix me and exact matches were rare	re previously identified	
gp160 (310–318)	This epitope was not con	HIGPGRAFY	HIV-1 infection	human (A*3002)	Sabbaj2002b
	<ul> <li>24 epitopes were describ</li> <li>Serial peptide truncations</li> <li>This epitope was newly of</li> <li>Subject 00RCH33 was on B*5301; AETFYVDGA,</li> </ul>	tope responses in HIV-1 ed – 8 were novel, 8 used s were used to define optilefined in this study in HAART had a viral loa RT(437-445), HLA B*4	infected minority women living in a low restricting elements but were mal epitopes for CTL cell lines iso d of 2900 and CD4 count of 727 and 501; and RSLYNTVATLY, p17(76-3/16 (19%) recognized this epitope	previously defined epitopes, and lated from 12 individuals, assaye and also recognized the epitopes Y 86), HLA A*3002	d by a Cr-release
gp160 (310–318)	<ul><li> Epitope name: Env-HY9</li><li> Among HIV+ individuals</li></ul>		HIV-1 infection 6/29 (21%) recognized this epitope	human (A02)	Sabbaj2002b
gp160 (310–323)	<ul><li>Epitope name: p97</li><li>The vaccine vCP205, car</li></ul>	narypox vector, MN gp12	Vaccine dovirion boost Strain: MN, IIIB 0 + Gag/Pro IIIB, with a HIV-1 pseus epitope in immunized BALB/c	eudovirion boost was given to mi	ce;)
gp160 (311–318)			Vaccine e Strain: MN HIV component: to V3 peptides induces mucosal IF		Golding2002a onses in BALB/c mice
gp160 (311–319)	<ul> <li>Transgenic mice expressis Mice given gp160deltaV region of gp120, KLTPL</li> <li>Greater resistance was consistent isolates (VI-06 and 89.6)</li> </ul>	ing a HLA-A2/Kb chime and a broader immune and CVTL, and the C-term resonferred by the gp160delta, and the resistance was considered.	Vaccine ant protein boost Strain: IIIB H ric protein were vaccinated with a f response than those given gp160, w rigion of gp41, SLLNATAIAV. raV3 than the gp160 vaccine to a ch conferred by CD8+ T-cells. 60 vaccine were directed at three V	full length gp160 or with gp160d with increased responses to consentallenge of vaccinia expressing here.	eltaV3, with the V3 loop deleted. rved HLA-A2 epitopes in the C1
gp160 (311–319)	gp120 (312–320 SF2) Vaccine Vector/Type: DN	IGPGRAFHT NA <i>Strain:</i> SF2 <i>HIV o</i>	Vaccine component: gp120	murine $(D^d)$	Selby1997

HXB2 Location	<b>Author's Location</b>	Sequence	Immunogen	Species (HLA)	References
	promoter		-	containing HIV-1 (SF2) gp120 generation containing HIV-1 (SF2) gp120 g	
gp160 (311–319)	<ul><li>CTL were induced by v</li><li>DNA vaccine with prot</li></ul>	vaccine, and restimulated ein boost stimulated both			Barnett1997
gp160 (311–320)	• Murine BALB/c (H-2 <sup>d</sup> )	and macaque both show			Okuda1997 oosted with a peptide including four
gp160 (311–320)		1 0		human d with a full-length env gene product 2 binding, which may relate to the in	
gp160 (311–320)	<ul><li>MIP-1alpha co-inocula</li><li>A MIP-1 alpha express</li></ul>	tion increased IgG1/IgG2	-	murine BALB/c ant: MIP-1alpha ine, as well as the T help response, p	Lu1999 resumably by the MIP-1 alpha
gp160 (311–320)	<ul> <li>Epitope name: P18</li> <li>gp120 encoding DNA of to bicistronic gp120 and</li> <li>Both mono and bicistronic gp120 and</li> </ul>	co-injected with a plasmid GMCSF cloned into the	e same vector and expressed from ed similar CTL responses directed	CD4+ T-cell responses in BALB/c m	Barouch2002 ice relative to the enhanced response eptide RGPGRAFTVTI in murine
gp160 (311–320)	<ul><li>Epitope name: Pep 09</li><li>Plasmid DNA encoding</li><li>Vaccine-induced CTL a</li></ul>	DNA Strain: BRU HI g gp160, tat, rev was give activity produced a low d	Vaccine V component: gp160, tat, rev  n i.m. to immunize BALB/c mice egree of cell lysis of V3-peptide ponses were observed, and weak A	oulsed target cells, using a B (RGPG	Arora2001  RAFVTI) or C (RIGGPGQTFYATG)
gp160 (311–320)		tide does not have the kn	in vitro stimulation an HIV negative donor. own binding motif for A2.1 A2.1 epitope was observed for a r	human (A $*0201$ ) nurine H-2 D $^d$ epitope	Alexander-Miller1996

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
gp160 (311–320)	gp120 (311–320 IIIB) • C. Brander notes this is	RGPGRAFVTI an A*0201 epitope		human (A*0201)	Brander2001
gp160 (311–320)	• Lysis only occurs with I	ed with rec vaccinia gp1 IIB P18 peptide pulsed o	60 IIIB and boosted with purified onto autologous targets; MN, RF, S	human (A2) gp160 SIMI P18 peptides fail to stimulate G 8 did not enhance the MN, RF, or SI	
gp160 (311–320)	<ul> <li>Individual was immuniz</li> <li>P18 MN and RF peptide (IGPGRAFYTT) and the</li> <li>The P18 IIIB peptide do</li> </ul>	ed with rec vaccinia gp1 ss were able to stimulate e P18 RF peptide (KGPO es not cross-react (RGPO	GRVIYAT) could cross-react GRAFVTI in the epitope region)		
gp160 (311–320)	studied in eight HIV-1-in	nfected subjects, two wit cognized in a given indiv	th acute infection, five with chroni	human (A2) and B alleles in individuals who coc c, and one long-term non-progresso e tended to be narrow and never dor	
gp160 (311–320)	<ul> <li>Epitope name: LR25</li> <li>The stability of peptide I SLYNTVATL (p17), SLI (GILGFVFTL), while R</li> <li>The four high-affinity peless than an hour.</li> <li>HLA-A2.1 transgenic mas adjuvants.</li> </ul>	binding to HLA-A2.1 was LNATDIAV (gp41) and GPGRAFVTI and VIYO optides formed stable contice were immunized with QYMDDL induced a stopping to the binding of the properties of	as determined for six HLA-A2.1 p LLWKGEGAV (RT) all bound wi QYMDDL bound with a lower affi mplexes with half-lives ranging be h the six HIV-1 peptides and P30,	murine (A2.1) s adjuvant (IFA), Montanide (ISA 72 septides included in this vaccine stude th high affinity comparable to a influent (relative binding activity = 0.01 stween 8 and 32 hours, while the low as a universal T-helper epitope, with a says - stronger responses were obse	ly – ILKEPVHGV (RT), uenza epitope reference ). v affinity peptides had half lives of n IFA or Montanide or microspheres
gp160 (311–320)		ined as the optimal pepti	Vaccine IV component: V3 de for vaccination, out of RIQRG djuvant, could stimulate Env speci		Nehete1995
gp160 (311–320)	gp160 (318–327 IIIB)  Vaccine Vector/Type: pe  • Successful priming with		Vaccine IV component: V3 pulsed splenic dendritic cells	murine $(D^d)$	Takahashi1993

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
gp160 (311–320)	peptide	to free peptide corresp	Vaccine  HIV component: V3  ponding to the epitope results in stron  ', where the CTL is inactivated by a C	-	
gp160 (311–320)	gp160 Vaccine Vector/Type: D Induction of HIV-1 specexpressing Env boost If IL-12 was also deliver critical parameter for su	RGPGRAFVTI NA, vaccinia HIV co cific CD8 gamma IFN s red as a boost from the ccess with DNA and v	Vaccine omponent: env Adjuvant: IL-12 secreting cells was enhanced when IL viral vector, impairment of the IL-12 accinia vectors used in combination v delivered with the boost involved nitr	murine $(H-2^d)$ $-12$ and Env were given together in the effects was noted, indicating that with immunomodulators	Gherardi2000 n a prime, followed by a VV
gp160 (311–320)	<ul> <li>A study of the DNA vac</li> <li>Intranasal immunization</li> <li>Co-administration of IL</li> <li>Both the CTL (peptide period)</li> </ul>	ccine pCMV160IIIB/R n of BALB/c mice with -15 with IL-12 or IL-2 pulsed targets) and DT	Vaccine  IV component: gp160, rev Adjuvant EV with IL-15 and IL-2 or IL-12 expanded to the IL-15 plasmid induced plasmids did not alter the effect of IL-14 response (injection of peptide into the IL-15 plasmids did not alter the affect of IL-15 plasmids did not alter the effect of IL-15 plasmids did not alter the affect of I	ression plasmids. Ed increased Th1 and CTL respons -15 footpad) to this peptide was monito	ored
gp160 (311–320)	<ul> <li>Class I tetramer staining</li> <li>vp18 had more gamma I</li> <li>The overall decline in C</li> </ul>	expressed in two differ s showed that up to 139 IFN secreting splenocy D8+ T cells in the tran	Vaccine component: V3 rent vaccine vectors and the CTL resp % of the CD8+ splenocytes were p18 rtes and activated CD4+ and CD8+ T sition into memory was 2-3 fold for b memory cytotoxic T cells, although r	specific in the acute response using cells both vectors	g vaccinia, only 4% using Sindbis
gp160 (311–320)	Env (318–327)  • A series of protease and and from within a chime • Lactacystin, a proteason pathway can be used • Both TAP dependent and • 1,10-phenanthrolin (met) • The Tap-independent pathway can be used	eric hepatitis B protein ne inhibitor, partially in d TAP-independent pa tallopeptidases inhibito athway does not involve dominant in mice, and	or) blocks epitope presentation demone e processing by metalloproteinases is presented by multiple human HLA	epitope suggesting both a proteas	ome pathway and an additional
gp160 (311–320)	gp120 <b>Vaccine</b> Vector/Type: va	RGPGRAFVTI accinia HIV compone	Vaccine vat: polyepitope	murine (H-2 <sup>d</sup> )	Hanke1998a, Hanke1998b

HXB2 Location	<b>Author's Location</b>	Sequence	Immunogen	Species (HLA)	References
	types, one murine HIV	epitope and three maca	accine of CTL epitopes expressed toge aque HIV epitopes, delivered in a vacc generating CTL when given i.v. rather	inia virus Ankara (VVA) construct	
gp160 (311–320)	<ul><li>B cell epitope HGP-30</li><li>Vaccine combined HGF</li></ul>	also serves as a CTL ep-30, V3 loop peptide v	Vaccine nt: V3, HPG30, CD4BS Adjuvant: I pitope variants, and CD4 binding site peptide accination enhanced the CTL response		) Hamajima1997
gp160 (311–320)	Low-dosage 8 Br-cAMI	P given in combination	Vaccine IV component: gp160 Adjuvant: 8 E with a DNA vaccine to BALB/c mice and by activation of the CMV promotor	increased IgG and sIgA levels, an	Arai2000 d enhanced Th1, Th2 and CTL
gp160 (311–320)	Anthrax lethal toxin car	n deliver proteins to the g the delivery domain o	Vaccine rax delivery domain HIV component e cytosol of eukaryotic cells of the anthrax protein to gp120 achieve		Goletz1997 processed allowing presentation of
gp160 (311–320)	dependent IL-2 unrespo	onsiveness that might b	in vitro stimulation  CTL with peptide without APCs redue to IL-2Rbeta down regulation by addition of anti-IFN-gamma, TNF-a		• •
gp160 (311–320)	Helicobacter pylori indu	uces Th1 responses ear	Vaccine  HIV component: gp160  ly, but predominantly Th2 responses late to HIV gp160-vaccinia vaccination is		
gp160 (311–320)	• Three class I MHC, H-2	$2^{d,p,u}$ , that differ in seq	Vaccine  HIV component: gp160  uence and serology, cross-present this or strong CTL activity with all three M		Shirai 1997 her haplotypes
gp160 (311–320)	gp160  Vaccine Vector/Type: v.  MVA is an attenuated v  γ IFN and CTL activity  An MVA boost enhance	accinia that can not rep were induced after a s	olicate in mammalian cells – strings of	murine (H- $2^{d17}$ ) CTL epitopes were delivered and	Hanke1998a expressed in a MVA DNA vector
gp160 (311–320)	Env (89.6) Vaccine Vector/Type: v	IGPGRARYAR accinia Strain: 89.6	Vaccine HIV component: gp160	murine BALB/c (H-2D	) Belyakov1998b

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References	
	vector for this vaccine s • A single intrarectal much	tudy cosal immunization resu	MVA), an attenuated vaccina which halted in long lasting mucosal CTL resing mucosal CTL as replicating recom	ponses and production of proinflan		
gp160 (311–320)		cosal CTL response was	Vaccine HIV component: V3 s studied – an HIV peptide immunogoing Abs did not play a role, demonstr		ressing vaccinia in a murine	
gp160 (311–320)	gp120 (MN)  Vaccine Vector/Type: B  B. abortus-peptide conj		Vaccine gate pecific CTL response in CD4+ lymph	murine (H-2 $\mathbf{D}^d$ ) nocyte depleted mice	Lapham1996	
gp160 (311–320)	<ul> <li>A good HIV-1 Env imm</li> <li>5'splice-donor site sequ</li> <li>Administration of monor for a CTL response com</li> </ul>	nune response using nor ence and the presence oc ocistronic RAd501 expr parable to that induced	Vaccine us Strain: IIIB HIV component: In-replicating adenovirus vectors in Base of Rev essing env and RAd46 expressing rev by the bicistronic virus RAd142 TL response, but no humoral response	ALB/c mice is dependent upon the presulted in a positive CTL response	se, but required two immunizations	
gp160 (311–320)	gp120 (MN)  Vaccine Vector/Type: B  B. abortus-peptide conj		Vaccine gate pecific CTL response in CD4+ lymph	murine (H-2 $\mathbf{D}^d$ ) nocyte depleted mice	Lapham1996	
gp160 (311–320)	gp160 (318–327 IIIB) • XGPXRXXXXI are cri	RGPGRAFVTI tical for binding, consis	Peptide-HLA interaction tent with H-2D $^d$ motif XGPX(RKH)		Takeshita1995	
gp160 (311–320)	Env RGPGRAFTVTI Vaccine murine (H-2D <sup>d</sup> ) Hanke1999a, Hanke1999b  Vaccine Vector/Type: DNA HIV component: V3  • Vaccinated mice elicited a CTL response to a gene gun-delivered multiepitope vaccine to two epitopes studied that are known to elicit CTL in mice:  SYIPSAEKI from Plasmodium berghei and RGPGRAFTVTI from HIV-1 Env  • Different vaccination protocols were tested and it was found that a gene gun mediated delivery followed by an MVA boost was as good as i. m. immunization followed by a MVA boost – this is advantageous as gene gun delivery requires far less DNA than i.m. DNA priming  • CTL activity was high (60% - 70% specific lysis at effector target) when vaccinated with a single gene gun immunization and an MVA boost, and improve with two gene gun vaccinations					
gp160 (311–320)			in vitro stimulation etitive restimulation of BALB/c splee epitope within the previously describe			

HXB2 Location	<b>Author's Location</b>	Sequence	Immunogen	Species (HLA)	References
			moval of the 2 C-terminal residues ( r target cell presentation of RIQRGI		1-converting-enzyme) in sera to
gp160 (311-320)	<ul> <li>Epitope name: p18-110</li> <li>BALB/c mice were vac Gag in vaccinia virus (</li> <li>Primary CTL response the CD8+ cells were te</li> <li>Vaccinating with GagE Gag-rVSV or Env-rVS</li> </ul>	ecinated with rec vesicular VVs). The primary resp is to the immunodominant tramer positive, and this env-rVSV carrying both V alone.	Vaccine (VSV), vaccinia Strain: Env, IIIB ar stomatitis virus (rVSV) expressing sonse was determined by cell lysis, content Env (RGPGRAFVTI) epitope peal response was 6-fold higher than the Gag and Env allowed recognition of d CTL responses that were strong by	g either HIV-1 Gag, Env, or both, a ytokine production and tetramer st ked 5-7 days after intraperitoneal v response to Env-rVV. both HIV-1 proteins, but at reduce	and compared to using rec Env and taining. vaccination with Env-rVSV, 40% of ed levels compared to either
gp160 (311-320)	<ul> <li>Epitope name: p18-I10</li> <li>BALB/c mice were vacand recall responses we</li> <li>Seven months after vacmemory phenotype, CI</li> <li>Env in rec vaccinia vim (expressing CD62L-Lc</li> <li>A prime with Env-rVS splenocytes being Env</li> <li>A Gag-rVSV or EnvGathe fraction of IFN-gar</li> </ul>	ecinated with rec vesicular ere studied by tetramer streination with Env-rVSV D44-Hi positive.  Its (Env-rVV) elicited a solo, and capable of IFN-gaV and heterologous boost specific memory cells 15 ag-rVSV prime and with the man producing cells was	taining and IFN-gamma production. 6% of the CD8+ cells were tetrame trong recall response, with up to 450 mma production. st of Env-rVV gave remarkably high	g either HIV-1 Gag or Env, or both er positive for the immunodominar % to the CD8+ T-cell population to levels of memory cells, with appro- g-rVV boost combination gave 40% bous vector prime-boost combination	a, and retention of memory responses at Env epitope; these cells had a etramer positive and activated oximately 1/3 of the CD8+ % tetramer positive CD8+ cells, but on showed a profound benefit.
gp160 (311–320)	<ul> <li>Cholera toxin (CT) is a BALB/c mice V3 pepti</li> <li>Peptide vaccine induce activity than any single</li> <li>Combinations of cytok immunization was obse</li> <li>Nasal immunization was</li> </ul>	potent adjuvant used in des to attempt to replace d CTL activity was signi eytokine. ins could be more potent erved with IL-lalpha plu ith HIV peptide in the pro- , and was associated with	CT as a potent adjuvant. Ificantly increased by IL-1alpha, IL- It that CT as an adjuvant. The highests IL-18 as adjuvant. IL-12 and GM- IL-14 that GM- IL-19 the pregulation of MHC class II and	nans, so combinations of cytokins 18, and GMCSF given alone as act tetramer binding of H-2Dd peptic CSF induced IFN-gamma-secreti	were used in nasal immunization of ljuvant, but CT gave more potent CTI de-specific PBMC after nasal ng cells in the cervical lymph node,
gp160 (311–320)	gp160 (318–327 IIIB)	RGPGRAFVTI	Vaccine a boost Strain: IIIB HIV compon	murine (H-2D <sup>d</sup> )  ent: gp160 Adjuvant: PLG-micr	Wierzbicki2002 roparticle, liposome, beta-glucan

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
	with addition of muring immunodominant epito	e IL-2/Ig plasmid or lenting pe RGPGRAFVTI, but d	nan-associated liposomes. Lentinar	n increased CTL activity as measur acreased both type I and II activitie	of rec gp160 vaccinia vectors (rVV) red by Cr-release assays against the s, and increased Env specific CTL and
gp160 (311–320)	<ul> <li>Epitope name: P18</li> <li>Immunostimulatory see</li> <li>Intranasal immunization than immunizing with sonly i.n. immunization</li> <li>The highest mucosal C conjugate.</li> </ul>	quences (ISS), also known n (i.n.) of BALB/c mice was p120 and separate ISS may gave IgA responses. TL activity in both the Land CTL responses follow	n as CpG motifs, stimulate innate i was more effective than intraderma solecule – increased IgG1, IgG2a, mina Propria and the Peyer's Patcl		cific immune responses. p120-ISS conjugate was more potent 1-beta production was observed, and al delivery with the gp120/ISS
gp160 (311–320)	<ul> <li>Epitope name: I10</li> <li>During acute infection,</li> <li>Recently stimulated CT with antigenic peptide</li> <li>Restimulated CTL shows</li> </ul>	CL from BALB/c mice value or H-2Dd/peptide tetrame wed an upregulation of Clarapoptosis was inhibited	t in "clonal exhaustion", a depletio ecinated with gp160-vaccinia showers. D3-chain phosphorylation in comp	ved a dose- and time-dependent ind	Takahashi2002  luction of apoptosis when stimulated et cells, indicative of TCR-mediated ecific for the ERK1/ERK2 MAPK
gp160 (311–320)	<ul> <li>Epitope name: MNT10</li> <li>During acute infection,</li> <li>Recently stimulated CT with antigenic peptide</li> <li>Restimulated CTL shows</li> </ul>	high doses of virus result TL from BALB/c mice value or H-2Dd/peptide tetrame wed an upregulation of Class, apoptosis was inhibited	t in "clonal exhaustion", a depletio ecinated with gp160-vaccinia showers. D3-chain phosphorylation in comp	ved a dose- and time-dependent ind	Takahashi2002  luction of apoptosis when stimulated et cells, indicative of TCR-mediated ecific for the ERK1/ERK2 MAPK
gp160 (311–320)	<ul><li>An HIV-1 Env vaccine</li><li>The rapidly degraded f</li><li>The rapidly degraded f</li></ul>	orm rapidly stimulated Co			Tobery 1997

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References	
gp160 (312–320)	<ul> <li>BALB/c mice were vacc LR150, JY1, RF, MN, I</li> <li>Intraperitoneal immuniz immunization. Intraperi</li> <li>The immunodominant rethe response by Elispot</li> <li>Low CTL responses were</li> </ul>	cinated with a polyepitope V3 v BRVA and IIIB with 5-aa linker ation elicited the strongest V3- toneal immunization conferred esponse was directed against the was GPGRAFVTI).	Vaccine IIB, JY1, RF, MN, BRVA HIV convaccine in a fowlpoxvirus carrying or setween, fused to the N-term of prespecific IFN-gamma response in specific IFN are recombinant vaccini at IIIB peptide (the IIIB immunizing SRGIRIGPGRAILAT) and RF (RKIVIYAT), or MN (RKRIHIGPGRAF	concatonated 15 mer sections of 64K protein from Neisseria lenocytes, compared to intrata virus challenge model. g peptide was SIRIQRGPGR	of the V3 loops of HIV-1 isolates meningitidis. venous and subcutaneous	
gp160 (314–322)	gp120 (314–322) • Study of peptide binding	GRAFVTIGK g to HLA-B27	Peptide-HLA interaction	human (B27)	Jardetzky1991	
gp160 (337–361)		KWNNTLKQIDSKLREQFGN NKTIIF accinia HIV component: gp16 obtained from an HIV-1 vaccin	60	human (CD4+ CTL)	Johnson1994a	
gp160 (339–354)		NNTLKQIDSKLREQFG accinia HIV component: gp16 m LAI IIIB gp160 vaccinees	Vaccine 60	human (CD4+ CTL)	Johnson1994b	
gp160 (340–348)	<ul> <li>HLA-A11 is very command CTL responses were</li> </ul>	8 7-1 exposed persistently serones non in this population, and was be found in 8/8 HIV+ controls, a	HIV-1 infection  gative (HEPS) female sex workers in enriched among the HEPS sexwork and 0/9 HIV- women that were not e y subject 053 who carried HLA-A1	ers – weak CTL responses w exposed		
gp160 (340–348)	<ul> <li>This epitope was weakly reactive in HIV+ control study subject 053 who carried HLA-A11</li> <li>gp120 (346–354 CM243 RVLKQVTEK HIV-1 infection human (A11) Bond2001 subtype CRF01)</li> <li>HLA-A11 CRF01 (called subtype E in Bond et al.) epitopes were identified that stimulated CTL from HIV+ female sex workers (FSW) from Northern Thailand, of whom more than half were HLA-A11 positive</li> <li>77 possible HLA-A11 epitopes were first defined using EpiMatrix, these were screened for binding to A11 finding and 26 bound, and 12 of these were epitopes for CTL responses from 8 HLA-A11 positive FSWs, six were novel, six were previously identified</li> <li>This is one of the new A11 epitopes identified through the streamlined EpiMatrix method, and 2/8 tested FSWs recognized it</li> <li>This epitope was not conserved in other subtypes, and exact matches were rare</li> </ul>					
gp160 (340–349)	An HIV-1 rgp120 vaccin		Vaccine 6.ID HIV component: gp120 cellular immune response in sibling epitope	-	Balla-Jhagjhoorsingh1999a of the two made a detectable CTL	

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References		
gp160 (369–375)	gp120 (374–380 BRU) • Defined through blockin	PEIVTHS g CTL activity, and Er	HIV-1 infection av deletions	human (A2)	Dadaglio1991		
gp160 (375–383)	gp120 (379–387 LAI)  • C. Brander notes this is	SFNCGGEFF a B*1516 epitope	HIV-1 infection	human (B*1516)	Brander2001		
gp160 (375–383)	<ul> <li>Detection of CTL escape infants</li> </ul>	e mutants in the mothe at gave a positive, thou	HIV-1 infection  In the context of mother-to-infant transmission  It was associated with transmission, but the Context of the	CTL-susceptible forms of the	Wilson1999a ne virus tended to be found in infected		
gp160 (375–383)	<ul> <li>individuals treated durin</li> <li>The breadth and specific individuals with primary (Group 3), using 259 ove</li> <li>Previously described and</li> </ul>	g chronic infection city of the response way infection but post-ser- erlapping peptides spand d newly defined optima	HIV-1 infection ed in a narrower CTL response, stronger T h s determined using ELISPOT by studying 19 oconversion therapy (Group 2), and 10 indivening p17, p24, RT, gp41, gp120 and Nef all epitopes were tested for CTL response cTL response to this epitope broken down by	9 individuals with pre-serocyiduals who responded to H	conversion therapy (Group 1), 11 AART given during chronic infection		
gp160 (375–383)	• Predominant form in pro	oviral DNA of the indiv	HIV-1 infection that recognize this epitope in the context of vidual with B15 restricted CTL was SFTCG-NCRGEFF) from the B15 donor was greatly	GEFF and this was recogni-			
gp160 (375–383)	gp120 (376–383 PV22) • C. Brander notes this is		HIV-1 infection	human (C*0401)	Brander2001		
gp160 (375–383)	gp120 SFNCGGEFF HIV-1 infection human (Cw*0401, Bird2002 Cw*0407)  • 4/123 (2 HIV-1 positive, 2 HEPS) Kenyan female sex workers carried the novel allele HLA Cw*0407.  • HLA Cw*0407 did not differ from Cw*0401 in the region associated with the binding pocket, and Cw*0407 was shown to cross-present a previously defined Cw*0401 epitope, SFNCGGEFF (gp120).						
gp160 (375–383)	gp120 (376–383 PV22) • Conserved epitope	SFNCGGEFF	HIV-1 infection	human (Cw4)	Johnson1993		
gp160 (375–383)	gp120 (376–383 PV22) • Longitudinal study of ep	SFNCGGEFF bitope variation in vivo	HIV-1 infection	human (Cw4)	Wolinsky1996		
gp160 (375–383)	gp120 (376–383)  • ELISPOT was used to st	•	HIV-1 infection, HIV-1 exposed seronegative a panel of 54 predefined HIV-1 epitopes in 9		Kaul2001a ntly seronegative (HEPS) and 87		

HIV-1-infected female Nairobi sex workers

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
	reduced risk of infection women  43/91 HEPS women have Among HLA-Cw4 work	on, and there was a shift ad CD8+ responses and men, 1/2 HEPS and 10/	r, and focused on different epitopes with in the response in the HEPS women undetection of HIV-1-specific CTL in HI 11 HIV-1 infected women recognized to this epitope in 6 of the 10/11 response.	pon late seroconversion to epitop EPS women increased with the d this epitope	uration of viral exposure
gp160 (376–383)	deletion in CCR5	osure to both HIV-1 and	posed African female sex workers in G d HIV-2, CTL responses to B35 epitopotivity [Johnson1993]		
gp160 (376–384)	<ul> <li>FNCRGEFFY and FNO from the host</li> </ul>	CRGGFFY are major a	HIV-1 infection s derived from two different donors and minor autologous variants in one of re present in the other donor, and the C		
gp160 (376–384)		pe mutants in the mothe	HIV-1 infection in the context of mother-to-infant transer was associated with transmission, but		Wilson1999a  the virus tended to be found in infected
gp160 (376–384)	CD8+ cell IFNgamma • In general, during the f specificities that were r HIV-specific responses	production to measure first month of treatment not previously detectable diminished	HIV-1 infection  les was tested in 14 HIV+ patients froi responses viral load decreased and frequencies of e were newly detected, as were CMV sonse: increases or decreases in pre-exis	of HIV-specific CTL tripled and be specific CD8+ PBL – but with co	proadened – eight new HIV ontinued viral suppression,
gp160 (376–384)	CD4 proliferative responsible HAART had no HIV spundetectable  One of the 7/8 study su Patient SC19(HLA A1	onses and were able to a pecific CD4 proliferation bjects that were HLA I 1/12, B8/44, Cw06/070	HIV-1 infection  fection (three with sustained therapy, to maintain a CTL response even with under responses and lost their CTL responses are recognized this CTL epitope 11, DR3/7, DR52/53, DQ 2/8) had a CT GGEFFY that declined during therapy in the company in	detectable viral load – three patieses when HAART was eventually	ents that had delayed initiation of y given and their viral loads became

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
gp160 (376–384)	gp160  ◆ Epitope name: FNC	FNCGGEFFY	HIV-1 infection	human (B8)	Oxenius2002b
	period including therapy	with standard treatmen	), Oxenius2001a] in an IFNgamma Elispot as t interruptions (STI). opes, but there was no correlation between C		-
gp160 (376–387)	gp120 (381–392 BRU)  • Defined through blocking	KNCGGEFFYCNS ag CTL activity, and Env	HIV-1 infection deletions	human (A2)	Dadaglio1991
gp160 (377–387)	gp120 (377–387) • Peptides recognized by or	NSGGEFFYSNS class I restricted CTL ca	n bind to class II	human (A2)	Hickling1990
gp160 (383–391)	Phe, Leu or Ile at the C t  This peptide induced CT	term) – 53 of the 59 pep TL in 1/4 HIV-1+ people			
gp160 (410–429)	<ul> <li>CTL were studied throughter</li> <li>Human CD4+ CTL clonicells – natural variants of the Low concentrations of the low concentratio</li></ul>	gh PBMC stimulation in the (Een217) is an MHC of the epitope resulted in the HXB2-derived variantiantials.	INMWQE in vitro stimulation in vitro by gp120 pulsed autologous monocyte class II HLA-DRA restricted CTL clone that an anergic response it (GSDTITLPCRIKQIINMWQK) induced TNTNITLQCRIKQIIKMVAG) and Z3 (CTG)	can lyse antigen presenting Conference	centrations could induce proliferation
gp160 (416–424)	<ul> <li>Med. 2:405, 1996;Lance</li> <li>15% of Japanese popula</li> <li>Of the 172 HIV-1 peptid positive individuals, and</li> </ul>	et 22:1187, 1986;Hum Intions carry HLA-B51 where with HLA-B*5101 and six were properly process.	HIV-1 infection low progression to AIDS, while HLA-B35, - mmunol 22:73, 1988;Hum Immunol 44:156, hile HLA-B27 and -B57 are detected in less nchor residues, 33 bound to HLA-B*5101, so essed among B subtype sequences, LPCRIKQII is a	1995) than 0.3% even of these peptides we	
gp160 (416–424)	gp160 (416–424 LAI) • C. Brander notes this is	LPCRIKQII a B*5101 epitope		human (B*5101)	Brander2001
gp160 (416–424)	gp120 (378–385)	LPCRIKQII	HIV-1 infection, HIV-1 exposed seronegative	human (B51)	Kaul2001a
	ELISPOT was used to st HIV-1-infected female N	•	panel of 54 predefined HIV-1 epitopes in 91	HIV-1-exposed, persister	ntly seronegative (HEPS) and 87

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
gp160 (416–429)	gp120 (410–429 H3DCG) • CD4+ CTL restricted by	LPCRIKQFINMWQE  class II HLA-DR4, targets prim	HIV-1 infection and by CD4 mediated uptake of gp12	human (DR4 CD4+)	Siliciano1988
gp160 (416–435)	gp120 (421–440 LAI) • Defined through blockin	LPCRIKQFINMWQEVGKAMY g CTL activity, and Env deletion		human (A2)	Dadaglio1991
gp160 (419–427)	gp120 (424–432 HXB2) • C. Brander notes that thi	RIKQIINMW s is an A*3201 epitope in the 19	199 database	human (A*3201)	Harrer1996b
gp160 (419–427)	gp120 (419–427 HXB2) • C. Brander notes this is a			human (A*3201)	Brander2001
gp160 (419–427)	<ul><li>95 optimally-defined per</li><li>1/11 of the A2+ individu</li></ul>	otides from this database were usuals was A29 and responded to R	HIV-1 infection acted to SLYNTVATL, calling into consect to screen for INFγ responses to RIKQIINMW, and another respondent peptide 32 gp120 419–427 and the	other epitopes r was A32 and these are tho	ught to be presenting molecules
gp160 (419–427)			HIV-1 infection uals, and in both cases strain-specific N and RF were KIKQFINMW and F		
gp160 (419–427)	gp120 (420–428)  • This epitope is processed	RIKQIINMW d by a TAP1/2 dependent mecha	HIV-1 infection nism	human (A32)	Ferris1999
gp160 (419–427)	<ul> <li>CTL epitopes (http://hiv.)</li> <li>60 epitope responses we magnitude of the respondence of the res</li></ul>	and lymph node (LN) CD8+ T-cell-web.lanl.gov/content/hiv-db/RE re detected in both PB and LN sees was similar in LN and PB, but in the LN.  It the thin the patients studied, the responses in the PB became unfollowing HAART induced result the PB, and the addition of 9 novesponses were shown for 4 indiv PB and LN samples, while a thin	the magnitude of the CD8 T-cell responses to 5/26 in the detectable, in contrast to 5/26 in the detectable in increased viremia accompanies well epitope responses.	th person's class I HLA alleleditional 8 responses were detected the LN is lower so the number onse was decreased in both LN.  The detect response to epitope B4-V10(gp120) was only detected.	es. etected only in LN. The total ber of HIV-specific cells per million LN and PB, but more dramatically detection of 13 epitopes that had 4-AW11(p24) and also responded to ed in the LN sample. Patient D
gp160 (421–435)	gp120 (421–440 LAI) • Defined through blockin	KQFINMWQEVGKAMY g CTL activity, and Env deletion	HIV-1 infection	human (A2)	Dadaglio1991

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
gp160 (421–436)	gp120 (428–443 IIIB) • CTL and T helper cell re	KQIINMWQEVGKAMYA eactivity in healthcare workers	HIV-1 exposed seronegative exposed to HIV	human	Pinto1995
gp160 (421–436)	CTL response may acco		HIV-1 infection zed with adenovirus-HIV-1 MN gp equent HIV-1 SF2 challenge in a chi peptide (T1)		Lubeck1997 ing antibodies
gp160 (421–436)	gp120 (428–443 IIIB)  • Helper and cytotoxic T of	KQIINMWQEVGKAMYA cells can be stimulated by this p	HIV-1 infection peptide (T1)	human (A2)	Clerici1991a
gp160 (421–436)	gp120 (428–443 IIIB)  • Helper and cytotoxic T of	KQIINMWQEVGKAMYA cells can be stimulated by this p	HIV-1 infection peptide (T1)	human (A2)	Cease1987
gp160 (421–436)		KQIINMWQEVGKAMYA accinia <i>Strain:</i> IIIB <i>HIV con</i> iple class I molecules can preso		murine $(H-2^{a,b,f})$	Shirai1992
gp160 (432–451)	A VLP is a non-infection     V3+CD4 linear domains     neutralizing response occupintervenous challenge was a compared to the compared to	Gag and Env specific CTL we	nent: gag, gp120, V3, CD4BS  abled from HIV Pr55 gag – macaque  are stimulated in each case, and Aba  anot V3+CD4 – despite the CTL and  acck	response to gag and gp120	was elicited, but the gp120
gp160 (434–443)	gp120 (431–440)  Vaccine Vector/Type: pe  Tolerization of CTL resp	MYAPPIGGQI eptide conse with continued administr	Vaccine ration of soluble peptide	murine (H-2K <sup>d</sup> )	Duarte1996
gp160 (435–443)	<ul> <li>Epitope name: p41A</li> <li>Monkeys that received the responses, stable CD4+ mortality by day 140 aft</li> <li>IL2/Ig consisting of interior as DNA – both enhand</li> <li>Responses to a dominant tracked and had good duty</li> </ul>	the DNA vaccines augmented w T-cell counts, preserved virus-ser challenge – monkeys that go rleukin-2 (IL-2) for immune sti ce the CTL response to vaccina t Mamu A*01 gag epitope SIV trability prior to challenge, and detected in the vaccinated mon- reserved CD4+ T-cells	Vaccine onent: SIVmac239 Gag and HIV-1 with IL-2/Ig were infected when charspecific CD4+ T-cell responses, low at a sham vaccine had high viral load imulation, and the Fc portion of immation, DNA IL2/Ig giving the most if Gag p11C (CTPYDINQM) and a sthe higher the prechallenge peak plankeys prior to challenge, and compared	llenged with pathogenic SF to undetectable viral loads d, progressed to disease, an nunoglobulin G (IgG) for s intense response subdominant epitope HIV-11C CTL response, the low	HIV-89.6P, but had potent CTL, and no evidence of disease or d were half were dead by day 140 tability, was delivered either as protein Env p41A (YAPPISGQI) were er the post-challenge viral load

	Author's Location	Sequence	Immunogen	Species (HLA)	References
gp160 (435–443)	Env (89.6)  Vaccine Vector/Type: v  • Epitope name: p41A	YAPPISGQI vaccinia <i>Strain:</i> 89.6 <i>HIV c</i>	Vaccine component: SIVmac239 Gag/Po	Rhesus macaque ol and HIV-1 89.6P Env Adjuvan	Barouch2001b at: IL2/Ig
	<ul> <li>animals, and 1/4 made</li> <li>The animals were infecting preservation of CD4+ 7</li> </ul>	a response to the HIV Env epi ted when challenged with patl	tope YAPPISGQI, as determined thogenic SHIV-89.6P, but had post, and no evidence of disease or 1	d by tetramer staining and chrom	Ab responses upon challenge, partial
gp160 (435–443)		YAPPISGQI	SHIV infection	Rhesus macaque (Man A*01)	-
			es of response to the SIVmac epi e STPPLVRLV and HIV-1 env e	itope gag p11C,C-M (CTPYDING epitope YAPPISGQI	QM) but only a fraction of A*01
gp160 (435–443)	gp41 (89.6)	YAPPISGQI	SHIV infection, Vaccine	Rhesus macaque (Man A*01)	nu Barouch2001a
	<ul> <li>Epitope name: p41A</li> <li>Mamu-A*01+ rhesus n and a subdominant resp</li> <li>The binding affinities a</li> <li>Monkeys vaccinated with</li> </ul>	nonkeys infected with SHIV-8 bonse to HIV-1 Env p41A epite re the same for the two Mamu ith MVA vectors carrying SIV observed and the response to p	9.6 and SHIV-HXBc2 make imrope (YAPPISGQI)  A*01 epitopes, so that is not will gag/pol and HIV-1 env showed	hat dictates the dominance. the same p11C epitope dominance	Gag p11C epitope (CTPYDINQM)  te and p41A epitope subdominance, nd HIV genes under CMV promotor
		RCSSNITGLL		human (B56)	De Groot2001
gp160 (444–453)	• A subset of the potentia B58) epitopes were ide	was used in conjunction with al epitopes was identified that ntified that could stimulate IFI	could bind to the appropriate HIN $\gamma$ production in an ELISPOT a	entify conservered regions of HIV LA-allele, and 15 of the predicted assay	
gp160 (444–453) gp160 (489–508)	<ul> <li>The program Epimatrix</li> <li>A subset of the potentia B58) epitopes were ide</li> <li>RCSSNITGLL was nev</li> <li>Env (496–506 BH10, LAI)</li> </ul>	was used in conjunction with al epitopes was identified that ntified that could stimulate IFI wly defined as an epitope in th VKIEPLGVAPTKAKRRVV	could bind to the appropriate HI N $\gamma$ production in an ELISPOT a is study, and was shown to stime	entify conservered regions of HIV LA-allele, and 15 of the predicted assay ulate an ELISPOT response, desp human	That might serve as epitopes B7 superfamily (HLA B7, B8, and
	<ul> <li>The program Epimatrix</li> <li>A subset of the potentia B58) epitopes were ide</li> <li>RCSSNITGLL was nev</li> <li>Env (496–506 BH10, LAI)</li> <li>This study employs an</li> <li>This CTL epitope (the</li> </ul>	was used in conjunction with al epitopes was identified that ntified that could stimulate IFI wly defined as an epitope in th VKIEPLGVAPTKAKRRVV antigenic similarity matrix to	could bind to the appropriate HI Nγ production in an ELISPOT a is study, and was shown to stime /QR HIV-1 infection compare HIV-1 antigenic determn similarity to a human protein or	entify conservered regions of HIV LA-allele, and 15 of the predicted assay ulate an ELISPOT response, desp human	7 that might serve as epitopes B7 superfamily (HLA B7, B8, and ite not detectably binding to HLA-B

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
gp160 (489–508)	gp120 (494–513 BRU) • Defined through blockin	VKIEPLGVAPTKAKRRVVQR g CTL activity, and Env deletions		human (A2)	Dadaglio1991
gp160 (519–543)	gp41 (519–543)	FLGFLGAAGSTMGAASLTL- TVQARC	HIV-1 infection	human (Cw7)	Nehete1998a
	<ul><li>CTLs – Cw7 specific CT</li><li>HLA-C antigens are exp</li><li>HLA-C confers protection</li></ul>	CL were found against three pepti ressed on lymphoid cells to a less on against lysis by natural killer c	HIV+ individual were studied and for des, including this one ser extent, 10% of either HLA-A or rells and by non-MHC-restricted effor an expression and class I expression in	HLA-B ector T cells and Cw7 direc	tly governs this resistance to lysis –
gp160 (552–571)	<ul><li>each HIV protein.</li><li>Nef and p24 had the high</li></ul>	hest percentage of reactive peptid	HIV-1 infection 105 HIV-1 positive Botswanans; Eles, and p24 had the highest magnitutides from among over 350 tested spanning to the spanning of the spanning of the spanning over 350 tested spanni	ide of HIV-1 responses.	Novitsky2002 m between 55 and 64 subjects for
gp160 (557–565)			HIV-1 infection ndation ARIEL Project, a mother-in riants, were found in mother and are		Wilson1996 y
gp160 (557–565)	• 95 optimally-defined per	otides from this database were use	HIV-1 infection cted to SLYNTVATL, calling into qued to screen for INFγ responses to cook, B78, and responded to RAIEAQQ	ther epitopes	
gp160 (557–565)	<ul> <li>Detection of CTL escape infants</li> </ul>		HIV-1 infection ext of mother-to-infant transmission ciated with transmission, but the CT	human L-susceptible forms of the	Wilson1999a virus tended to be found in infected
gp160 (557–565)	• This CTL epitope (the H		HIV-1 infection  pare HIV-1 antigenic determinants v  nilarity to a human protein overlapp  LRLMEDQQHMA.		Maksiutov2002  AQQHLL) has similarity with
gp160 (557–565)	gp41 (557–565 IIIB)  • C. Brander notes this is a	RAIEAQQHL a B*5101 epitope	HIV-1 infection	human (B*5101)	Brander2001
gp160 (557–565)	gp41 (557–665) • Epitope name: E3 • The epitope was recogni	RAIEAQQWQ zed by patient 246#1 in a study o	HIV-1 infection of the effects of therapy escape muta	human (B*5101) tions on CTL recognition	Samri2000

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
gp160 (557–565)	gp41 (557–565 IIIB)  • HIV IIIB proteins were  • KAIEAQQHL, a varian  • RAIEAQQHM, a varian  • RAIDAQQHL, a varian  • RAIKAQQHL, a varian	t found in HIV-1 NY5 nt found in HIV-1 JRC t found in HIV-1 ETR	SF, was also recognized , was also recognized	human (B51) workers accidentally infected w	Sipsas1997 vith HIV-1 IIIB
gp160 (557–565)	gp41 (557–565)  • This epitope can be produced by the produced	RAIEAQQHL cessed by a TAP1/2 de	HIV-1 infection ependent mechanism	human (B51)	Ferris1999
gp160 (557–565)	CD4 proliferative respo HAART had no HIV sp undetectable	nses and were able to ecific CD4 proliferation	HIV-1 infection  affection (three with sustained therapy, two maintain a CTL response even with unde we responses and lost their CTL responses epitope but none were HLA B51+	etectable viral load – three patie	ents that had delayed initiation of
gp160 (557–565)	gp41 (47–55)  • One of the 51 HIV-1 epi HLA alleles	RAIEAQQHL itopes selected by Ferr	HIV-1 infection rari et al. as good candidate CTL epitopes	human (B51) s for vaccines by virtue of bein	Ferrari2000 g conserved and presented by common
gp160 (557–565)	<ul> <li>CD8+ cell IFNgamma p</li> <li>In general, during the firspecificities that were not HIV-specific responses</li> </ul>	production to measure rst month of treatment ot previously detectab diminished	HIV-1 infection  eles was tested in 14 HIV+ patients from responses  viral load decreased and frequencies of le were newly detected, as were CMV sponse: increases or decreases in pre-existing	HIV-specific CTL tripled and becific CD8+ PBL – but with co	oroadened – eight new HIV ontinued viral suppression,
gp160 (557–565)	<ul><li>assays of target cells ex</li><li>CTL from subject US10</li></ul>	s were found in PBM0 pressing recombinant 01, infected with a clad	HIV-1 infection C isolated from individuals infected with vaccinia viruses expressing HIV-1 gag, ede B virus, displayed broad cross-reactiving the C-term position that was tolerated.	nv, nef and pol from many clac ty to HIV-1 clade A, B, C, D, O	les. CRF01_AE, F G, recognized this
gp160 (565–573)	for the A3 supertype) w • Progressors had memor • A positive correlation be	hile the effector cells y resting CD8+ T-cells etween effector CD8+	HIV-1 infection g memory resting CD8+ T-cell responses of long-term nonprogressors recognized a s that recognized far fewer epitopes than T-cells and plasma viremia and a negative ty of LTNPs to clear virus	far fewer epitopes LTNPs	es tested, (18 for the A2 supertype, 16

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References				
	• This epitope can bind for	our of the five HLA-A2 supertype	s alleles (A*0201, A*020 2, A*0203	, A*0206 and A*6802)					
gp160 (570–589)	gp41 (571–590 LAI)	VWGIKQLQARILAVERYLKD	Vaccine	human (CD4+ CTL(DR-1))	Kent1997a				
	<ul> <li>Vaccine Vector/Type: vaccinia prime with rgp160 boost Strain: LAI HIV component: gp160</li> <li>VWGIKQLQARILAVERYLKD, present in HIV-1 LAI, was the immunizing strain</li> <li>VWGIKQLQARVLAVERYLKD, present in HIV-1 MN, was also recognized</li> </ul>								
	• Lysis of the target cells	by CD4+ CTL was inhibited with	the autologous strain that infected to the addition of the peptide representative functions of the CD4+ CTL clor	ing the autologous strain					
	• The behavior of the auto the ability of CTL to rec		mechanism for vaccine failure since	the infecting virus not only	escapes CTL activity, but inhibits				
gp160 (572–590)	gp41 (572–590 BRU)  Vaccine Vector/Type: re  CD4+ CTL	GIKQLQARILAVERYLKDQ combinant protein Strain: BRU	Vaccine  J. HIV component: gp160	human (DPw4.2)	Hammond1991				
gp160 (575–599)	gp41 (575–599 IIIB)	QLQARILAVERYLKDQQLL- GIWGCS	HIV-1 infection	human (B14)	Jassoy1992				
450 (700 700)		CTL clone derived from CSF							
gp160 (583–592)	gp41 (583–592 PV22) • HIV-1 specific CTLs rel	VERYLKDQQL ease $\gamma$ -IFN, and $\alpha$ - and $\beta$ -TNF	HIV-1 infection	human (B14)	Jassoy1993				
gp160 (584–592)	gp41 (584–592)  ◆ Study of cytokines relea	ERYLKDQQL seed by HIV-1 specific activated C	HIV-1 infection TTL	human	Price1995				
gp160 (584–592)	restricted CTL response		HIV-1 infection ion controlled their viral infection we ized this peptide	human ell and mounted an early, st	Borrow1994 rong HIV-1 specific MHC				
gp160 (584–592)	gp41 (584–592 HXB2) ERYLKDQQL HIV-1 infection human (A32, B14) Mollet2000  • Epitope name: E4  • A panel of 16 epitopes covering 15 class I alleles was tested in 14 HIV+ patients from an unselected Caucasian population treated with HAART, using CD8+ cell IFNgamma production to measure responses								
	<ul> <li>In general, during the firspecificities that were not HIV-specific responses</li> </ul>	rst month of treatment viral load of the previously detectable were new diminished	decreased and frequencies of HIV-specific Courses or decreases in pre-existing responses	D8+ PBL – but with contin	nued viral suppression,				
gp160 (584–592)			HIV-1 infection kers caused a functional deficiency in tetramer assays, while not affecting						

HXB2 Location	<b>Author's Location</b>	Sequence	Immunogen	Species (HLA)	References
			esponses in 4 HIV-1 exposed persis n 2 HEPS subjects were shown to h		
gp160 (584–592)	gp41 (584–592 PV22) • C. Brander notes this is	ERYLKDQQL a B*1402 epitope	HIV-1 infection	human (B*1402)	Brander2001
gp160 (584–592)			HIV-1 infection t the mediators of both the cytolytic used as markers) anti-viral response		Wagner1998a ne marker) and non-cytolytic (HIV-1 'L's cytotoxic granules
gp160 (584–592)	that by day 260 CTL act  ERYLKDQQL was the of Sporadic breakthrough i Peptide-tetramer staining	ivities were undetectable dominant response in one of t n viremia resulted in increase g demonstrated that declining	he individuals, SLYNTVATL subdo s in CTLp levels of in vivo-activated CTL we	ominant ere associated with a decrease	Kalams1999b V in vivo activated specific CTL such e in expression of CD38 and then decreased with the decline of
gp160 (584–592)	<ul><li> Eleven subjects had CTI</li><li> One of these 11 had CTI</li></ul>	ERYLKDQQL  I CTL specific for more than 1  L that could recognize vaccini  L response to this peptide  was HLA-A3, -A32, -B7, -B1	a-expressed LAI gp160	human (B14)	Lieberman1997a
gp160 (584–592)	The consensus sequence	ERYLKDQQL  for clades B, C, and D is ER  for clade A is ERYLRDQQL  for clade E is ERYLKDQKF	and it is equally reactive	human (B14)	Cao1997a
gp160 (584–592)	and D clades - such cros		inst both A and D and confer prote		Rowland-Jones 1998a opes that tended to be conserved in A subtypes are circulating
gp160 (584–592)	gp41 (584–592) • HIV IIIB proteins were	ERYLKDQQL used to define the range of CT	HIV-1 infection FL epitopes recognized by 3 lab wo	human (B14) orkers accidentally infected w	Sipsas1997 rith HIV-1 IIIB
gp160 (584–592)	<ul><li>Clones specific for RT ly</li><li>The distinction was thou</li></ul>	ysed HIV-1 infected cells at lo	HIV-1 infection ed to determine their susceptibility ower levels than Env or Gag specifi- sion of RT relative to Env and Gag ibly prior to viral production	c clones	Yang1996
gp160 (584–592)	gp41 (584–592) • CTL inhibit HIV-1 replic	ERYLKDQQL cation at effector cell concent	HIV-1 infection rations comparable to those found	human (B14) in vivo	Yang1997a

HXB2 Location	<b>Author's Location</b>	Sequence	Immunogen	Species (HLA)	References
	<ul><li>CTL produced HIV-1-su</li><li>CTL suppress HIV repli</li></ul>		rs – MIP-1 $\alpha$ , MIP-1 $\beta$ , RANTES, after a in HLA-matched cells	intigen-specific activation	
gp160 (584–592)	gp41 (584–592 PV22) • Two overlapping CTL ep	ERYLKDQQL pitopes were mapped w	HIV-1 infection rith different HLA restriction (also see Y	human (B14) LKDQQLL HLA-B8)	Johnson1992
gp160 (584–592)	gp41 (584–592 PV22) • HIV-1 specific CTLs rel	ERYLKDQQL ease $\gamma$ -IFN, and $lpha$ - and	HIV-1 infection $\beta$ -TNF	human (B14)	Jassoy1993
gp160 (584–592)	gp41 (584–592 HXB2)  • Longitudinal study of T  • Persistence of oligoclone			human (B14)	Kalams1994, Kalams1996
gp160 (584–592)	gp41 (584–592) • Epitope studied in the co	ERYLKDQQL ontext of HLA-B14 bind	Peptide-HLA interaction ding	human (B14)	DiBrino1994a
gp160 (584–592)	gp41 (584–592)  • This peptide can be proc	ERYLKDQQL essed for HLA-B14 pro	HIV-1 infection esentation in a TAP-1/2 independent path	human (B14) nway	Hammond1995
gp160 (584–592)	<ul> <li>A diverse repertoire of T</li> <li>3/5 subjects showed no</li> <li>A minor CTL response seven when it was the minor CTL response seven when it was the</li></ul>	ected in all five, and CT CRs recognized this ep- variation in viral sequer specific for the ERYLQ nority form substitutions were well	HIV-1 infection HLA-B14 positive persons FL clones were isolated from 4/5 bitope, with similar fine specificities nce, 2/5 had a dominant variant that resul DQQL could be detected by two individual tolerated by most of the CTL clones test	uals, but the major CTL resp	ponse was to the ERYLKDQQL form
gp160 (584–592)	gp120 (584–592)  ◆ This epitope is processed	ERYLKDQQL d by both TAP1/2 depen	HIV-1 infection ndent and independent mechanisms	human (B14)	Ferris1999, Hammond1995
gp160 (584–592)	deletion in CCR5	sure to both HIV-1 and	osed African female sex workers in Gam HIV-2, CTL responses to B35 epitopes in activity [Johnson1992]		
gp160 (584–592)	recognized during the in	itial decline in viremia SLYNTVATL, was no	HIV-1 infection epitope in initial control of viremia in act t evident until 18 months post-presentation y infected subjects		Goulder2001a several subdominant CTL epitopes

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
gp160 (584–592)	gp41 (584–592) • Epitope name: 588K	ERYLKDQQL	HIV-1 infection	human (B14)	Islam2001
	collected 6-11 years por recognizes the A2 epitor	st infection: clone M2	m patient 115, with a chronic and stable 1 and E15 recognize ERYLKDQQL,and	clone D87 recognizes variant	ERYLQDQQL, and clone p175b
	gene, and D87 uses Vb • Responses were stable	eta8, ALNRVD, Jbeta2 even through HAART	OGA, Jbeta 1.2 TCR beta gene, and clone 2.1 with undetectable viral loads but frequen at to 3.78% for M21, with the relative fre	ncies varied over time by 100-f	fold, ranging from 0.012% of the total
gp160 (584–592)	<ul> <li>individuals treated duri</li> <li>The breadth and specification individuals with primar (Group 3), using 259 or</li> <li>Previously described an</li> </ul>	ng chronic infection city of the response wary infection but post-ser werlapping peptides spand and newly defined optime	HIV-1 infection ted in a narrower CTL response, stronger as determined using ELISPOT by studyir roconversion therapy (Group 2), and 10 i unning p17, p24, RT, gp41, gp120 and No al epitopes were tested for CTL response CTL response to this epitope broken dow	ng 19 individuals with pre-sero individuals who responded to l ef e	oconversion therapy (Group 1), 11 HAART given during chronic infection
gp160 (584–592)	gp41 (589–597)  • ELISPOT was used to HIV-1-infected female		HIV-1 infection, HIV-1 exp seronegative o a panel of 54 predefined HIV-1 epitopes		Kaul2001a ently seronegative (HEPS) and 87
gp160 (584–592)	<ul><li>with the B14-restricted</li><li>Primary monocytes and lymphocytes and could</li></ul>	CTL clone 15160/D75 I monocyte-derived DC also be inhibited by M cultures allowed vigor	HIV-1 infection hismatched lymphocytes from uninfected specific for ERYLKDQQL, and viral in C were generated from the same donors, in HC-restricted CTL rous viral replication and MHC-restricted	chibition was MHC-restricted replication of HIV-1 in these constants.	ell types was less efficient than in
gp160 (584–592)	gp41 (SF2)  This epitope was mapp an HLA-B60 individua		HIV-1 infection udy identifying new HLA-B60 epitopes,	human (B14) and was one of the epitopes p	Altfeld2000b resented by another HLA molecule in
gp160 (584–592)	suppression of replicati	on. The "EpiNef" cons	HIV-1 infection to contain Env and Pol epitopes to enabl- truct was inserted into a recombinant var and Pol epitopes indicating that they we	ccinia virus which was used to	

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References				
gp160 (584–592)	than NL-43 with an in	tact Nef. The effect was	HIV-1 infection and this study demonstrates directly shown to be specific for class I presen clone 15160D75, specific for the clas	tation of epitopes, and unlike N					
gp160 (584–592)	<ul> <li>CTL epitopes (http://ht</li> <li>60 epitope responses of magnitude of the responses of the responses of the responses of the response of the response</li></ul>	and lymph node (LN) CI iv-web.lanl.gov/content/lywere detected in both PB onse was similar in LN are in the LN. reatment in five patients so the performance in the PB but following HAART results, and the addition of 9 note responses were shown in	tudied, the magnitude of the CD8 T-ce ecame undetectable, in contrast to 5/2 ted in increased viremia accompanied ovel epitope responses. or 4 individuals. Patient A displayed	for each person's class I HLA and an additional 8 responses were cells in the LN is lower so the number of the LN.  I by the restoration of the detect	lleles. e detected only in LN. The total umber of HIV-specific cells per million oth LN and PB, but more dramatically				
gp160 (584–592)	<ul> <li>The HIV-1 subtype A which could direct the conserved, often immediately the conserved. A DNA and M included in the polyeption Multiple CD4+ or CD assays after vaccination.</li> </ul>	B7-TL9(p24), and responses to B7-TM9(Nef) and A32-PW10(RT).  gp41 ERYLKDQQL HIV-1 infection, Vaccine human (B14) Hanke2000, Wee2002  Vaccine Vector/Type: DNA prime with vaccinia MVA boost Strain: subtype A HIV component: p17, p24, polyepitope  • The HIV-1 subtype A focused vaccine HIVA contains p24 and p17, in a reversed order relative to the Gag polyprotein to prevent myristylation of p17, which could direct the protein to the cell membrane and inhibit efficient peptide processing and class I presentation, as well as a polyepitope string of conserved, often immunodominant epitopes that were selected to have particularly good cross-reactive potential for the A-clade epidemic in Nairobi, Kenya. A DNA and MVA prime-boost vaccination protocol using the HIVA antigen will be used in a phase III clinical trial in Kenya. This epitope is included in the polyepitope string [Hanke2000].  • Multiple CD4+ or CD8+ T-cell vaccine-induced responses to peptide pools were detected using intracellular cytokine staining and IFNgamma Elispot assays after vaccination of 5 macaques. The response to the Mamu A*01 SIV p27 epitope p11C (CTPYDINQM), included in the polyepitope region, was not immunodominant in the Mamu A*01 vaccinated macaques, possibly because of processing limitations in context of the artificial polyepitope string							
gp160 (584–592)	<ul> <li>Seroprevalence in this</li> <li>Most isolated HIV stresponses are frequent</li> <li>This epitope is conser</li> </ul>	cohort is 90-95% and the ains are clade A in Nairol		se CTL may confer protection est in the world	,				
gp160 (585–592)	_	RYLRDQQL immunogenetics – 59 HI C term) – 53 of the 59 pep		human (A*2402) edicted by searching for A*2402	Ikeda-Moore1997 anchors in HIV proteins (Tyr at 2, and				

HXB2 Location	<b>Author's Location</b>	Sequence	Immunogen	Species (HLA)	References				
	<ul> <li>This peptide induced CTL in 2/4 HIV-1+ people tested</li> <li>RYLRDQQL bound to A*2402 weakly, the epitope can be processed in a vaccinia construct and presented – two specific CTL clones were obtained</li> </ul>								
gp160 (585-592)	gp41 (590–597 LAI)	RYLKDQQL	HIV-1 infection	human (B27)	Shankar1996				
gp160 (585–593)	Phe, Leu or Ile at the C  This peptide induced C	term) – 53 of the 59 pept TL in 4/4 HIV-1+ people	ides bound A*2402		Ikeda-Moore1997 anchors in HIV proteins (Tyr at 2, and becific CTL clones were obtained				
gp160 (585–593)	gp41 (591–598 LAI) • C. Brander notes this is	RYLKDQQLL an A*2402 epitope		human (A*2402)	Brander2001				
gp160 (585–593)	<ul> <li>CTL epitopes (http://hi</li> <li>60 epitope responses w magnitude of the responses w magnitude of the responses with the response of the response of</li></ul>	and lymph node (LN) CDev-web.lanl.gov/content/hir ere detected in both PB and in the LN. catment in five patients study are responses in the PB because of the PB, and the addition responses were shown fo	adied, the magnitude of the CD8 T-c came undetectable, in contrast to 5/2 ed resulted in increased viremia according of 9 novel epitope responses.	for each person's class I HLA all and an additional 8 responses were cells in the LN is lower so the nut ell response was decreased in bot 6 in the LN.  Impanied by the restoration of the the greatest response to B27-KK.	eles. detected only in LN. The total mber of HIV-specific cells per million h LN and PB, but more dramatically				
gp160 (585–595)	Phe, Leu or Ile at the C  This peptide induced C	term) – 53 of the 59 pept TL in 4/4 HIV-1+ people	ides bound A*2402		Ikeda-Moore1997 anchors in HIV proteins (Tyr at 2, and resented – two specific CTL clones				
gp160 (585–595)	<ul> <li>Epitope name: Env584</li> <li>A Sendai virus vector s responses and has the p</li> <li>MHC class I/peptide te</li> </ul>	-11 ystem (SeV) was develop otential to elicit immune s tramers could be made us	Vaccine I (SeV) HIV component: class I/pe d that expressed HLA-A*2402-restr responses. ing this system that bound to epitop A*2402-HIV epitope complexes ind	ricted class I/peptide complexes; te-specific CTLs in PBMCs.					

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
gp160 (586–593)	<ul><li>sex workers eventually</li><li>The epidemiological factorism working for a period or</li></ul>	seroconverted, and for ctor associated with se retire	HIV-1 infection  xposed, persistently seronegative individuals is in these HIV CTL reactive epitopes have reconversion was stopping sex work and H  x worker controls, ML887	ad been defined while serones	gative
gp160 (586–593)	gp41 (584–591 NL43) • The lysine (K) is critica • C. Brander notes that the		HIV-1 infection A24 CTL response oe in the 1999 database, and suggested that	human (A*2402) t the epitope is RYLKQQLL	Dai1992
gp160 (586–593)	<ul> <li>HIV-1-infected female</li> <li>Responses in HEPS wo reduced risk of infectio women</li> <li>43/91 HEPS women ha</li> <li>Among HLA-A24 wom and infected women, R</li> <li>The dominant response</li> </ul>	study CTL responses to Nairobi sex workers omen tended to be lowe in, and there was a shift d CD8+ responses and nen, 3/4 HEPS and 10/ DYVDRFFKTL in inf to this HLA allele was specificity were only so	or a panel of 54 predefined HIV-1 epitopes or, and focused on different epitopes with Fit in the response in the HEPS women upon a detection of HIV-1-specific CTL in HEPS 10 HIV-1 infected women recognized this fected women only so to this epitope in all 3/4 HEPS cases but the en for responses restricted by class I HLA	in 91 HIV-1-exposed, persisted HLA presenting molecules that a late seroconversion to epitops women increased with the depitope, and (R)YL(R/K)DQ in only 4 of the 10/10 HIV-1	at have previously been associated with pes recognized by the HIV-1 infected duration of viral exposure QLL tended to be reactive in HEPS infected women
gp160 (586–593)	<ul><li>epitopes in this group, a</li><li>The only HLA-A24 FS</li></ul>	ort of HIV+ female se although E clade version W tested did not recog	HIV-1 infection  x workers (FSW) from Northern Thailand ons of previously defined B-clade A2 and a mized the E clade version of this epitope R h an additional amino acid added on	A24 epitopes were also tested	l.
gp160 (586–593)	<ul> <li>The HIV-1 subtype A for which could direct the processerved, often immunity</li> </ul>	ocused vaccine HIVA oprotein to the cell mem nodominant epitopes the VA prime-boost vaccin	HIV-1 infection, Vaccine hia MVA boost <i>Strain:</i> subtype A <i>HIV</i> contains p24 and p17, in a reversed order rubrane and inhibit efficient peptide process hat were selected to have particularly good ation protocol using the HIVA antigen wil 0].	relative to the Gag polyprotein sing and class I presentation, a I cross-reactive potential for the	oitope  n to prevent myristylation of p17, as well as a polyepitope string of the A-clade epidemic in Nairobi,

HXB2 Location	<b>Author's Location</b>	Sequence	Immunogen	Species (HLA)	References
	assays after vaccination	of 5 macaques. The resp	responses to peptide pools were detected us ponse to the Mamu A*01 SIV p27 epitope plated macaques, possibly because of procession	1C (CTPYDINQM), inc	cluded in the polyepitope region, was
gp160 (586–593)	gp41 (586–593 LAI)	YLKDQQLL	HIV-1 infection	human (A24, B8)	Mollet2000
	<ul><li>Epitope name: E1</li><li>A panel of 16 epitopes of CD8+ cell IFNgamma p</li></ul>		es was tested in 14 HIV+ patients from an uns sponses	selected Caucasian popul	lation treated with HAART, using
	specificities that were no HIV-specific responses	ot previously detectable diminished	iral load decreased and frequencies of HIV-sp were newly detected, as were CMV specific se: increases or decreases in pre-existing resp	CD8+ PBL – but with co	ontinued viral suppression,
gp160 (586–593)	gp41 (586–593) • C. Brander notes this is	YLKDQQLL a B*0801 epitope	HIV-1 infection	human (B*0801)	Brander2001
gp160 (586–593)	gp41 (586–593) • Two overlapping CTL e	YLKDQQLL pitopes were mapped with	HIV-1 infection ith different HLA restriction (also see ERYL)	human (B8) KDQQL HLA-B14)	Johnson1992
gp160 (586–593)	gp41 (586–593) • Predicted epitope based	YLKDQQLL on B8-binding motifs, f	Peptide-HLA interaction From larger peptide QLQARILAVERYLKDQ	human (B8) QQLLGIWGCS	Sutton1993
gp160 (586–593)	gp41 (76–83) • Included in a study of the	YLKDQQLL ne B8 binding motif		human (B8)	Goulder1997g
gp160 (586–593)	deletion in CCR5	sure to both HIV-1 and	osed African female sex workers in Gambia a HIV-2, CTL responses to B35 epitopes in exp ivity [Johnson1992]		
gp160 (586–593)	gp41 (586–593)	YLKDQQLL	HIV-1 infection, HIV-1 exposed seronegative	human (B8)	Kaul2001a
	<ul> <li>ELISPOT was used to st HIV-1-infected female N</li> </ul>		n panel of 54 predefined HIV-1 epitopes in 91	HIV-1-exposed, persiste	ently seronegative (HEPS) and 87
gp160 (586–593)	gp41 (586–593)  • B8-restricted CTL accord	YLKDQQLL unted for about 1/3 of th	HIV-1 infection the total CTL response in one individual	human (B8)	Day2001
gp160 (586–598)	CTLs – Cw7 specific C	ΓL were found against the	HIV-1 infection ptomatic HIV+ individual were studied and for three peptides, including this one ls to a lesser extent, 10% of either HLA-A or		Nehete1998a I C-restricted CD8+ Env-specific

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References		
					rectly governs this resistance to lysis – gulate Cw7, thus triggering non-MHC		
gp160 (594–608)	patients – this observati	on may be partially due HIV-1 specific memory	AV HIV-1 infection was associated decreased the IL-2-expa e to a reduction and impaired function cells (CTLp) was observed in three pa	of T helper cells, CTL exhaustio	n and APC dysfunction		
gp160 (606–614)	gp41 (605–615 LAI)  Vaccine Vector/Type: v  C. Brander notes this is	-	Vaccine ent: gp160	human (B*3501)	Brander2001		
gp160 (606–614)	gp41 (606–614 HXB2)  • Natural form of this per		HIV-1 infection d, suggesting initial Class I processing	human (B*3501) may occur in the cytosol	Ferris1996		
gp160 (606–614)	gp41 (605–615 LAI)  Vaccine Vector/Type: v  • Epitope for vaccine ind		Vaccine ent: gp160	human (B35)	Johnson1994b		
gp160 (606–614)	gp41 (606–614 LAI)  Vaccine Vector/Type: v  HLA restricted CTL res	-	Vaccine ent: gp160 V-1 vaccinia-env vaccinees	human (B35)	Johnson1994a		
gp160 (606–614)	gp41 (606–614 LAI)  Vaccine Vector/Type: v  • Peptide only processed			human (B35)	Hammond1995		
gp160 (606–614)	gp41 (606–614)  • This epitope is processor	TAVPWNASW ed by a TAP1/2 dependent	HIV-1 infection ent mechanism	human (B35)	Ferris1999		
gp160 (606–614)	gp41 (subtype B) TAVPWNASW HIV-1 exposed seronegative human (B35) Rowland-Jones1998b  • HIV-specific CTL were found in exposed seronegative prostitutes from Nairobi – these CTL may confer protection  • Seroprevalence in this cohort is 90-95% and their HIV-1 exposure is among the highest in the world  • Most isolated HIV strains are clade A in Nairobi, although clades C and D are also found – B clade epitopes are often cross-reactive, however stronger responses are frequently observed using A or D clade versions of epitopes  • This epitope is conserved among A, B and D clade viruses						
gp160 (606–614)	gp41 (606–614)  • ELISPOT was used to s HIV-1-infected female		HIV-1 infection, HIV-1 ex seronegative a panel of 54 predefined HIV-1 epitop		Kaul2001a ently seronegative (HEPS) and 87		
gp160 (634–648)	gp41 (641–655 SF2) • Of 25 patients, most ha	EIDNYTNTIYTLL d CTL specific for mor		human	Lieberman1997a		

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
	<ul><li>One of these 11 had CT.</li><li>The responding subject</li></ul>	L response to this peptide was HLA-A1, A2, B51, and B57	7		
gp160 (678–686)	Env (679–687 subtype B)	WLWYIKIFI	Vaccine	human (A2.1)	Kundu1998a
	<ul> <li>Ten HIV-1+ HLA A2 as</li> <li>Two hundred and fifty the in gp160, of which 25 h</li> <li>Eleven peptides were stream</li> </ul>	hree HIV-1 peptides of 9 or 10 as ad a high or intermediate binding udied that had high HLA-A2 bin mmunization may include recall	ven two courses of HIV-1 MN rgp10 a possessing the HLA-A2.1 binding	motif (Leu at position 2, V detected to 9/11 peptides in	al at the C terminus) were identified at least 1 individual
gp160 (680–688)	Phe, Leu or Ile at the C  This peptide induced CT	term) – 53 of the 59 peptides bot $\Gamma$ L in 1/4 HIV-1+ people tested			Ikeda-Moore1997 nchors in HIV proteins (Tyr at 2, and cific CTL clones were obtained
gp160 (685–693)	<ul> <li>Ten HIV-1+ HLA A2 as</li> <li>Two hundred and fifty the in gp160, of which 25 h</li> <li>Eleven peptides were stream of the CTL responses after reindetectable CTL responses</li> </ul>	hree HIV-1 peptides of 9 or 10 as ad a high or intermediate binding udied that had high HLA-A2 bin mmunization may include recall es	ven two courses of HIV-1 MN rgp10 a possessing the HLA-A2.1 binding	motif (Leu at position 2, V detected to 9/11 peptides in accine cross-reactive seque	al at the C terminus) were identified at least 1 individual nees prior to vaccination showed
gp160 (698–707)	<ul> <li>characterize the immune</li> <li>The anchor motif for HI used to define 82 potent cultures from 1/3 HLA.</li> <li>CTL clones were isolate</li> </ul>	e response in this population. LA*3303 (A, I, L, V, F, Y in posi- ially reactive peptides in Env; 37 A*3303 positive individuals tested that killed target cells in a con- pressed from a vaccinia vector. B		o, and R (K is also tolerated 7 peptides could induce per	) in the C-terminal position) was btide-specific CTL in bulk PBMC (NR peptide, that could also kill cells
gp160 (700–708)	Env (695–705 BH10, LAI) • This study employs an a	AVLSVVNRV	HIV-1 infection  npare HIV-1 antigenic determinants	human with human proteins.	Maksiutov2002

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
		IV-1 LAI fragment with high sires fragment LRLVFALVTAV.	nilarity to a human protein o	verlapping this epitope is LRIVFA	AVLSVV) has similarity with the
gp160 (700–708)	gp41 (705–714) • This epitope is processed	AVLSVVNRV I by a TAP1/2 dependent mechan	HIV-1 infection	human (A2)	Ferris1999
gp160 (701–720)	gp41 (701–720 BH10) • Recognized by CTL deri	VLSIVNRVRQGYSPLSFQTH ved from acute seroconverter	HIV-1 infection	human (A32)	Safrit1994a
gp160 (702–721)	<ul><li>each HIV protein.</li><li>Nef and p24 had the high</li></ul>	nest percentage of reactive peption	n 105 HIV-1 positive Botswardes, and p24 had the highest	-	Novitsky2002 om between 55 and 64 subjects for
gp160 (704–712)	gp160 (704–712 LAI) • C. Brander notes this is a	IVNRNRQGY an <b>A*3002</b> epitope		human (A*3002)	Brander2001, Goulder2001a
gp160 (704–712)	<ul> <li>characterized that are presented.</li> <li>A rapid method was deviwere defined – this meth</li> <li>Two individuals were stu African-Caribbean</li> <li>In both HLA-A*3002 in</li> <li>In subject 199 four addit</li> </ul>	mmon in African populations, 50 esented by this HLA molecule eloped combining ELISPOT with od was completed within 48 to 7 idied: Subject 199 (HLA A*020 dividuals the response to RSLYN ional A*3002 epitopes were identifications).	h intracellular IFN-γ staining 2 hours of receipt of blood 1/*3002 B*4402/51 Cw2/5), VTVATLY was dominant ntified		pes, then HLA presenting molecules HLA A*3002/ B53/*5801 Cw4/7) at
gp160 (742–761)	<ul><li>each HIV protein.</li><li>Nef and p24 had the high</li></ul>	nest percentage of reactive peption	105 HIV-1 positive Botswardes, and p24 had the highest	-	Novitsky2002 om between 55 and 64 subjects for
gp160 (747–755)	gp41 (747–755) • Studied in the context of	RLVNGSLAL HLA-A2 peptide binding	HIV-1 infection	human (A2)	Parker1992
gp160 (747–755)	gp41 (741–749 CM243 subtype CRF01) • Epitope name: E747-755	RLVSGFLAL	HIV-1 infection	human (A2)	Sriwanthana2001

• HLA-A11 is very common in this population, and was enriched among the HEPS sexworkers – weak CTL responses were detected in 4/7 HEPS women,

• This was a study of HIV-1 exposed persistently seronegative (HEPS) female sex workers in Chiang Mai, northern Thailand

and CTL responses were found in 8/8 HIV+ controls, and 0/9 HIV- women that were not exposed

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
	This epitope was reactive	e in HIV+ control study	subject 144 who carried HLA-A2		
gp160 (747–755)	gp41 (741–749 CM243 subtype CRF01)	RLVSGFLAL	HIV-1 infection	human (A2)	Bond2001
			vorkers (FSW) from Northern Thailan		
	<ul> <li>2/4 tested FSWs recogni RLVNGSLAL</li> </ul>	zed the E clade version	of previously defined B-clade A2 an of this epitope, which differs from the		
	This epitope was somew	hat conserved 4/8 subty	pes: CRF01 (E), B, C, and G		
gp160 (754–768)	patients – this observation	on may be partially due of IIV-1 specific memory of	HIV-1 infection as associated decreased the IL-2-expa to a reduction and impaired function of the ells (CTLp) was observed in three pa	of T helper cells, CTL exhaustio	n and APC dysfunction
gp160 (767–775)	Phe, Leu or Ile at the C t  This peptide induced CT	term) – 53 of the 59 pep L in 1/4 HIV-1+ people	tides bound A*2402		Ikeda-Moore1997 anchors in HIV proteins (Tyr at 2, and o specific CTL clones were obtained
gp160 (767–780)	gp41 (606–614 LAI) • Peptide only processed be • CTL from an acute served	•	HIV-1 infection pathway	human (A31)	Hammond1995
gp160 (769–777)	gp41 (769–777 BH10) • Recognized by CTL deri	HRLRDLLLI ived from acute serocon	HIV-1 infection verter	human	Safrit1994a
gp160 (770–778)	<ul><li>have A2 anchor residues</li><li>The C terminal epitopes</li></ul>	(D2 and 5.3) were high	HIV-1 infection es were studied: D2: LLNATAIAV, 5  ly variable and the variability was cor l and gave evidence of high levels of 0	nsidered responsible for limited	· ·
	<ul> <li>Peptides 5.3 and D2 bou</li> </ul>		2	CTL response in vitro	
gp160 (770–780)	gp41 (775–785)  • Only 4/11 HLA-A2+ HI  • 95 optimally-defined per	RLRDLLLIVTR V+ individuals had CTI otides from this database	HIV-1 infection  that reacted to SLYNTVATL, calling were used to screen for INFγ respons R, B51 and responded to this epitope	ises to other epitopes	
gp160 (770–780)	gp41 (768–778 NL43) • CD8+ T cell clone	RLRDLLLIVTR	HIV-1 infection	human (A*0301)	Takahashi 1991

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
gp160 (770–780)	gp41 (775–785 LAI) • C. Brander notes this is a	RLRDLLLIVTR an A*0301 epitope	HIV-1 infection	human (A*0301)	Brander2001
gp160 (770–780)	•	RLRDLLLIVTR ived from acute seroconverter s is an A*3101 epitope in the 19	HIV-1 infection	human (A*3101)	Safrit1994a, Safrit1994b
gp160 (770–780)	gp160 (770–780 LAI)  • C. Brander notes this is a	RLRDLLLIVTR an A*3002 epitope		human (A*3101)	Brander2001
gp160 (770–780)	The consensus peptide o	RLRDLLLIVTR f clade B is RLRDLLLIVTR f clades A, C and E is RLRDFI f clade D is SLRDLLLIVTR an		human (A3)	Cao1997a
gp160 (770–780)	gp41 (775–785)  • ELISPOT was used to st HIV-1-infected female N		HIV-1 infection, HIV-1 exposed seronegative f 54 predefined HIV-1 epitopes in 91	human (A3) HIV-1-exposed, persistentl	Kaul2001a y seronegative (HEPS) and 87
gp160 (770–780)	studied in eight HIV-1-ir  2 to 17 epitopes were recepitopes were targeted by	nfected subjects, two with acute cognized in a given individual, A y at least one person	HIV-1 infection estricted by HLA class I A and B allele infection, five with chronic, and one l A2-restricted CTL response tended to epitopes, but none was clearly domin	long-term non-progressor ( be narrow and never domin	LTNP)
gp160 (770–780)	<ul> <li>studied in eight HIV-1-ir</li> <li>2 to 17 epitopes were recepitopes were targeted b</li> <li>All patients recognized a</li> </ul>	nfected subjects, two with acute cognized in a given individual, A y at least one person	HIV-1 infection estricted by HLA class I A and B allele infection, five with chronic, and one lA2-restricted CTL response tended to epitopes, but none was clearly dominnt epitope	long-term non-progressor ( be narrow and never domin	LTNP)
gp160 (770–780)	<ul> <li>One individual, AC-06, vinterruptions (STI). He has restricted by HLA-A3, 1</li> <li>0/14 HLA-A3 positive in</li> </ul>	ntely HIV-infected HLA-A3 (n= was homozygous at all three cla had only two detectable CTL res 1 by HLA-B7, and 1 by HLA-C ndividuals had detectable A3-res	HIV-1 infection  7) or -B7 (n=4) or both -A3 and B7 (rest I alleles (A3, B7, Cw7), was treated ponses during acute infection, but after Ew7.  Stricted responses to this epitope during an to have detectable responses to this	d during acute infection and er STI this broadened to 27 ag acute infection, but only	d had supervised treatment distinct epitopes including 15

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
gp160 (770–780)	gp41 (770–780) • This epitope is processed	RLRDLLLIVTR I by a TAP1/2 dependent mechan	HIV-1 infection nism	human (A31)	Ferris1999, Hammond1995
gp160 (777–785)	gp41 (782–790 LAI)  • C. Brander notes this is a	IVTRIVELL an A*6802 epitope		human (A*6802)	Brander2001
gp160 (781–802)	gp120 (788–809)	IVELLGRRGWEALKYWWNL- LQY		human	Lieberman1995
		developed by ex vivo stimulation			
gp160 (781–802)	gp41 (788–809 HXB2)  • CTL epitope defined by	IVELLGRRGWEALKYWWNL- LQY T cell line and peptide mapping	HIV-1 infection	human (B27)	Lieberman1992
gp160 (786–794)	gp41 (791–799 LAI) • Review of HIV CTL epi	GRRGWEALK	HIV-1 infection	human (B27)	McMichael1994
gp160 (786–795)	gp41 (791–800 LAI)  • C. Brander notes this is a	GRRGWEALKY a B*2705 epitope	HIV-1 infection	human (B*2705)	Brander2001
gp160 (786–795)	gp41 (791–800 LAI)  • Optimal peptide mapped	GRRGWEALKY by titration J. Lieberman, Pers.	HIV-1 infection Comm.	human (B27)	Lieberman1998
gp160 (786–795)	gp41 (786–795)	GRRGWEALKY	HIV-1 infection	human (B27)	Day2001
gp160 (794–802)	gp160 (794–802 LAI)  • C. Brander notes this is a	KYCWNLLQY an <b>A*3002</b> epitope		human (A*3002)	Brander2001, Goulder2001a
gp160 (794–802)	<ul> <li>characterized that are present a rapid method was devenued and the method was</li></ul>	mmon in African populations, 50 esented by this HLA molecule eloped combining ELISPOT with od was completed within 48 to 7 idied: Subject 199 (HLA A*020 dividuals the response to RSLYN ional A*3002 epitopes were iden	1/*3002 B*4402/51 Cw2/5), a Cauca WTVATLY was dominant	ACs to map optimal epitopoasian, and Subject 6007 (H	es, then HLA presenting molecules LA A*3002/ B53/*5801 Cw4/7) an
gp160 (794–814)	gp41 (SF2)  • This epitope was mapped an HLA-B60 individual	KYCWNLLQYWSQELKNSAV- SL d by ELISPOT in a study identify	HIV-1 infection  ying new HLA-B60 epitopes, and wa	human as one of the epitopes prese	Altfeld2000b ented by another HLA molecule in

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
	The response to the pepti	ide was CD8 dependent, but the l	HLA presenting molecule and op	timal epitope were not determ	ined
gp160 (795–816)	gp41 (802–823 HXB2)	YWWNLLQYWSQELKNSAVN- LLN	HIV-1 infection	human	Lieberman 1992
	• CTL epitope defined by	Γ cell line and peptide mapping			
gp160 (799–807)	Env (800–808 subtype B)	LLQYWSQEL	Vaccine	human (A2.1)	Kundu1998a
	<ul> <li>Ten HIV-1+ HLA A2 asy</li> <li>Two hundred and fifty th in gp160, of which 25 ha</li> <li>Eleven peptides were stu</li> </ul>	ree HIV-1 peptides of 9 or 10 aa d a high or intermediate binding died that had high HLA-A2 bind nmunization may include recall r	en two courses of HIV-1 MN rgp possessing the HLA-A2.1 bindin	ng motif (Leu at position 2, Va as detected to 9/11 peptides in	l at the C terminus) were identified at least 1 individual
gp160 (805–814)	Env (799–813 BH10, LAI)	QELKNSAVSL	HIV-1 infection pare HIV-1 antigenic determinant	human	Maksiutov2002
	<ul> <li>This CTL epitope (the H the complement compon</li> <li>This CTL epitope (the H</li> </ul>	IV-1 LAI fragment with high siment C6 fragment LTQFSSEELKI IV-1 LAI fragment with high sim	nilarity to a human protein overlag	pping this epitope is LLQYW pping this epitope is NSAVSI	SQELKNSAVS) has similarity with LNATAIAVA) also has similarity
gp160 (805–814)	gp41 (810–819 LAI) • C. Brander notes this is a	QELKNSAVSL a B*4001,B60 epitope		human (B*4001)	Brander2001
gp160 (805–814)		QELKNSAVSL  d by ELISPOT in a study identify  of the Caucasoid and very com		human (B60(B*4001))	Altfeld2000b
gp160 (805–814)		QELKNSAVSL sponses were detected to five B61 bitopes were reactive in another s	HIV-1 infection -restricted epitopes tested subject, and the B60-restricted res	human (B60/B61) sponses together contributed of	Day2001 over one-third of the total CTL
gp160 (813–822)	• Of two CTL clones, one	SLLNATDIAV combinant protein <i>Strain:</i> MN reacted only with 815-823, the obtained on the strain of t		human (A*0201)	Dupuis1995
gp160 (813–822)	gp41 (818–827 LAI)  Vaccine Vector/Type: rec  C. Brander notes this is a		Vaccine HIV component: gp160	human (A*0201)	Brander2001

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References	
gp160 (813–822)	monthly into six HIV-in  1/6 showed increased er no change – pulsed DCs  SLLNATDIAV is a cons detectable CTL response	fected patients av-specific CTL and ince were well tolerated served HLA-A2 epitope e – the other two had ei	HIV-1 infection from HLA-identical siblings, pulsed v reased lymphoproliferative responses, e included in this study – 4/6 patients h ther the sequence SLFNAIDIAV or SI et, epitope is naturally processed and en	2/6 showed increase only in pro ad this sequence as their HIV d LNTTDIVV and no detectable	oliferative responses, and 3/6 showed irect sequence, and 3 of these had a	
gp160 (813–822)	• 95 optimally-defined pe	ptides from this databas	HIV-1 infection L that reacted to SLYNTVATL, calling se were used to screen for INFγ resport to SLYNTVATL reacted with seven of	ises to other epitopes		
gp160 (813–822)			HIV-1 infection tient AC13– response to this epitope coidentified in the acute phase, but a response to the content of the con			
gp160 (813–822)	<ul> <li>individuals treated durin</li> <li>The breadth and specific individuals with primary (Group 3), using 259 ov</li> <li>Previously described and</li> </ul>	ng chronic infection  begin to the response was  y infection but post-sero  erlapping peptides spard  d newly defined optima	determined using ELISPOT by studyi	ing 19 individuals with pre-sero individuals who responded to H Jef se	IAART given during chronic infection	
gp160 (813–822)	gp41 (814–823 CM243 SLLNATAIAV HIV-1 infection human (A2) Sriwanthana2001 subtype CRF01)  • Epitope name: E813-82  • This was a study of HIV-1 exposed persistently seronegative (HEPS) female sex workers in Chiang Mai, northern Thailand  • HLA-A11 is very common in this population, and was enriched among the HEPS sexworkers – weak CTL responses were detected in 4/7 HEPS women, and CTL responses were found in 8/8 HIV+ controls, and 0/9 HIV- women that were not exposed  • This epitope was reactive in HIV+ control study subjects 125 and 144 who carried HLA-A2					
gp160 (813–822)	<ul><li>epitopes in this group, a</li><li>1/4 tested FSWs recogni</li></ul>	Ithough E clade version ized the E clade version	HIV-1 infection workers (FSW) from Northern Thailans of previously defined B-clade A2 and of this epitope, which differs from the types: CRF01 (E), B, D, and F	d A24 epitopes were also tested		

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
gp160 (813–822)	studied in eight HIV-1 • 2 to 17 epitopes were	l-infected subjects, two wit	HIV-1 infection topes restricted by HLA class I A and the acute infection, five with chronic, yidual, A2-restricted CTL response	and one long-term non-progress	
gp160 (813–822)	<ul> <li>IL-12p40)</li> <li>Epitope name: D2</li> <li>Transgenic mice expression of gp160delt.</li> <li>region of gp120, KLT.</li> <li>Greater resistance was</li> </ul>	essing a HLA-A2/Kb chimaV3 had a broader immuno PLCVTL, and the C-term so conferred by the gp160de	Vaccine nant protein boost Strain: IIIB H eric protein were vaccinated with a eresponse than those given gp160, v region of gp41, SLLNATAIAV. eltaV3 than the gp160 vaccine to a c conferred by CD8+ T-cells.	full length gp160 or with gp1600 with increased responses to conse	erved HLA-A2 epitopes in the C1
gp160 (813–822)	<ul> <li>Ten HIV-1+ HLA A2</li> <li>Two hundred and fifty in gp160, of which 25</li> <li>Eleven peptides were</li> <li>CTL responses after redetectable CTL responses</li> <li>CTL to overlapping period</li> <li>ALTERNATIVE EPIT</li> </ul>	recombinant protein Stra asymptomatic individuals three HIV-1 peptides of 9 had a high or intermediate studied that had high HLA eimmunization may includenses eptides in this region gave FOPES: LLNATDIAV and		binding motif (Leu at position 2, ase was detected to 9/11 peptides s with vaccine cross-reactive sequence of patients d by vaccine in those that had the	Val at the C terminus) were identified in at least 1 individual uences prior to vaccination showed
gp160 (813–822)	<ul> <li>Epitope name: LR27</li> <li>The stability of peptid SLYNTVATL (p17), S (GILGFVFTL), while</li> <li>The four high-affinity less than an hour.</li> <li>HLA-A2.1 transgenic as adjuvants.</li> <li>All peptides except VI</li> </ul>	le binding to HLA-A2.1 was SLLNATDIAV (gp41) and RGPGRAFVTI and VIYO peptides formed stable commice were immunized with	h the six HIV-1 peptides and P30, a	ptides included in this vaccine stubling affinity comparable to a infity (relative binding activity = 0.0 ween 8 and 32 hours, while the loss a universal T-helper epitope, with	ndy – ILKEPVHGV (RT), fluenza epitope reference

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
gp160 (813–822)	<ul> <li>Epitope name: LR27</li> <li>When HIV-1 peptides vigiven individually, but counteract immunodom</li> </ul>	were used to vaccinate immunodominance lin inance in BALB/c mice	Vaccine  Adjuvant: P30, incomplete Freund's ad  HLA-A2.1 transgenic A2-Kb mice, stronited the response to some of the peptide ce, so it was given with the multiple epite b CTL responses. This was possibly a co	ng responses to five peptides we s when they were given in comb ope vaccination, and was instead	pination [Peter2001]. IL-12 can d found to specifically eliminate the
gp160 (813-822)	<ul> <li>criteria, and 30 of these</li> <li>Three additional previor recognized at least one maximum of 2)</li> <li>This epitope binds to the This epitope did not eli</li> </ul>	Il peptides which carrie bound to HLA-A*020 busly described HLA-A of the 23 peptides (me aree HLA-A2 supertyp cit an ELISPOT respon	HIV-1 infection  ed the A2-supermotif pattern conserved in 201 – 20/30 bound to at least 3/5 of HLA- 22 epitopes were added to the set of 20, a dian of 2 and maximum of 6), while 6/1  e alleles: A*6802 (highest affinity), A*0 are in 22 chronic HIV HLA-A2 infection 344/14 and also had a strong response to	A2 supertype alleles tested and 18/22 chronically infected F 2 acute infected individuals reconcept and A*0203 (but not A*02 ns, but elicited a strong response	JLA-A2 individuals had CTL that ognized at least 1 (median of 1 and 01 and not A*0206)
gp160 (814–822)	<ul> <li>have A2 anchor residue</li> <li>The C terminal epitopes</li> <li>N-terminal epitopes, we</li> <li>Peptides 5.3 and D2 bo</li> <li>Substitutions in peptide</li> </ul>	es. s (D2 and 5.3) were hi ere much more conser- und to HLA A*0201 v 2 D2: llnTIaiav did not	HIV-1 infection copes were studied: D2: LLNATAIAV, 5. ghly variable and the variability was conved and gave evidence of high levels of Covith low affinity and were variable, particular abrogate the response, but diminished it the variable D2 epitope diminished over the copies of the control	nsidered responsible for limited of CTL response in vitro. cularly D2.	CTL response, while D1 and 4.3,
gp160 (814–822)		-	Vaccine  Strain: MN HIV component: gp160 5-823, the other with 814-823 and 815-8	human (A2)	Dupuis1995
gp160 (814–822)	Env (815–823) • Increased CTL respons	LLNATAIAV e to cells expressing a	HIV-1 infection VV construct ΔV3 mutant compared with	human (A2) th a full-length env gene produc	Kmieciak1998b t
gp160 (822–832)	<ul> <li>individuals treated duri</li> <li>The breadth and specification individuals with primar (Group 3), using 259 or</li> </ul>	ng chronic infection city of the response way infection but post-se werlapping peptides spa	HIV-1 infection ted in a narrower CTL response, stronge as determined using ELISPOT by studyi roconversion therapy (Group 2), and 10 anning p17, p24, RT, gp41, gp120 and N nal epitopes were tested for CTL respons	ng 19 individuals with pre-serod individuals who responded to H	conversion therapy (Group 1), 11

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References		
	• Number of individuals t group 3	hat had a CTL response to this ep	pitope (HLA presenting molecule	uncertain) broken down by	group: 0 group 1, 1 group 2, and 0		
gp160 (827–841)	gp41 (834–848 IIIB)  • CTL and T helper cell r	DRVIEVVQGAYRAIR eactivity in healthcare workers ex	HIV-1 exposed seronegative posed to HIV	human	Pinto1995		
gp160 (827–841)	gp41 (834–848 IIIB) • Helper and cytotoxic T	DRVIEVVQGAYRAIR cells can be stimulated by this pe	HIV-1 infection ptide (Th4)	human (A2)	Clerici1991a		
gp160 (827–841)		DRVIEVVQGAYRAIR accinia Strain: IIIB HIV comptiple class I molecules can presen		murine $(H-2^{d,p,u,q})$	Shirai1992		
gp160 (827–841)		DRVIEVVQGAYRAIR accinia HIV component: gp160 can cross-present this epitope (HI	Vaccine P53), and P18 RIQRGPGRAFVTI	murine (H- $2^{d,p,u,q}$ ) GK, to specific CTL	Shirai1996b		
gp160 (828–836)		RVIEVLQRA ecombinant protein Strain: MN elitive subject react with this peption		human (A2)	Dupuis1995		
gp160 (828–836)	<ul><li>epitopes in this group, a</li><li>1/4 tested FSWs recogn</li></ul>	ort of HIV+ female sex workers ( although E clade versions of previ		4 epitopes were also tested.	Bond2001 this study concentrated on A11 sion by three amino acids, RvievLqRa		
gp160 (828–836)	Env (829–837 subtype RVIEVLQRA Vaccine human (A2.1) Kundu1998a  B)  Vaccine Vector/Type: recombinant protein Strain: MN HIV component: gp160  • Ten HIV-1+ HLA A2 asymptomatic individuals were given two courses of HIV-1 MN rgp160 vaccine over a 2 year period  • Two hundred and fifty three HIV-1 peptides of 9 or 10 aa possessing the HLA-A2.1 binding motif (Leu at position 2, Val at the C terminus) were identified in gp160, of which 25 had a high or intermediate binding affinity  • Eleven peptides were studied that had high HLA-A2 binding affinity – a CTL response was detected to 9/11 peptides in at least 1 individual  • CTL responses after reimmunization may include recall responses – individuals with vaccine cross-reactive sequences prior to vaccination showed detectable CTL responses						
gp160 (830–854)	gp41 (831–853)  • Study of cytokines relea	IEVVQGAYRAIIRHIPRRI- RQGLERI ased by HIV-1 specific activated (		human	Price1995		
gp160 (831–838)	Env (830–837) • HLA-A33 a very comm	EVAQRAYR	HIV-1 infection 303 the most common among the	human (A*3303) Japanese. New A*3303 epi	Hossain2001, Takiguchi2000 stopes were defined to better		

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
	used to define 82 potent cultures from 1/3 HLA • 2/3 peptides that reacted shown to be the one tha • CTL clones were isolated	tially reactive peptides in Env; 3 A*3303 positive individuals test d with the bulk culture, EVAQR t was reactive with a CTL clone ed that killed target cells in a copressed from a vaccinia vector.	37/82 peptides bound to sted. AYR and VIEVAQRAY e. oncentration dependent n	nost strongly), and R (K is also tolerated A*3303; 3/37 peptides could induce pe R, were overlapping, with one encompananner after pulsing with the EVAQRA'd from six additional people, and only	eptide-specific CTL in bulk PBMC assing the other, but EVAQRAYR was YR peptide, that could also kill cells
gp160 (835–843)	<ul> <li>Med. 2:405, 1996;Lanc</li> <li>15% of Japanese popula</li> <li>Of the 172 HIV-1 peptic positive individuals, and</li> <li>This peptide could stim</li> </ul>	et 22:1187, 1986;Hum Immuno ations carry HLA-B51 while HI des with HLA-B*5101 anchor r d six were properly processed ulate CTL from one person, ho	ol 22:73, 1988;Hum Imm LA-B27 and -B57 are de residues, 33 bound to HL wever this CTL clone die		re reactive with CTL from 3 B*5101
gp160 (837–856)	gp120 (844–863) • HIV-specific CTL lines	YRAIRHIPRRIRQGLERII developed by ex vivo stimulation		human	Lieberman1995
gp160 (837–856)	<ul><li> Eleven subjects had CT</li><li> One of these 11 had CT</li></ul>	YRAIRHIPRRIRQGLERII d CTL specific for more than 1 L that could recognize vaccinia L response to this peptide was HLA-A2, A26, B7, and B3	HIV-1 protein -expressed LAI gp160	human	Lieberman1997a
gp160 (837–856)	gp120 (844–863 LAI)	YRAIRHIPRRIRQGLERII	L HIV-1 infection	human (B35)	Shankar1996
gp160 (837–856)	gp41 (844–863 HXB2) • CTL epitope defined by	YRAIRHIPRRIRQGLERIL  T cell line and peptide mappin		human (B8)	Lieberman1992
gp160 (842–856)	from 7 proteins, suggest		sponses are underestimat	human all HIV-1 proteins in an ELISPOT and sed if accessory proteins are not include	
gp160 (843–851)	gp41 (848–856 LAI) • C. Brander notes this is	IPRRIRQGL a B*0702 epitope		human (B*0702)	Brander2001
gp160 (843–851)	gp41 (848–856 LAI) • Epitope defined in the c	IPRRIRQGL context of the Pediatric AIDS Fo	oundation ARIEL Projec	human (B7) et, a mother-infant HIV transmission stu	Brander1995b udy
gp160 (843–851)	Following primary infection one individual and in V		HIV-1 infection n and accumulation of m	human (B7) autations of HIV-env nucleotide sequen	Soudeyns1999 ces was observed, focused in V2 in

<b>HXB2</b> Location	<b>Author's Location</b>	Sequence	Immunogen	Species (HLA)	References
	• The patient with the V8	diversification had an i	only transient CTL against Env and N immunodominant CTL response to V8 the CT response in vitro, and also ipr	B epitope IPRRIRQGL, and mul-	tiple escape variants emerged within a diminished responses.
gp160 (843–851)	gp41 (848–856 LAI)  • The consensus peptide companies to the consensus peptide			human (B7)	Cao1997a
gp160 (843–851)	<ul><li>cross-reactivity was obse</li><li>Two HLA B7 individual note that the B7 epitope</li></ul>	clade cross-reactivity for erved is had CTL response to IPRRIRQGL is conser	HIV-1 infection  rom CTL isolated from individuals net B_LAI, A_92UG037 and C_92BR02  rved between the LAI and clade A and expecificity of the response in the HLA	5 gp160, but were B clade strain C strains, but that MN has a no	
gp160 (843–851)	<ul> <li>interestingly, no response</li> <li>The individual showed at Despite the initial narrow</li> <li>No HIV-specific lympho</li> <li>Variants were observed iprrTrqgl; the other form reduced</li> </ul>	RQGL was the immund to to commonly immund a strong initial CTL rest was response to two epitoproliferative responses in vivo, the most common detected were iprring	HIV-1 infection odominant response in a rapid progres to a rapid progres addominant HLA A*0201 epitope SLY ponse at the time of the initial drop in opes, no other CTL responses developes were detected in this patient, and neuron form of the viral epitope at presenting printing prin	YNTVATL, although this individ viremia, but it was quickly lost, ed attralizing antibody response was tation at 3 months was the only fuld elicit a CTL response although	ual was HLA A*0201 although memory cells persisted weak form that did not elicit a CTL response:
gp160 (843–851)	cross-reactive CTL resp and D • Proteins corresponding was extensive inter-subt	onses in Ugandans to A to the subtype of the in- type cross-reactivity with	fecting strains tended to trigger higher th B clade proteins and the co-circulat	a viruses expressing Gag, Env, I r levels of CTL response measur ing subtype	Pol, RT or Nef from HIV-1 clades A, B
gp160 (843–851)	<ul> <li>This individual had a do subdominant response to variation occurred with</li> <li>At 3 months post-preser WAASS, two used Vbet</li> </ul>	minant response to IPF o SPAIFQSSM – during in both epitopes atation, seven IPRRIRQ a16S1, ERSPPGD, Jbe	HIV-1 infection acute infection through death, and had RRIRQGL with strong in vivo activate g the course of disease progression (4  QGL CTL clones were obtained, five u ta 2.7 and one CTL clone isolated at 3 n, even to time of death, despite the los	d responses and in vitro stimula Years), the functional CTL responded the T-cell receptor Vbeta 6S 39 months was Vbeta 14S1, CR3	onses were lost and no sequence 1 and Jbeta 2.7 and had the CDR3 3 PTAAG, and Jbeta 2.1 – all of these

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
gp160 (843–851)	<ul> <li>individuals treated durin</li> <li>The breadth and specific individuals with primary (Group 3), using 259 ov</li> <li>Previously described an</li> </ul>	ng chronic infection city of the response wa y infection but post-ser verlapping peptides spa d newly defined optim	HIV-1 infection ed in a narrower CTL response, stronger s determined using ELISPOT by studyin occonversion therapy (Group 2), and 10 in nning p17, p24, RT, gp41, gp120 and Neal epitopes were tested for CTL response TL response to this epitope broken down	g 19 individuals with pre-sero ndividuals who responded to lef	oconversion therapy (Group 1), 11 HAART given during chronic infection
gp160 (843–851)	<ul> <li>HIV-1-infected female I</li> <li>Responses in HEPS worked reduced risk of infection women</li> <li>43/91 HEPS women had</li> <li>Among HLA-B7 wome</li> <li>The dominant response HEPS cases</li> <li>Subject ML 1203 started</li> </ul>	tudy CTL responses to Nairobi sex workers men tended to be lower n, and there was a shift d CD8+ responses and n, 2/5 HEPS and 5/6 H to this HLA allele was d with CTL responses	HIV-1 infection, HIV-1 exposeronegative d D a panel of 54 predefined HIV-1 epitopes c, and focused on different epitopes with in the response in the HEPS women upon detection of HIV-1-specific CTL in HEP IV-1 infected women recognized this epitope in 2 of the 5/6 HIV-1 infector to A*6802 DTVLEDINL and to B7 FPV YFILKL which became dominant, B7 TI	s in 91 HIV-1-exposed, persist HLA presenting molecules the on late seroconversion to epitor PS women increased with the citope exceed women that responded to TTPQVPLR prior to seroconversion.	at have previously been associated with pes recognized by the HIV-1 infected duration of viral exposure to the epitope, but in neither of the 2/5 ersion, and upon seroconversion
gp160 (843–851)	gp41 (843–851)  The CTL response to opstudied in eight HIV-1-i  to 17 epitopes were reepitopes were targeted be Subjects with chronic H  An acute seroconvertor  The other acute serocon	IPRRIRQGL otimally defined CTL e infected subjects, two v ecognized in a given inc by at least one person IIV-1 infection recogni homozygous for the B evertor failed to recogni	HIV-1 infection pitopes restricted by HLA class I A and with acute infection, five with chronic, an dividual, A2-restricted CTL response ten zed between 2-8 out of 11 B7-restricted epi 7 allele recognized five B7-restricted epi ize any of the 11 B7-restricted epitopes t uriable and there was no clearly dominan	human (B7) B alleles in individuals who c ad one long-term non-progress ded to be narrow and never de epitopes topes ested	Day2001 oexpressed HLA A2, A3, and B7 was or (LTNP)
gp160 (843–851)	gp41 (SF2)  This epitope was mappe an HLA-B60 individual		HIV-1 infection ady identifying new HLA-B60 epitopes,	human (B7) and was one of the epitopes p	Altfeld2000b resented by another HLA molecule in
gp160 (843–851)	• One individual, AC-06,	was homozygous at al had only two detectabl	HIV-1 infection  A-A3 (n=7) or -B7 (n=4) or both -A3 and three class I alleles (A3, B7, Cw7), was e CTL responses during acute infection, by HLA-Cw7.	s treated during acute infection	and had supervised treatment

HXB2 Location	<b>Author's Location</b>	Sequence	Immunogen	Species (HLA)	References
	was the first targeted pe  • 6/11 HLA-B7 individua	ptide, and remained immur ls had detectable B7-restric	nodominant through the 34 month	study period.  ng acute infection – 10/15 of HLa	d Gag GPGHKARVL. GPGHKARVL  A-B7 epitopes tested were targeted by
gp160 (843–851)	<ul> <li>CTL epitopes (http://hiv</li> <li>60 epitope responses we magnitude of the responses to CD8+ T-cells is higher in 1 year post-HAART tree in PB, and 13/25 epitope</li> <li>Treatment interruption in become undetectable in</li> <li>Breakdowns of epitope</li> </ul>	and lymph node (LN) CD8-tr-web.lanl.gov/content/hiv- ere detected in both PB and asse was similar in LN and I in the LN. atment in five patients studie responses in the PB becate following HAART induced the PB, and the addition of responses were shown for the PB in the content of the PB.	db/REVIEWS/brander2001.html) d LN samples of the 15 patients, an PB, but the percentage of CD8+ T died, the magnitude of the CD8 T-come undetectable, in contrast to 5/20 resulted in increased viremia accord 9 novel epitope responses.	for each person's class I HLA all ad an additional 8 responses were cells in the LN is lower so the nu ell response was decreased in bot 6 in the LN.  Impanied by the restoration of the the greatest response to B27-KK	detected only in LN. The total mber of HIV-specific cells per million th LN and PB, but more dramatically
gp160 (845–856)	gp41 (852–863 HXB2) • CTL epitope defined by	RRIRQGLERILL  T cell line and peptide ma	HIV-1 infection	human (A30, B8)	Lieberman1992
gp160 (845–856)	gp41 (852–863 LAI)	RRIRQGLERILL	HIV-1 infection	human (B7)	Shankar1996
gp160 (846–854)		RIRQGLERA	HIV-1 infection	human (A*0205)	Sabbaj2002b

## II-B-19 Env CTL Epitopes

HXB2 Location	<b>Author's Location</b>	Sequence	Immunogen	Species (HLA)	References
Env	The live canarypox va	ccine ALVAC-HIV(vCI	Vaccine gp120 boost Strain: MN, LAI, SF2 P205) carrying MN gp120, LAI gp41, Grag CD8+ CTL were detected in 64%	Gag and Protease, and boosted w	
Env	delivery of protein alo <ul><li>Chloroquine administr</li></ul>	ne	HIV-1 infection 24 NY5) to human dendritic cells (DC presentation, and brefeldin A and pept me pathway		
Env	HIV+ infants • No HIV+ infants had a disease, and not in rap	no demonstrable CTL a pid progressors	HIV-1 infection had lower Th1 responses and decrease t birth, but Th1 responses accompanied g dilution using autologous B cells infe	l by CTL responses developed in	children with slowly progressive
Env	(HAART) decrease gle	obal CD8 T cell oligocl	HIV-1 infection region repertoire indicates that antiret onality during primary HIV infection clones was observed in HAART-treate		Soudeyns2000 y active antiretroviral therapy
Env	<ul><li>The vaccine used was</li><li>Twenty HIV negative</li><li>Immunization with vC</li></ul>	a rec canarypox with H subjects were vaccinate CP205 induced HIV-1-sp	Vaccine II, MN HIV component: gp41, Gag, IIV-1 gp120 MN, tm/gag/protease LAI d in phase I trial with combinations of pecific ABs to gp120, V3, and p24 antits against Env, Gag and Pol, but the CI	(vCP205), alone or with p24E-V vCP205 and CLTB-36 gens, and CTL immune response	es against vCP205 were detected after
Env	responses to Gag, Pol, <ul><li>Data suggests that the</li></ul>	Env or Nef antigens functional and genetic	HIV-1 infection showed CD8 T cell proliferation and d integrity of the CD8 T cell repertoire (*Tell control co		-
Env	Env (LAI, MN)  Vaccine Vector/Type:  • The vaccine used was	canarypox prime with r	Vaccine gp120 boost <i>Strain:</i> LAI and SF2 <i>I</i> and HIV-1 env, gag, pol, nef and proteas Env, Gag, Pol, and Nef antigens was o	se (vCP300) with or without adm	inistration of HIV-1 SF-2 rgp120

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
	• The combination of vo	CP300 and vP1291 toge	ther resulted in an overall increase in	CTL induction and detection sensi	tivity
Env	Env (LAI) • In infants with positive subtypes	e CTL responses, most i	HIV-1 infection responses showed cross-clade reactive	human ity with somewhat diminished reco	Buseyne1998b gnition of epitopes from different
Env			Vaccine IV component: gp120, gp160 gp120 or gp160 DNA vaccine elicite	Rhesus macaque ed a strong CD8 cytotoxic T cell res	Shiver1997 ponse
Env	<ul><li>A strong CTL respons</li><li>The CTL response pea</li></ul>	se against env, pol and ga aked by 4 weeks and dec	HIV-1 infection the infection within 6 months, so it is agantigens can be detected clined dramatically by 8 weeks al blood was comparable	Macaca nemestrina is of interest to examine their initial	Kent1997b immune response
Env	<ul> <li>A gag/pol, vif or env I increase in both the cy</li> </ul>	DNA vaccine, when deligitotoxic and proliferative	Vaccine : Gag, Pol, Vif, Env Adjuvant: B7, vered in conjunction with the plasmic responses in mice be detected even without in vitro stir	d encoding the co-stimulatory mole	Kim1997c cules B7 and IL-12, gave a dramatic
Env	<ul> <li>A gag/pol or env DNA both the cytotoxic and</li> </ul>	A vaccine, when delivered proliferative responses	Vaccine : Gag, Pol, Vif, Env Adjuvant: B7, d in conjunction with the plasmid en in mice I be detected even without in vitro sti	coding the co-stimulatory molecule	Kim1997d es CD86, gave a dramatic increase in
Env	<ul> <li>Vaccination of Macaq response, and type-spo</li> </ul>	ues mulatta (Rhesus mo ecific neutralizing antibo	Vaccine ) boost Strain: HXBc2 HIV comp nkeys) with an HXBc2 env DNA prindies (B2 were protected from infection		Letvin1997 cell proliferative response, a CTL
Env	<ul><li>An HIV DNA env and</li><li>The CTL response to</li></ul>	I rev vaccine given to 15 gp120 was enhanced in	Vaccine IV component: Env, Rev asymptomatic HIV+ individuals at t 0/4 patients in the 30 µg group, 2/3 p and a strong CTL response prior to va	patients in the 100 $\mu$ g group, and 0/	3 in the 300 $\mu$ g group – but the
Env			HIV-1 infection and with their own lymphocytes, cryop seen in 7/12, and an increase in the C		
Env	gp120 (LAI) • Seventeen recently inf	fected patients were teste	HIV-1 infection ed for CTL response to HIV proteins	human Env, Gag, Pol, Rev, Nef, Vif and Ta	Legrand1997 at

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
	<ul><li>An early response (with Early responses to Pol</li></ul>		PI) was noted in 87% of the subjects to rare	o Gag, 75% to Env, and 50% to N	lef
Env	<ul> <li>Vaccinia-naive subject</li> </ul>	s were vaccinated with	Vaccine b120 boost Strain: LAI, SF2, MN F vaccinia-gp160 LAI and boosted with se that were boosted with gp120 tender	gp120 SF2, LAI, MN, or 160 MI	
Env	Env proteins		HIV-1 infection clade virus had CTL that were able to a particular protein, and the level	-	-
Env	• Anti-NKR IgM MAb	masked this inhibitory f	HIV-1 infection receptor (NKR+) can exhibit down reg function and increased HIV-1 specific 0 e other case anti-NKR MAb brought H	CTL activity in phytohemaggluting	
Env			HIV-1 infection n between HIV Type I plasma viral loa term survivors (LTS) of HIV-1 infection		Betts1999 nst HIV-1 Pol, and stronger combined
Env		orrelation between strong CD4 and CD8 cells, and		human nse in 7-12 month old infants, and	Buseyne1998a I remaining AIDS-free for the first year
Env	CTL activity was corre	elated with a CCR5 wile	dtype genotype	IIV-1 specific CTL against Env, C	Goh1999 Gag, Pol, or a combination of proteins – ar individuals had responses to multiple
Env	<ul> <li>A Canarypox vaccine</li> </ul>	expressing gp120, gp41	Vaccine onent: gp120, gp41, Gag, Pro, Nef, RT , Gag, Protease, Nef and Pol CTL epit cted 3-6 months after the last vaccinati	topes gave rise to CTL that could	Evans 1999 be detected in 61% of the volunteers –
Env	<ul> <li>Priming with an HIV-I</li> <li>The proliferative response fold increase in the median</li> </ul>	DNA vaccine and boost onse to Env and Gag aft	Vaccine nia boost Strain: LAI HIV compone ing with a vaccinia construct induced g er the DNA vaccination had a mean SI Env. The T help response happened de as also enhanced	greater levels of HIV T cell immu of 1.5-4, but after boosting with	rHIV-fowlpox virus, there was a 6-17

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
Env			Vaccine I, LAI HIV component: gp120, gp41, G MN gp120 and LAI gp41/gag/protease co		Salmon-Ceron1999 oproliferative response in healthy,
Env	• The study explores the	use of co-stimulatory n	Vaccine Env, Gag, Pol Adjuvant: CD86, CD80 nolecules co-expressed with an HIV-1 imically increased both HIV Env and Gag/P	munogen in a DNA vaccine to	
Env	<ul> <li>Immunization of SIV F the HIV antigens in Se</li> </ul>	Pr56Gag-derived VLPs mliki-Forest Viruses en	Vaccine th virus-like particle boost Strain: IIIB with HIV-1 gp120 anchored on their surfa hanced the immunological outcome nowed a more rapid reduction of plasma v	ice induced Abs, CTL and Th	
Env		nt HIV-1-resistance in ea ed to HIV-1 specific CT	HIV-1 exposed seronegative exposed and uninfected individuals is not continuously.		Akridge1999 deletion in the HIV-1 co-receptor
Env			HIV-1 infection elease assay in bulk culture showed no co CD4 and time to death	human orrelation between CTL-activi	Aladdin1999 ty (gp120, Gag, Pol and Nef) and
Env			HIV-1 infection hancement of CD4 cell counts that was a fon was ultimately enhanced	human ccompanied by a decrease in 0	Aladdin2000 CTL activity – IL-2 therapy did not
Env	found in non-transmitti (Lazuriaga95);	ing mothers than in tran	HIV-1 infection  n HIV-1 infected pregnant women, and hig smitting mothers – Nef CTL responses had d in env depending on whether IIIB, MN.	ave been found in uninfected i	nfants born to HIV+ women
Env	<ul> <li>This paper is a review of vaccinia to very efficient</li> </ul>	ntly boost memory T-ce	xt of vaccines strategies that use different		
Env	Rhesus macaques were		Vaccine IV component: complete genome ection with naked plasmid DNA carrying a	Rhesus macaque an HIV-1 complete genome va	Akahata2000 accine, strain ZF1, with a mutated zing

finger in the nucleocapsid to prevent packaging

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
	<ul> <li>2/4 monkeys (MM146</li> <li>PBMC from all vaccir MM145, the animal w</li> <li>4 weeks post-challeng detection limit</li> </ul>	and MM143) produced nated monkeys produced ith the strongest CTL re e with SHIV NM-3rN p	sponses were induced in 2/4 vaccinated antibodies against p24 and/or gp160, I IFN-gamma, in response to HIV-1 gp sponse blasma viral loads of both MM145 and I plasma viral loads of both MM146 ar	but no CTL response was detected 160, indicating a Th response – MM153 (with a homologous E	teted this response was 5 times higher in nv) decreased to near or below the
Env	<ul><li>tested increased lysis l</li><li>2/10 individuals with</li></ul>	by > 5%) if the culture v <200 CD4 cells/ul, and	was derived from HIV+ individuals wh	no had CD4 cells/ul > 500 ls/ul, had an increase of >5% up	Young2001 20 vaccinia expressed antigens (11/15 con treatment of the culture with rhIL12,
Env	cross-reactive CTL res HIV-1 clades A, B, an • Proteins corresponding	D dominate the Ugand sponses in HIV infected d D g to the subtype of the is	HIV-1 infection an epidemic, and a vaccine trial using a Ugandans to A, D, and B clade recom infecting strains tended to trigger highe ith B clade proteins and the co-circula	binant vaccinia viruses expressi r levels of CTL response measu	
Env	Protease Adjuvant: I • 26/42 subjects who rea a CTL response	MF-59 adjuvant ceived CP vac-env-pro v		by Cr-release, while only 3/17 v	AVEG022PT2001 F2 gp120 HIV component: Env, Gag, who were vaccinated with rec gp120 had % of subjects
Env		vity was detected in the	HIV-1 infection female reproductive tract of only 1/3 l	human HIV-infected women who under	White2001 rwent a hysterectomy, although CTL
Env		and Pol expressed in va	HIV-1 infection ed in long term non-progressors (LTNF ccinia in autologous targets low viral load	human P) with low viral load using limi	Jin2000a iting dilution analysis and measuring
Env	by therapy, using a tet	ramer assay	HIV-1 infection ed in long term non-progressors (LTNI low viral load, while HAART patient		Jin2000a tients whose virus was well-suppressed ow viral load
Env	Env • This is a review that so	ummarizes observations	HIV-1 exposed seronegat about HIV-specific CTL found in the		Rowland-Jones2001 onegative (HEPS) population

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References		
	<ul> <li>of a lower magnitude to CD8+ CTL responses clear if there is a stable</li> <li>CD8+ CTL responses and ELISPOT, and the individuals relative to</li> <li>HIV-1 specific CD8+ of CD8+ o</li></ul>	than in chronic HIV-1 in tend to be detectable in the memory population in in the HEPS population authors consider the population HIV-1 infected individual CTL responses in HIV-1	nfections – the responses in HEPS cas HEPS subjects only if they are recent HEPS cases are associated with HIV-1 specific Cossibility that HIV-1-specific T-help relials, who tend to have a poor HIV-1-specific T-help relials.	es are below the level of detection by exposed, and the response dimensional distribution of the response dimensional distribution of the responses improve the "quality" of the presponse distribution of the response dis	ninishes if exposure is reduced – it is no y proliferation assays, IL-2 secretion, f the CD8+ response in HEPS may not mature properly, and although		
Env			Vaccine	murine	Nabel2002		
	<ul> <li>Env DNA constructs v Env expression levels, responses, when inject</li> </ul>	deletions in the cleavag	codon optimized for human genes, ex	e constructs increased Ab respon	regulatory protein Rev, both increasing uses to Env, while not diminishing CTL as has been seen in analogous SIV		
Env	• 6/24 HIV uninfected i: • Reviewed in [Kuhn200]		HIV-1 exposed seronega ths) born to HIV+ mothers had HIV-1		De Maria1994, Kuhn2002 nia-expressed Nef, Gag/Pol, Env.		
Env	<ul> <li>remained very low in 3</li> <li>The two infants with h</li> <li>Stronger responses we</li> <li>Two babies that were n</li> </ul>	HIV-1 infection human Kuhn2002, Wasik1999  In HIV-infected infants HIV-specific, CTL responses were not detectable in cord blood or in PBMC collected shortly after birth and were absent or remained very low in 3 infants with a rapidly progressive disease. For those who progressed more slowly, the HIV-specific CTL activity varied.  The two infants with high levels of Env peptide-stimulated IL-2 responses had the highest CTLp frequencies.  Stronger responses were detected after initiation of the antiretroviral therapy.  Two babies that were not infected though born to HIV+ mothers had detectable though low HIV-specific CTLp responses to Env (1/2), Pol (2/2), Gag (1 cord blood and transiently in PBMC after birth.					
Env	responses were detected	ed at all time points.  That were not infected the	HIV-1 infection d HIV-1 specific CTL responses to vac- lough born to HIV+ mothers had detect	•	Aldhous1994, Kuhn2002 /6), Env (1/6), or Gag (1/6), but not all /2), Gag (1/2).		
Env	were found in PBMC	from 91% and 78% of I ot infected though born	HIV-1 infection TL against Env or Gag in unstimulated HIV-infected children, respectively, wi to HIV+ mothers had detectable respectively.	th high precursor frequencies.	Kuhn2002, McFarland1994 of PBMC, Gag and Env specific CTL		

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
Env	variable regions found  • While the uneven distrused to probe the immediate to not be found in C-te virus where variation is and turn regions in the	in Nef, Env and p17. ibution of epitopes may une response and autologrminal positions of epit is best tolerated traces of proteins.	HIV-1 infection ture and included in this database tend to clu be in part due to a limited cross-recognition ogous strains, regions with a paucity of defir opes, and had lower cleavage prediction sco f immune escape have left an imprint on the	n of specific responses becaused epitopes also had higherers for epitope processing a viral population. Epitopes	ause of differences between peptides or frequencies of amino acids that tend. This suggests that in the regions of the
Env	from the individuals re	eceiving ART showed in	HIV-1 infection  Env expressing targets from 25 HIV+ patient acreased TNFalpha production and a reduction a potential benefit of immunomodulants	on of perforin and granzyr	
Env	<ul><li>Nef and/or Pol CTL re</li><li>The magnitude and bre</li><li>Pol and Int CTL response</li></ul>	esponses were detected is eadth of Gag and p24 T nses correlated positive	HIV-1 infection ted patients elicited gamma-IFN CD8+ T-ce in 86% of the subjects -cell responses correlated with absolute CD4 ly with absolute CD4+ T-cell count either CD4 counts or viral load		Edwards2002 related with viral load
Env	<ul> <li>Vaccination route of H application of DNA dir responses, IFN-gamma</li> <li>DNA delivered topical</li> </ul>	IIV-1 DNA immunization rectly on the skin after of a and IL-4 production, ally with adjuvant-like cases.	Vaccine  IV component: gp160, Rev Adjuvant: cation with gp160 and Rev genes was compared elimination of keratinocyte layers using a strund delayed type hypersensitivity (DTH). To tionic liposomes gave a stronger response the cytotoxic activity and DTH.	including intranasal (i.n.), rong adhesive. Topical expopical application favored	nitramuscular (i.m.), and topical osure resulted in high level CTL Fh2 responses.
Env	patients on successful	HAART treatment, rela	HIV-1 infection ccinia expressing Gag, Pol, Nef and Env coutive to autologous monocytes. Some weak retection of low frequency memory cells.		
Env		s were obtained in 14 d	HIV-1 infection sion of CD8+ and CD4+ T-cells with the goays with optimized concentrations of IL-2, a		
Env			HIV-1 and HCV co-infection ied in 22 individuals who were co-infected cells using targets expressing either Gag, RT		

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
	recognized Nef. Robus  Despite high HCV vira strong anti-HCV respo	st CTL activity was ind al loads, very few HCV onses were mounted.	0/22 patients recognized RT, 17/22 patients of disease progression or vira CD8+ T-cell Elispot responses were detected in 9/17 coinfected patients,	al load. etected. In a control HCV infector	•
Env	<ul><li>varied at different time</li><li>2/4 infants infected int</li></ul>	point. Pol responses wrapartum had detectabl		one not until 42 months.	Luzuriaga1995 months of age. Levels of the responses
Env	<ul> <li>A safety and immunog</li> </ul>	geniticity study of a vac	Vaccine gp120 boost HIV component: gag, er cine dosing schedule was studied in a t Env CTL response by day 728.		
Env	<ul> <li>Before ART 2/13 infar became undetectable a</li> <li>One older infant, at 23 group. 3/4 infants olde</li> </ul>	nts <6 months of age sh fter successful therapy- months, had CTL resp or than 6 months of age	HIV-1 infection ART were studied in 13 HIV-1 vertically owed IFNgamma Elispot CD8+ T-cell - 3 infants were coinfected with CMV onses against all for proteins tested, Garesponded to either Nef or Pol. ned the HIV-1-specific CTL response is	responses, one to Nef and one to and all 3 had CMV-specific CD8 ag, Pol, Nef and Env, and had the	DEnv and Nef, and these responses + T-cell responses. Elowest plasma viremia of the study
Env	boosted HIV-1 specific rebound to pretreatmen gp160, Gag p55, RT-Po	c CTL responses and ele nt levels and CD4 T-cel ol and Nef expressed in	HIV-1 infection infected patients undergoing HAART evated CTL responses were maintained count decline was observed. CD8 responses had an augmented neutralizat	l up to 22 weeks after the last tre ponses in PBMC were measured	atment interruption, but viral load
Env	was inhibited by an HI		, relative to a Nef-deleted virus; while		Tomiyama2002 ted HIV-1-epitope specific CTL clones regulation inhibited lysis, it did not
Env	HLA-A*0201 and HL	A-B*3501 HIV T-cell e	computer prediction works, hidden Markov models, binding epitope candidates from 533 Gag, Enva risons to known epitopes and between	and Pol sequences of which 374	

HIV CTL Epitope Tables Env CTL Epitopes

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References			
Env			Vaccine	human (A1, A2, A24, B62, A25, A26, A30, A31, B8, B17, B39, B51, B57, B60, B62, B70)	Ferrari2001			
	<ul> <li>component: gp120, gp</li> <li>HLA-B62 responses down against the MN pe</li> <li>Class I presentation of</li> <li>Class I presentation of</li> <li>Class I presentation of</li> </ul>	41, Gag, Pol and Nef of commanded the response optide 381-400; a response in Env CTL responses in the command of the com	rgp120 boost, canarypox prime with rgp1 epitope rich regions is against an Env vaccine in an individual onse diminished by half was observed again vaccinee 022A12K: A25 > B39, A1 and a vaccinee 022A12N: B57 » A2 > A26 and vaccinee 034GP3: A31 > A24 > B62 > B4 vaccinee 0348PP: B17 > B70, A1 and A3 vaccinee 0348PP: B17 × B70 vaccinee 0348PP: B17 vaccinee 0348PP: B17 vaccinee 0348PP: B17 vaccinee 0348PP: B17 vac	60 boost Strain: gp41 LAI, G (022JAV) who was HLA A2, A2 inst vaccinia expressed clade A B8 were undetectable. d B60. B51.	26, B35, B62. The strongest response			
Env	gp120 (303–327)	Ziii C1Z Teopenses II	HIV-1 infection	human (A2, A3, A11, B27)	Ferrari2000			
	<ul> <li>One of the 51 HIV-1 epitopes selected by Ferrari et al. as good candidate CTL epitopes for vaccines by virtue of being conserved and presented by common HLA alleles</li> <li>For this cluster of epitopes spanning the tip of the V3 loop, they suggest including a sequence from each clade</li> </ul>							
Env	component: gp120, gp-	41, Gag, Pol and Nef 6 8 responses were mad	e against the Env vaccine in individuals c					
Env	<ul> <li>Of 32 patients with HL 69% to Gag, 50% to N</li> <li>The overall magnitude in those that had lower</li> </ul>	A-B*35 alleles CD8+ ef, and 41% to Env. of CTL responses did RNA levels that carrie	HIV-1 infection *3503, B*3504, and B*5301 tend to proc CTL responses were quantified using an not differ between those bearing B*3501 ed B*3501, and there was a negative asso to protection in B*3501 individuals, but r	intracellular cytokine staining a and the others. A higher percer ciation with viral load and CTL	assay – 75% had responses to Pol, ntage of Gag responses was observed activity. The data is consistent with			
Env			HIV-1 infection  vo HIV-specific CTL showed that in early accumulate prior to down-regulation of v		Pantaleo1997, Soudeyns1997 ones preferentially accumulate in			
Env	<ul> <li>Mammalian codon opt yields a higher antibod</li> </ul>	imization renders gp10 y response with an ear	Vaccine HIV component: gp160, gp120, codon-op 60 expression Rev independent, increases elier onset than wild type nan membrane bound gp160		Vinner1999 NA vaccination of BALB/c mice			

HXB2 Location	<b>Author's Location</b>	Sequence	Immunogen	Species (HLA)	References
	In contrast to antibodic	es, synthetic codon-option	mized DNA did not alter the CTL resp	ponse, wild type genes generated	equally strong CTL responses
Env	<ul><li>A multicomponent per</li><li>Immunization of BAL</li></ul>	otide vaccine VC1 with B/c mice with VC1 and	Vaccine  nt: V3 Adjuvant: Cholera Toxin adjuto toxin adjuvant was given to more common to the common of the common	nice. which was enhanced by IL-12 exp.	
Env	<ul><li>A PLG-microparticle</li><li>Oral DNA vaccination</li></ul>	encapsulated DNA enco of BALB/c mice induce	Vaccine IV component: gp160 Adjuvant: PI ding gp160 was given to mice. ed mucosal and systemic gp160 glyco -env expressing vaccinia intrarectal cl	oprotein-specific cellular and hum	
Env			Vaccine tor with cationic liposome HIV com arrying gp160 and Rev linked to a cyto		Ishii1997
Env	<ul><li>An AAV vector expres</li><li>A single injection stim</li></ul>	ssing HIV-1 env, tat, and nulated and long lasting	Vaccine (AAV) HIV component: Env, Tat, Relative genes (AAV-HIV vector) was use serum IgG, fecal IgA, and HIV-specif IL2 enhanced T-cell immunity	ed to vaccinate BALB/c mice	Xin2001
Env	• The use of two differe response in Balb/c mid	nt live vectors for priming on the cocurred when they we	Vaccine rain: IIIB HIV component: V3, Env ng and boosting has a synergistic effer vere immunized with rec influenza vir V-Env) expressing the complete HIV-	ct on the immune response agains us (Flu-Env) expressing the V3 lo	oop epitope from HIV-1 strain IIIB, and
Env	<ul><li>BALB/c were immuni</li><li>A single vaccination in</li><li>Although the greatest</li></ul>	zed with a replication conduced induced strong a specific lysis was achiev	Vaccine L4-3, 89.6 HIV component: gp160 competent recombinant rabies virus (R' nd long-lasting (4.5 months) gp160-s yed when the vaccine strain was also us to clade HIV-1 envelope proteins, imply	pecific CTL cytotoxic responses used as the in vitro the target strai	n to assess the response, there was

HXB2 Location	<b>Author's Location</b>	Sequence	Immunogen	Species (HLA)	References			
Env	Env (SIV)		SIV infection	Rhesus macaque	Dzuris2000			
				(Mamu-A*11, -B*03,				
				-B*04, and -B*17)				
	• Cell binding assays for Mamu molecules were employed to describe the peptide binding motifs for Mamu-A*11, -B*03, -B*03, -B*04, and -B*17 CTL							
	epitopes – a similarity for so not specifically listed		numan HLA-B*44 and -B*27, respect	ively, was observed – all ep	pitopes studied were SIV epitopes,			

## **II-B-20** Nef CTL Epitopes

HXB2 Location	<b>Author's Location</b>	Sequence	Immunogen	Species (HLA)	References
Nef (1–16)	<ul><li>each HIV protein.</li><li>Nef and p24 had the hi</li></ul>	ghest percentage of reactive p	peptides, and p24 had the highes	human anans; Elispot data was obtained fr t magnitude of HIV-1 responses. d tested spanning all HIV proteins.	Novitsky2002 rom between 55 and 64 subjects for
Nef (13–20)	Nef (13–20 LAI) • C. Brander notes this is	WPTVRERM s a B*0801 epitope	HIV-1 infection	human (B*0801)	Brander2001, Goulder1997g
Nef (13–20)	molecules. Such a cons		e as a more potent immunogen.		Peng2001 egulation of MHC class I and CD4 at would be disputed by this deletion
Nef (13–20)	Nef (13–20 LAI) • Unusual epitope for Hl	WPTVRERM  LA-B8, but compatible with c	HIV-1 infection rystal structure predictions	human (B8)	Goulder1997g
Nef (13–20)	<ul> <li>95 optimally-defined p</li> </ul>	eptides from this database we	HIV-1 infection t reacted to SLYNTVATL, calling the used to screen for INFγ responses to this epitop		Betts2000 unodominant
Nef (13–20)	<ul> <li>individuals treated duri</li> <li>The breadth and specifindividuals with primate (Group 3), using 259 of Previously described a</li> </ul>	ing chronic infection  neity of the response was dete  ry infection but post-seroconv  verlapping peptides spanning  nd newly defined optimal epit	rmined using ELISPOT by study ersion therapy (Group 2), and 10 p17, p24, RT, gp41, gp120 and opes were tested for CTL respon	ying 19 individuals with pre-seroco 0 individuals who responded to HA Nef	AART given during chronic infection
Nef (13–20)	Nef (13–20) • B8-restricted CTL acco	WPTVRERM ounted for about 1/3 of the tot	HIV-1 infection al CTL response in one individu	human (B8) nal	Day2001
Nef (42–50)			Vaccine  3 HIV component: Nef Adjusted with HI A.	murine (HLA-A201 transgenic)  vant: Freund's adjuvant  A*0201 – of these, four did bind str	Sandberg2000

- Ten Nef 9-mer peptides were predicted to have a strong binding affinity with HLA-A\*0201 of these, four did bind strongly by a T2 class I stabilization assay, several others bound weakly
- A CTL immune response to only 3/10 peptides was detected by a 51Cr-release assay after immunization of HLA-A201 transgenic mice with either nef DNA under the control of a CMV promotor, coated on gold particles delivered to abdominal skin by gene gun
- ALTSSNTAA was also tested by subcutaneous injection of Nef peptides in Freund's adjuvant

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
	ALTSSNTAA bound w peptide vaccination	reakly to HLA-A2, but i	it had the strongest CTL response amo	ong the three elicited by the DNA	vaccine and a strong response to the
Nef (48–56)	Nef (58–66 JRFL) <b>Vaccine</b> Vector/Type: I	TAATNADCA DNA <i>Strain:</i> JRFL	Vaccine	murine (H-2 <sup>b</sup> )	Liang2002
	<ul> <li>The Nef mutant that laits ability to elicit induand the di-leucine moti</li> <li>N-terminal addition of</li> </ul>	cked the myristylation of tion of Nef-specific CE f for the down-regulation thuman tissue plasminos		ucine motif (L -> A at positions I myristylation site is critical for Ne mutation of these regions could y CD8+ T-cell responses and could	74 and 175) was impaired in terms of ff membrane localization and function, ield a safer vaccine. compensate for the G2A, L174A,
Nef (62–81)	Nef (61–80) • HIV-specific CTL lines		PLRPMTY HIV-1 infection stimulation with peptide	human	Lieberman1995
Nef (62–81)	• Two of these 12 had C	d CTL specific for more ΓL that could recognize ΓL response to this pept	vaccinia-expressed LAI Nef	human	Lieberman1997a
Nef (62–81)	Nef (61–80 SF2) • CTL expanded ex vivo	EEEEVGFVTPQVP: were later infused into		human	Lieberman1997b
Nef (62–81)	<ul><li>from 7 proteins, sugges</li><li>Nef peptides PQVPLR</li></ul>	6 was tested for reactive sting that the breadth of RMTYKAAVDLSHFL	PLRPMTY HIV-1 infection coverlapping peptides spanning all HI CTL responses are underestimated if , KAAVDLSHFLKEKGGLEGLI and st and last share PQVPLRPMTY	accessory proteins are not includ	ed in the study
Nef (66–80)	Nef (66–80 BRU) • HIV-1 specific CTLs d	VGFPVTPQVPLRM etected in lymphoid org	T HIV-1 infection ans of HIV-1 infected patients	human (A1, B8)	Hadida1992
Nef (66–80)	Nef (64–78) • One of the 51 HIV-1 ep HLA alleles	VGFPVTPQVPLRMinitopes selected by Ferra		human (A1, B8) pes for vaccines by virtue of being	Ferrari2000 g conserved and presented by common
Nef (66–97)	<ul> <li>Anti-HIV lipopeptide v administered in a phase</li> </ul>	VDLSHFLKEKGGL ipopeptide HIV composaccine consisting of six E I trial		-	Gahery-Segard2000  ins modified by a palmitoyl chain was to this Nef peptide
		CTL response to at least	t one of the six peptides; each of the s		

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
Nef (67–81)	<ul><li>each HIV protein.</li><li>Nef and p24 had the high</li></ul>	ghest percentage of reactive p	eptides, and p24 had the highes	human anans; Elispot data was obtained t magnitude of HIV-1 responses. d tested spanning all HIV proteins	Novitsky2002 from between 55 and 64 subjects for
Nef (68–76)	• 3/7 B35-positive individ	FPVRPQVPL e to this epitope was obtained duals had a CTL response to t at position 4 abrogates specifi		human (B*3501)	Tomiyama1997
Nef (68–76)	<ul><li>A significant increase in healthy individuals</li><li>CD28-CD45RA- cells a</li></ul>	n CD28-CD45RA- cells and a are likely to be effector cells a	and have high levels of perforin	cells was observed in chronically in their cytoplasm	Tomiyama2000a  HIV-1-infected individuals relative to rison to HIV-1-uninfected individuals
Nef (68–76)	Nef (72–80 SF2) • Binds HLA-B*3501	FPVRPQVPL	HIV-1 infection	human (B35)	Shiga1996
Nef (68–76)	• The sequences of 9 prev	ubstitutions that were more co	CTL epitopes were obtained in	human (B35)  10 HLA B35+ and 19 HLA B35- n in B35- individuals, but this wa	
Nef (68–76)	Nef (66–74) • One of the 51 HIV-1 ep HLA alleles	FPVRPQVPL itopes selected by Ferrari et a	HIV-1 infection  1. as good candidate CTL epitop	human (B35) pes for vaccines by virtue of being	Ferrari2000 g conserved and presented by common
Nef (68–76)	<ul> <li>73 peptides had 81 mot directly related to the m</li> <li>20s proteasome cleavag</li> <li>The frequency of recog</li> </ul>	ifs. 54% bound to the predict umber of individuals that reco ge of the Nef protein positions nition may be in part dictated	ed HLA molecule, particularly a ognized a protein. 66-100 showed a large fraction by the cleavage step in process	A2, B7/35, and B8. The strength of peptides were cleaved endinging.	Choppin2001 A2, A3, A24, B7, B8, and B35; these of HLA-peptide binding was not at: 87L, 83A, 81Y, 71P, 68F and 67G.  6. It was a high affinity HLA binder.
Nef (68–76)	donors		•		Wilson1999b T cells cultured from HIV negative g from peptide, or expressed from

<b>HXB2</b> Location	<b>Author's Location</b>	Sequence	Immunogen	Species (HLA)	References
	B7 and A2 Nef epitope	es were studied – FPVTF	QVPL has a high affinity for B7		
Nef (68–76)	studied in eight HIV-1  • 2 to 17 epitopes were repitopes were targeted  • Subjects with chronic l  • An acute seroconvertor  • The other acute seroco	infected subjects, two we recognized in a given ind by at least one person HIV-1 infection recognize the homozygous for the B7 invertor failed to recognize	HIV-1 infection bitopes restricted by HLA class I A an ith acute infection, five with chronic, ividual, A2-restricted CTL response t ed between 2-8 out of 11 B7-restricted allele recognized five B7-restricted e ze any of the 11 B7-restricted epitope riable and there was no clearly dominic	and one long-term non-progress rended to be narrow and never do ed epitopes epitopes s tested	
Nef (68–76)	73 peptides had 81 mo directly related to the r  • 20s proteasome cleava. The frequency of recognitions are recognitive to the recognition of the	tifs. 54% bound to the produmber of individuals that ge of the Nef protein posignition may be in part did	redicted HLA molecule, particularly A at recognized a protein.	A2, B7/35, and B8. The strength of peptides were cleaved endinging.	g at: 87L, 83A, 81Y, 71P, 68F and 67G.
Nef (68–76)	<ul> <li>One individual, AC-06 interruptions (STI). He restricted by HLA-A3,</li> <li>0/11 HLA-B7 individu</li> </ul>	was homozygous at all had only two detectable 11 by HLA-B7, and 1 b lals had detectable B7-re		vas treated during acute infection n, but after STI this broadened to ng acute infection – 10/15 of HL	and had supervised treatment o 27 distinct epitopes including 15 A-B7 epitopes tested were targeted by
Nef (68–77)	Nef (68–77 LAI) • C. Brander notes this is	FPVTPQVPLR s a B*0702 epitope	HIV-1 infection	human (B*0702)	Brander2001
Nef (68–77)	Nef (68–77 LAI)  There was a high degree variants, indicating imm		HIV-1 infection TL epitopes in Nef in four slow and n	human (B7) non-progressors, and variant spec	Haas1996 ific CTLs arose over time to eliminate
Nef (68–77)	<ul><li>sex workers eventually</li><li>FPVTPQVPLR was re</li><li>20/20 sequences of the</li></ul>	seroconverted, and for secondized in 1 of the 6 we infecting strain had no sector associated with seron retire	substitutions in this epitope, all were I occonversion was stopping sex work ar	s had been defined while serone as present in the last available san FPVTPQVPLR, so there was no	gative mple prior to seroconversion, 7 months evidence for escape

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
Nef (68–77)	Nef (66–75) • One of the 51 HIV-1 e HLA alleles	FPVRPQVPLR pitopes selected by Ferrar	HIV-1 infection ri et al. as good candidate CTL epitope	human (B7) es for vaccines by virtue of beir	Ferrari2000 ng conserved and presented by common
Nef (68–77)	<ul> <li>individuals treated dur</li> <li>The breadth and speci individuals with prima (Group 3), using 259 c</li> <li>Previously described a</li> </ul>	ring chronic infection ficity of the response was ary infection but post-sero overlapping peptides span and newly defined optimal	determined using ELISPOT by studyi	ing 19 individuals with pre-sero individuals who responded to lef se	HAART given during chronic infection
Nef (68–77)	<ul> <li>HIV-1-infected female</li> <li>Responses in HEPS w reduced risk of infecti women</li> <li>43/91 HEPS women h</li> <li>Subject ML 1203 start</li> </ul>	e Nairobi sex workers omen tended to be lower, on, and there was a shift i ad CD8+ responses and d ted with CTL responses to		es in 91 HIV-1-exposed, persist th HLA presenting molecules th pon late seroconversion to epito EPS women increased with the eVTPQVPLR prior to seroconversion	at have previously been associated with opes recognized by the HIV-1 infected duration of viral exposure ersion, and upon seroconversion
Nef (68–77)	<ul> <li>studied in eight HIV-1</li> <li>2 to 17 epitopes were epitopes were targeted</li> <li>Subjects with chronic</li> <li>An acute seroconverto</li> <li>The other acute seroco</li> </ul>	-infected subjects, two wirecognized in a given indi l by at least one person HIV-1 infection recognized or homozygous for the B7 powertor failed to recognized	HIV-1 infection itopes restricted by HLA class I A and ith acute infection, five with chronic, a vidual, A2-restricted CTL response te ed between 2-8 out of 11 B7-restricted allele recognized five B7-restricted ep te any of the 11 B7-restricted epitopes iable and there was no clearly domina	and one long-term non-progress ended to be narrow and never de d epitopes bitopes tested	
Nef (68–77)	<ul> <li>One individual, AC-06 interruptions (STI). He restricted by HLA-A3</li> <li>0/11 HLA-B7 individual</li> </ul>	6, was homozygous at all e had only two detectable , 11 by HLA-B7, and 1 by uals had detectable B7-res		as treated during acute infection, but after STI this broadened t g acute infection – 10/15 of HI	n and had supervised treatment to 27 distinct epitopes including 15 _A-B7 epitopes tested were targeted by

HIV CTL Epitope Tables

Nef CTL Epitopes

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
Nef (68–81)			HIV-1 infection udy epitope diversity in this geographics and the subtype		Guimaráes2002 ce is FPVTPQVPLRMTY, but
Nef (68–84)	subtype in nef and env	and 7 of the 41 strains were	s of HIV-1 A-H were genetically of	_	Jubier-Maurin1999 4 subtypes were classified in the same
Nef (71–79)	Nef (71–79 LAI) • C. Brander notes this is	TPQVPLRPM a B*0702 epitope	HIV-1 infection	human (B*0702)	Brander2001
Nef (71–79)	<ul><li>73 peptides had 81 mot directly related to the n</li><li>20s proteasome cleavag</li><li>The frequency of recog</li></ul>	ifs. 54% bound to the prediction of individuals that regree of the Nef protein position in may be in part dictated.	cted HLA molecule, particularly cognized a protein.  ns 66-100 showed a large fractioned by the cleavage step in process	A2, B7/35, and B8. The strength of peptides were cleaved endinging.	Choppin2001 A2, A3, A24, B7, B8, and B35; these of HLA-peptide binding was not at: 87L, 83A, 81Y, 71P, 68F and 67G.
Nef (71–79)	<ul> <li>individuals treated duri</li> <li>The breadth and specific individuals with primar (Group 3), using 259 or</li> <li>Previously described ar</li> </ul>	ng chronic infection city of the response was det y infection but post-serocon verlapping peptides spannin d newly defined optimal ep	termined using ELISPOT by stud	ying 19 individuals with pre-seroe 0 individuals who responded to H Nef nse	AART given during chronic infection
Nef (71–79)	studied in eight HIV-1- • 2 to 17 epitopes were re epitopes were targeted • Subjects with chronic F • An acute seroconvertor • The other acute serocon	infected subjects, two with ecognized in a given individ- by at least one person HV-1 infection recognized I homozygous for the B7 all- evertor failed to recognize a	HIV-1 infection pes restricted by HLA class I A ar acute infection, five with chronic, lual, A2-restricted CTL response between 2-8 out of 11 B7-restricted ele recognized five B7-restricted on ny of the 11 B7-restricted epitope le and there was no clearly domin	and one long-term non-progressor tended to be narrow and never do ed epitopes epitopes es tested	
Nef (71–79)	73 peptides had 81 mot		cted HLA molecule, particularly		Choppin2001 A2, A3, A24, B7, B8, and B35; these of HLA-peptide binding was not

**HIV CTL Epitope Tables** 

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
	The frequency of recog	gnition may be in part die	itions 66-100 showed a large fraction stated by the cleavage step in process f individuals with HLA B7, and 1/10	ing.	g at: 87L, 83A, 81Y, 71P, 68F and 67G.  5. It was a moderate affinity HLA
Nef (71–79)	<ul> <li>One individual, AC-06 interruptions (STI). He restricted by HLA-A3,</li> <li>0/11 HLA-B7 individual</li> </ul>	cutely HIV-infected HLA, was homozygous at all had only two detectable 11 by HLA-B7, and 1 beals had detectable B7-reserved.		was treated during acute infection on, but after STI this broadened to a gaute infection – 10/15 of HL	and had supervised treatment
Nef (71–79)	<ul> <li>CTL epitopes (http://hi</li> <li>60 epitope responses w magnitude of the responses were compared to the response of t</li></ul>	and lymph node (LN) Cliv-web.lanl.gov/content/livere detected in both PB onse was similar in LN are in the LN. eatment in five patients spe responses in the PB of following HAART indum the PB, and the addition responses were shown from the PB. TM9(Nef) are posses to B7-TM9(Nef) are responses to B7-TM9(Nef	tudied, the magnitude of the CD8 T-cecame undetectable, in contrast to 5/2 ced resulted in increased viremia according of 9 novel epitope responses.	of for each person's class I HLA all and an additional 8 responses were cells in the LN is lower so the number of the LN.  The cell response was decreased in both 26 in the LN.  The cell response was decreased in both 26 in the LN.  The cell response was decreased in both 40 in the LN.  The cell response was decreased in both 40 in the LN.  The cell response was decreased in both 40 in the LN.  The cell response was decreased in both 40 in the LN.  The cell response was decreased in both 40 in the LN.	lleles. e detected only in LN. The total umber of HIV-specific cells per million oth LN and PB, but more dramatically ne detection of 13 epitopes that had B14-EL9(gp41), a strong response to
Nef (71–81)	Nef (75–85 SF2)  • A CTL clone responsive  • 4/7 B35-positive indivition  • An R to T substitution  • An R to H substitution	iduals had a strong CTL at position 1 abrogates s	response to this epitope pecific lysis, but not binding to B*35	human (B*3501)	Tomiyama1997
Nef (71–81)	<ul> <li>A significant increase inhealthy individuals</li> <li>CD28-CD45RA- cells</li> </ul>	in CD28-CD45RA- cells are likely to be effector of	cells and have high levels of perforin	cells was observed in chronically in their cytoplasm	Tomiyama2000a y HIV-1-infected individuals relative to arison to HIV-1-uninfected individuals

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
Nef (71–81)	Nef (75–85 SF2) • Binds HLA-B*3501	RPQVPLRPMTY	HIV-1 infection	human (B35)	Shiga1996
Nef (71–81)	<ul> <li>The sequences of 9 prev</li> <li>3/9 CTL epitopes had so peptide to B35 and was</li> <li>rpqvplrpmtF was found</li> </ul>	ubstitutions that were more community shown to be an escape mutation	none of the B35- individuals—the Y	- individuals – only one of	these reduced the binding of the
Nef (71–81)	Nef (69–79) • One of the 51 HIV-1 ep HLA alleles	RPQVPLRPMTY itopes selected by Ferrari et al. as	HIV-1 infection s good candidate CTL epitopes for va	human (B35) accines by virtue of being co	Ferrari2000 onserved and presented by common
Nef (71–81)	73 peptides had 81 moti directly related to the nu • 20s proteasome cleavag The frequency of recogn • TPQVPLRPMTY was 1	ifs. 54% bound to the predicted I imber of individuals that recognie of the Nef protein positions 66 nition may be in part dictated by	-100 showed a large fraction of pepti	5, and B8. The strength of des were cleaved ending at:	HLA-peptide binding was not 87L, 83A, 81Y, 71P, 68F and 67G.
Nef (71–81)	<ul> <li>The HIV-1 subtype A for which could direct the processor conserved, often immur Kenya. A DNA and MV included in the polyepit</li> <li>Multiple CD4+ or CD8-assays after vaccination</li> </ul>	ocused vaccine HIVA contains particle of the cell membrane and modominant epitopes that were self-A prime-boost vaccination proto ope string [Hanke2000].  + T-cell vaccine-induced response of 5 macaques. The response to	HIV-1 infection, Vaccine cost <i>Strain:</i> subtype A <i>HIV comp</i> 24 and p17, in a reversed order relativishibit efficient peptide processing a elected to have particularly good crost ocol using the HIVA antigen will be used to peptide pools were detected using the Mamu A*01 SIV p27 epitope p1 caques, possibly because of processi	we to the Gag polyprotein to nd class I presentation, as we s-reactive potential for the used in a phase III clinical to ing intracellular cytokine sta 1C (CTPYDINQM), include	pe prevent myristylation of p17, vell as a polyepitope string of A-clade epidemic in Nairobi, rial in Kenya. This epitope is aining and IFNgamma Elispot led in the polyepitope region, was
Nef (71–81)	<ul><li>73 peptides had 81 motidirectly related to the nu</li><li>20s proteasome cleavag</li></ul>	ifs. 54% bound to the predicted I imber of individuals that recogni	-100 showed a large fraction of pepti	5, and B8. The strength of	HLA-peptide binding was not

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
		recognized in 9/12 (75%) of in- term Y readily cleaved in vitr	ndividuals with HLA B7, and 5/10 (50).	50%) of individuals with HL	A B35. It was a moderate affinity
Nef (72–86)	<ul><li>each HIV protein.</li><li>Nef and p24 had the hi</li></ul>	ghest percentage of reactive pe	HIV-1 infection from 105 HIV-1 positive Botswanans eptides, and p24 had the highest mag peptides from among over 350 tester	gnitude of HIV-1 responses.	Novitsky2002 from between 55 and 64 subjects for s.
Nef (72–91)	<ul><li>Eleven subjects had CT</li><li>Three of these 11 had CT</li></ul>	PQVPLRMTYKAAVDLSHE d CTL specific for more than L that could recognize vaccin CTL response to this peptide ts were HLA-A3, A32, B51, B	1 HIV-1 protein ia-expressed LAI Nef	human	Lieberman1997a
Nef (72–91)	Nef (71–90 SF2) • CTL expanded ex vivo	PQVPLRPMTYKAAVDLSF were later infused into HIV-1		human	Lieberman1997b
Nef (72–91)	from 7 proteins, sugges • Nef peptides PQVPLR	sting that the breadth of CTL r	apping peptides spanning all HIV-1 pesponses are underestimated if access VDLSHFLKEKGGLEGLI and EEE	ssory proteins are not includ	
Nef (73–82)		QVPLRPMTYK P1 specific for this epitope is a perforin-dependent Nef-speci	HIV-1 infection able to kill target cells via two mechanics.	human anisms	Garcia1997
	<ul> <li>Second: Ca<sup>2+</sup>-indepen</li> <li>Findings indicate that t</li> </ul>	dent, CD95-dependent apopto	sis that could also kill non-specific tatually exclusive in human CTL, as to		
Nef (73–82)	<ul> <li>Second: Ca<sup>2+</sup>-indepen</li> <li>Findings indicate that t</li> <li>CTL mediated CD95-d</li> <li>Nef (73–82 NL43)</li> <li>81 Tyr is critical for bin</li> </ul>	dent, CD95-dependent apopto he two mechanisms are not me ependent apoptosis may play a QVPLRPMTYK	sis that could also kill non-specific trutually exclusive in human CTL, as to a role in pathogenesis  HIV-1 infection		Koenig1990
Nef (73–82)	<ul> <li>Second: Ca<sup>2+</sup>-indepen</li> <li>Findings indicate that t</li> <li>CTL mediated CD95-d</li> <li>Nef (73–82 NL43)</li> <li>81 Tyr is critical for bin</li> </ul>	dent, CD95-dependent apopto he two mechanisms are not me ependent apoptosis may play a QVPLRPMTYK ading to A3.1 his is an A*0301 epitope in the QVPLRPMTYK	sis that could also kill non-specific trutually exclusive in human CTL, as to a role in pathogenesis  HIV-1 infection	they are in mice	Koenig1990 Brander2001

Vaccine Vector/Type: DNA prime with vaccinia MVA boost Strain: subtype A HIV component: p17, p24, polyepitope

• The HIV-1 subtype A focused vaccine HIVA contains p24 and p17, in a reversed order relative to the Gag polyprotein to prevent myristylation of p17, which could direct the protein to the cell membrane and inhibit efficient peptide processing and class I presentation, as well as a polyepitope string of conserved, often immunodominant epitopes that were selected to have particularly good cross-reactive potential for the A-clade epidemic in Nairobi, Kenya. A DNA and MVA prime-boost vaccination protocol using the HIVA antigen will be used in a phase III clinical trial in Kenya. This epitope is included in the polyepitope string [Hanke2000].

HXB2 Location	<b>Author's Location</b>	Sequence	Immunogen	Species (HLA)	References
	assays after vaccination	of 5 macaques. The res	responses to peptide pools were detections to the Mamu A*01 SIV p27 eparted macaques, possibly because of parted macaques.	oitope p11C (CTPYDINQM), inc	cluded in the polyepitope region, was
Nef (73–82)	<ul><li> Epitope name: Nef-QK</li><li> Among HIV+ individua</li></ul>		HIV-1 infection 3, 9/20 (45%) recognized this epitope	human (A03)	Sabbaj2002b
Nef (73–82)			HIV-1 infection '-specific cloned CTL line and an EB noncytotoxic mechanism	human (A11) V (Epstein-Barr-virus) CTL line	Le Borgne2000 inhibit viral replication, but do not
Nef (73–82)	<ul><li>[Hunziker1998] suggest</li><li>The initial assignment o</li></ul>	s that HLA-A2 does not f HLA-A2 presentation	HIV-1 infection of generate autologous CTL targets in fact present this epitope for this epitope was based on a serologous the correct presenting molecule (I		Robertson1993  y, the authors revisited the issue with nm., 2000)
Nef (73–82)	Nef (73–82 LAI)  • Mutational variation in l  • [Goulder1997a] is a revi		HIV-1 infection nals with appropriate HLA types can nat summarizes this study	human (A11) result in evasion of CTL respons	Couillin1994, Goulder1997a
Nef (73–82)	Nef (73–82 LAI) • Mutations found in this	QVPLRPMTYK epitope in HLA-A11 po	HIV-1 infection sitive and negative donors were chara	human (A11) acterized	Couillin1995
Nef (73–82)	(LAI)	QVPLRPMTYK		(A11)	Brander2001, Buseyne1999
Nef (73–82)	CD4 proliferative responsible HAART had no HIV sponsored undetectable  One of the 2/8 HLA-A1  Patient SC18(HLA A2/1)	nses and were able to mecific CD4 proliferative  1 study subjects recogni  1, B8/44, Cw06/0701,	aintain a CTL response even with uncoresponses and lost their CTL response zed this CTL epitope	detectable viral load – three pationses when HAART was eventually the epitopes ACQGVGGPGHK, one	y given and their viral loads became  QVPLRPMTYK, AVDLSHFLK, and
Nef (73–82)	Nef (73–82)	QVPLRPMTYK tudy CTL responses to a	HIV-1 infection, HIV-1 ex seronegative panel of 54 predefined HIV-1 epitop	xposed human (A11)	Kaul2001a
Nef (73–82)	Nef (73–82) • Combined tetramer and	QVPLRPMTYK intracellular cytokine st	HIV-1 infection aining was used to study the function	human (A11) n of circulating CD8+ T cells spe	Appay2000 cific for HIV and CMV

HXB2 Location	<b>Author's Location</b>	Sequence	Immunogen	Species (HLA)	References
	CD27 expression on HI	V-specific cells, suggesti	ls of perforin than CMV-specific CD8+ T ng impaired maturation tivated virus-specific CD8+ T cells produce		-
Nef (73–82)	Nef (71–80 93TH253 subtype CRF01) • Epitope name: N73-82	QVPLRPMTYK	HIV-1 infection, HIV-1 exposed seronegative	d human (A11)	Sriwanthana2001
	<ul> <li>HLA-A11 is very comm and CTL responses wer</li> <li>This epitope was weakl stimulation, in study sul</li> </ul>	non in this population, and e found in 8/8 HIV+ con y reactive in HEPS study oject 256 who was HLA	seronegative (HEPS) female sex workers in the days are riched among the HEPS sexwork trols, and 0/9 HIV- women that were not explained to subject 265 who was HLA A2/A11 and A11/33, making it the most reactive epitory subject 053 who carried HLA-A11	ters – weak CTL response exposed 128 who was HLA A11/A	s were detected in 4/7 HEPS women, A33, and after a second in vitro
Nef (73–82)	Thailand, of whom mor 77 possible HLA-A11 e epitopes for CTL respon This epitope was predic that had been previously 4/8 tested FSWs recogn An HLA-A11 tetramer population after in vitro	e than half were HLA-A pitopes were first defined uses from 8 HLA-A11 poted by the EpiMatrix mey defined ized this epitope was made for this epitope stimulation	HIV-1 infection  al.) epitopes were identified that stimulated 11 positive dusing EpiMatrix, these were screened for sitive FSWs, six were novel, six were prethod to be likely to bind to A11, and it serve, which was recognized by two subjects - types, and exact matches were common	r binding to A11 finding a viously identified ved as an epitope in the F	and 26 bound, and 12 of these were SWs, it was one of the six A11 epitopes
Nef (73–82)	period including therapy	with standard treatment	HIV-1 infection  One of the control		•
Nef (73–82)	<ul><li>specific T-cell responses</li><li>Nef epitope recognition HLA-A3, one using HL</li></ul>	s by Elispot and Tetrame was detected in all 4 sub A-A11	HIV-1 infection ressful anti-viral therapy but with ongoing r staining, maintained for 2-4 years after injects, gp120, Pol and Gag-specific in 1 or late maturation phenotype characterized by	nitiation of HAART. 2 subjects – two patients	recognized this epitope, one using

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
Nef (73–82)	Nef (73–81)	QVPLRPMTYK	HIV-1 infection	human (A2, A3, A11, B35)	Ferrari2000
	• One of the 51 HIV-1 e HLA alleles	epitopes selected by Ferrari	et al. as good candidate CTL epitop	pes for vaccines by virtue of being	conserved and presented by common
Nef (73–82)	Nef (73–82 LAI)  • Mutations in Nef that of proteasome process		HIV-1 infection ys and Ala83Gly, may account for a	human (A3) n observed loss of CTL reactivity,	Chassin1999 with escape due to the introduction
Nef (73–82)	<ul> <li>one A subtype infection</li> <li>Pol reactivity: 8/8 had</li> <li>Gag reactivity: 7/8 reactivity: 7/8 reactivity: 7/8 reactivity: 3/8 reactivity: 3/8</li></ul>	on from a person living in I I CTL to A subtype, and 7/ acted with A or B subtype acted with A subtype, and 5	France originally from Togo, to differ 8 to B subtype, and HIV-2 Pol was a gag, 3/8 with HIV-2 Gag 6/8 with B subtype, none with HIV-2 with B subtype, none with HIV-2 Envith B subtype, none with HIV-2 Envitage with HIV-2 Envitag	erent antigens expressed in vaccini not tested  2 Nef	Durali1998 and 1 AG recombinant infections) and ia
Nef (73–82)	<ul> <li>Both had a response to</li> </ul>		HIV-1 infection fected with the same batch of factor at summarizes this study	human (A3)	Goulder1997e, Goulder1997a
Nef (73–82)	<ul> <li>A sustained Gag, Env</li> </ul>	and Nef response was obs	HIV-1 infection ing-term non-progressors were isolaterved, and clones were restricted by tope, with 10/11 CTL clones being states.	multiple HLA epitopes, indicating	g a polyclonal response
Nef (73–82)	Nef (73–82) • Epitope name: N1 • The epitope was recog	QVPLRPMTYK gnized by patients 252#0 a	HIV-1 infection and 252#4 in a study of the effects of	human (A3)  therapy escape mutations on CTL	Samri2000 recognition
Nef (73–82)	<ul> <li>individuals treated du</li> <li>The breadth and speci individuals with prima (Group 3), using 259</li> <li>Previously described a</li> </ul>	ring chronic infection ificity of the response was of ary infection but post-seroe overlapping peptides spann and newly defined optimal	determined using ELISPOT by study	ying 19 individuals with pre-seroco 0 individuals who responded to Ha Nef nse	AART given during chronic infection
Nef (73–82)	Nef (SF2) • This epitope was map an HLA-B60 individu		HIV-1 infection y identifying new HLA-B60 epitope	human (A3) es, and was one of the epitopes pre	Altfeld2000b sented by another HLA molecule in

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References			
Nef (73–82)	Nef (73–82) • Epitope name: A3-QK	QVPLRPMTYK	HIV-1 infection	human (A3)	Yu2002a			
	<ul> <li>CTL responses in 18 acutely HIV-infected HLA-A3 (n=7) or -B7 (n=4) or both -A3 and B7 (n=7) positive individuals were studied.</li> <li>One individual, AC-06, was homozygous at all three class I alleles (A3, B7, Cw7), was treated during acute infection and had supervised treatment interruptions (STI). He had only two detectable CTL responses during acute infection, but after STI this broadened to 27 distinct epitopes including 15 restricted by HLA-A3, 11 by HLA-B7, and 1 by HLA-Cw7.</li> <li>3/14 HLA-A3 positive individuals had detectable A3-restricted responses to this epitope during acute infection, but only 5/15 of HLA-A3 epitopes tested were targeted during acute infection. 5/7 individuals had detectable responses to this epitope after STI.</li> </ul>							
Nef (73–82)	<ul><li>specific T-cell response</li><li>Nef epitope recognitio HLA-A3, one using H</li></ul>	es by Elispot and Tetrame on was detected in all 4 sub LA-A11.	HIV-1 infection ressful anti-viral therapy but with one restaining, maintained for 2-4 years a pjects, gp120, Pol and Gag-specific in attended the maturation phenotype characterization.	fter initiation of HAART.  1 or 2 subjects – two patients rec	rognized this epitope, one using			
Nef (73–82)	CD8+ cell IFNgamma • In general, during the specificities that were HIV-specific responses	production to measure rest first month of treatment vi not previously detectable s diminished	HIV-1 infection  s was tested in 14 HIV+ patients from sponses ral load decreased and frequencies of were newly detected, as were CMV see: increases or decreases in pre-exist	f HIV-specific CTL tripled and br pecific CD8+ PBL – but with con	padened – eight new HIV tinued viral suppression,			
Nef (73–82)	<ul> <li>for the A3 supertype)</li> <li>Progressors had memor</li> <li>A positive correlation observed, which may of</li> </ul>	while the effector cells of ory resting CD8+ T-cells the between effector CD8+ T- contribute to the inability of	HIV-1 infection memory resting CD8+ T-cell response long-term nonprogressors recognized nat recognized far fewer epitopes that cells and plasma viremia and a negat of LTNPs to clear virus eles (A*0301, A*1101, A*3101, A*	I far fewer epitopes 1 LTNPs ive correlation between CD8+ eff				
Nef (73–82)	Nef (73–82 BRU) • Nef CTL clones from	QVPLRPMTYK HIV+ donors	HIV-1 infection	human (A3, A11, B35)	Culmann1991			
Nef (73–82)	• Nef CTL clones (4N22	25) were infused into an H	HIV-1 infection A significantly decreased immunoger IV-1 infected volunteer to evaluate e resulted in higher viral load/accelera	ffects of infusion on viral load/pa	Koenig1995 ient health			
Nef (73–82)	•		HIV-1 infection  that reacted to SLYNTVATL, calling were used to screen for INFγ response.	- 1	Betts2000 unodominant			

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
	• 1/11 of the A2+ individ	luals was A3, and respo	nded to QVPLRPMTYK as well as two	other A3.1 epitopes	
Nef (73–82)	<ul> <li>CD8+ T cells were four viral load was also four</li> <li>All three patients were</li> <li>ELISPOT was used to a subjects showed a dom</li> <li>The subject with A*020</li> <li>Weak responses were of B*2705</li> <li>No acute response was</li> </ul>	nd prior to seroconversited B*2705, with HLA allewest a panel of CTL epiterinant response to the B*01 had a moderatly strought bserved to A*301-RLR detected to the following	HIV-1 infection scific CTL responses were studied during on, and there was a close temporal relativeles: A1, A30/31, B*2705, B35; A1, A* topes that had been defined earlier and w 2705 epitope KRWIILGGLNK ng response to SLYNTVATL PGGKKK, A*301-QVPLRPMTYK, an ag epitopes: A*201-ILKEPVHGV, A*30 PIPVGEIY, B35-NSSKVSQNY, B35-VI	ionship between the number of 0301, B7, B2705; and A*0201, ere appropriate for the HLA hand B7-TPGPGVRYPL in the sul 01-KIRLRPGGK, A*301-AIFQ	circulating HIV-specific T cells and A*0301, B2705, B39 plotypes of the study subjects – 3/3 pject who was HLA A1, A*0301, B7, PSSMTK, A*301-TVYYGVPVWK,
Nef (73–82)	Nef (73–82 LAI) • Optimal epitope mappe	QVPLRPMTYK od by peptide titration		human (B27)	Culmann1998
Nef (73–82)	• Epitopes recognized in	cytotoxic activity agair five children were map	HIV-1 infection to 39% ast at least one HIV protein was detected ped using synthetic peptides and second the epitopes in Nef, was infected via bloom	ary cultures	Buseyne1993a  nt from CDC stage P2A to P2E
Nef (73–83)	73 peptides had 81 mot directly related to the n  • 20s proteasome cleavage The frequency of recognitions and the second	ifs. 54% bound to the pumber of individuals the ge of the Nef protein ponition may be in part di	HIV-1 infection and based on putative anchor motifs in the redicted HLA molecule, particularly A2 at recognized a protein. Sitions 66-100 showed a large fraction of ctated by the cleavage step in processing %) of individuals with HLA A3. It was	2, B7/35, and B8. The strength of peptides were cleaved ending g.	of HLA-peptide binding was not
Nef (74–81)	Nef (74–82) • Included in HLA-A3 bi	VPLRPMTY inding peptide competit	ion study	human (A3)	Carreno1992
Nef (74–81)	Nef (73–82 LAI) • C. Brander notes this is	VPLRPMTY a B*3501 epitope	HIV-1 or HIV-2 infection	human (B*3501)	Brander2001
Nef (74–81)	Nef (75–82) • Crystal structure of VP	VPLRPMTY LRPMTY-class I B alle	Peptide-HLA interaction le HLA-B*3501 complex	human (B*3501)	Smith1996
Nef (74–81)	<ul> <li>Optimal expansion of I</li> </ul>	HIV-1-specific memory	HIV-1 infection rirus-specific memory CTL was studied CTL depended on CD4+ T cell help in 9 e degree in most of patients		Ostrowski2000 rimer (CD40LT) could enhance CTL

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References			
	<ul> <li>Those CTL that didn't respond to CD40LT could expand with IL2 present, and IL15 produced by dendritic cells also contributes</li> <li>The T-helper epitope used for CD4+ T cell stimulation was the universal tetanus helper epitope TET830-843 (QYIKANSKFIGITE)</li> </ul>							
Nef (74–81)	<ul><li>CD8+ T cell responses</li><li>Low risk individuals di</li><li>CD8+ T cell epitopes:</li></ul>	tended to be to the same d not have such CD8+ c	uals), SLYNVATL (4 individuals), LSP	IIV-specific CD8 gamma-IFN than cervical CD8+ T cell resp	ponses			
Nef (74–81)	<ul> <li>CD8+ T cells were four viral load was also four</li> <li>All three patients were</li> <li>ELISPOT was used to the subjects showed a domnown</li> <li>The subject with A*020</li> <li>Weak responses were of B*2705</li> <li>No acute response was</li> </ul>	nd prior to seroconversiond B*2705, with HLA allel test a panel of CTL epitorinant response to the B*01 had a moderatly stronubserved to A*301-RLRI detected to the following	HIV-1 infection cific CTL responses were studied during on, and there was a close temporal relatives: A1, A30/31, B*2705, B35; A1, A*0 opes that had been defined earlier and w 2705 epitope KRWIILGGLNK og response to SLYNTVATL PGGKKK, A*301-QVPLRPMTYK, an og epitopes: A*201-ILKEPVHGV, A*30 IPVGEIY, B35-NSSKVSQNY, B35-VF	ionship between the number of 0301, B7, B2705; and A*0201 were appropriate for the HLA hand B7-TPGPGVRYPL in the substitution of the HLA hand B7-T	f circulating HIV-specific T cells and A*0301, B2705, B39 aplotypes of the study subjects – 3/3 abject who was HLA A1, A*0301, B7, QSSMTK, A*301-TVYYGVPVWK,			
Nef (74–81)	Nef (73–82 LAI) • Review of HIV CTL ep	VPLRPMTY bitopes – defined by B35	HIV-1 or HIV-2 infection motif found within a larger peptide	human (B35)	Culmann1991, McMichael1994			
Nef (74–81)	Nef (73–82 LAI) • VPLRPMTY also recog	VPLRPMTY gnized by CTL from HI	HIV-1 or HIV-2 infection V-2 seropositives; epitope is conserved	human (B35)	Rowland-Jones1995b			
Nef (74–81)		oss-reactivity could prote	HIV-1 exposed seronegative affected prostitutes from Nairobi using pacet against both A and D and confer properties the B clade epitope	reviously-defined B clade epit				
Nef (74–81)	stimulate a primary res	ponse, only secondary – f the B35 presented test	in vitro stimulation timulation of CTLp using optimized pe peptide-specific CTLp counts could be peptides used in control experiments sh	obtained via staining with per	otide-Class I tetramers			
Nef (74–81)	<ul><li>Seroprevalence in this of</li><li>Most isolated HIV strain</li></ul>	cohort is 90-95% and the ins are clade A in Nairob	HIV-1 exposed seronegative egative prostitutes from Nairobi – these eir HIV-1 exposure is among the highes oi, although clades C and D are also four clade versions of epitopes	e CTL may confer protection t in the world	Rowland-Jones1998b n cross-reactive, however stronger			

HXB2 Location	<b>Author's Location</b>	Sequence	Immunogen	Species (HLA)	References
	This epitope is conser-	ved among A, B, and D	clade viruses		
Nef (74–81)	<ul><li>deletion in CCR5</li><li>In Gambia there is exp</li></ul>	oosure to both HIV-1 ar	sposed African female sex workers in Ga ad HIV-2, CTL responses to B35 epitope PLRPMTY, and CTLs are cross-reactive	es in exposed, uninfected wome	en are cross-reactive,
Nef (74–81)	[Rowland-Jones 1995b] Nef (74–81)	VPLRPMTY	HIV-1 infection	human (B35)	Oxenius2000
	CD4 proliferative resp HAART had no HIV s undetectable • One of two HLA B35-	conses and were able to specific CD4 proliferati + among the eight study 1/68, B8/35, Bw4/6, Cv	nfection (three with sustained therapy, two maintain a CTL response even with und we responses and lost their CTL response wallows subjects recognized this epitope wallo704) was given acute and sustained	letectable viral load – three pati es when HAART was eventual	ients that had delayed initiation of ly given and their viral loads became
Nef (74–81)	<ul><li>HIV-1-infected female</li><li>Responses in HEPS w</li></ul>	Nairobi sex workers omen tended to be lowe	HIV-1 infection, HIV-1 ex seronegative o a panel of 54 predefined HIV-1 epitoper, and focused on different epitopes with it in the response in the HEPS women up	es in 91 HIV-1-exposed, persist	at have previously been associated with
		ed from a A*6802 DTV	detection of HIV-1-specific CTL in HE LEDINL and B35 (H/N)PDIVIYQY res		•
Nef (74–81)		uals who carried HLA I	HIV-1 infection  335, 12/22 (55%) recognized this epitop 3*5301, 0/11 (0%) recognized this epito		Sabbaj2002b
Nef (74–81)	73 peptides had 81 modirectly related to the second 20s proteasome cleava. The frequency of reco	otifs. 54% bound to the number of individuals t age of the Nef protein p gnition may be in part of	HIV-1 infection ted based on putative anchor motifs in the predicted HLA molecule, particularly A hat recognized a protein. ositions 66-100 showed a large fraction dictated by the cleavage step in processing individuals with HLA B35, and it was	A2, B7/35, and B8. The strength of peptides were cleaved endining.	n of HLA-peptide binding was not g at: 87L, 83A, 81Y, 71P, 68F and 67G

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References		
Nef (74–81)	<ul> <li>The HIV-1 subtype A which could direct the conserved, often immu Kenya. A DNA and M included in the polyep.</li> <li>Multiple CD4+ or CD3 assays after vaccinatio</li> </ul>	focused vaccine HIVA of protein to the cell mem inodominant epitopes the VA prime-boost vaccin itope string [Hanke20008+ T-cell vaccine-induction of 5 macaques. The results of the control of the contro	HIV-1 infection, Vaccine hia MVA boost Strain: subtype A HIV contains p24 and p17, in a reversed order relabrane and inhibit efficient peptide processing the were selected to have particularly good cation protocol using the HIVA antigen will body.  Ded responses to peptide pools were detected esponse to the Mamu A*01 SIV p27 epitopoolinated macaques, possibly because of processing the MVA because of processing the macaques	lative to the Gag polyprotein to the gand class I presentation, as cross-reactive potential for the be used in a phase III clinical lusing intracellular cytokine see p11C (CTPYDINQM), included	well as a polyepitope string of A-clade epidemic in Nairobi, trial in Kenya. This epitope is staining and IFNgamma Elispot aded in the polyepitope region, was		
Nef (74–82)	Nef (73–82) • Exploration of A11 bir	VPLRPMTYK nding motif	Peptide-HLA interaction	human (A11)	Zhang1993		
Nef (75–82)	Nef (75–82 LAI)  Review of HIV CTL e  C. Brander notes that t		HIV-1 infection se in the 1999 database	human (A*1101)	McMichael1994		
Nef (75–82)	Nef (75–82 LAI) • C. Brander notes this i	PLRPMTYK s an A*1101 epitope	HIV-1 infection	human (A*1101)	Brander2001		
Nef (77–85)	Nef (77–85 LAI)  Structural constraints of Noted in Brander 1999			human (B*0702)	Bauer1997		
Nef (77–85)	Nef (77–85 LAI) • C. Brander notes this i	RPMTYKAAL s a B*0702 epitope	HIV-1 infection	human (B*0702)	Brander2001		
Nef (77–85)	Nef (75–83 IIIB) RPMTYKAAL HIV-1 infection human (B7) Oxenius2001b  • Study of tetramer staining of B7 around RPMTYKAAL gave quantitative results that were very different than functional measurements based on an ELISPOT assay  • Autologous clones were checked and 39/40 clones from two time points had the variant sequence RPMTYKGAL – tetramers based on RPMTYKGAL gave a more intense and uniform staining and bound with higher affinity to the RPMTYKGAL Vbeta14 TCR						
Nef (77–85)	<ul> <li>individuals treated dur</li> <li>The breadth and specifindividuals with prima (Group 3), using 259 c</li> <li>Previously described a</li> </ul>	ing chronic infection ficity of the response wary infection but post-se overlapping peptides spand and newly defined optime	HIV-1 infection ted in a narrower CTL response, stronger T as determined using ELISPOT by studying a roconversion therapy (Group 2), and 10 indianning p17, p24, RT, gp41, gp120 and Nef tal epitopes were tested for CTL response tTL response to this epitope broken down by	19 individuals with pre-seroco ividuals who responded to HA	onversion therapy (Group 1), 11 AART given during chronic infection		

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References		
Nef (77–85)	<ul> <li>studied in eight HIV-1</li> <li>2 to 17 epitopes were repitopes were targeted</li> <li>Subjects with chronic</li> <li>An acute seroconverto</li> <li>The other acute serocon</li> </ul>	-infected subjects, two veccognized in a given in by at least one person HIV-1 infection recogning homozygous for the Bonvertor failed to recogn	HIV-1 infection epitopes restricted by HLA class I A and with acute infection, five with chronic, a dividual, A2-restricted CTL response terms at the example of the B7-restricted epitopes ariable and there was no clearly dominar	nd one long-term non-progress nded to be narrow and never do epitopes itopes tested	or (LTNP)		
Nef (77–85)	Nef (77–85) RPMTYKAAV HIV-1 infection human (B7) Day2001  • The CTL response to optimally defined CTL epitopes restricted by HLA class I A and B alleles in individuals who coexpressed HLA A2, A3, and B7 was studied in eight HIV-1-infected subjects, two with acute infection, five with chronic, and one long-term non-progressor (LTNP)  • 2 to 17 epitopes were recognized in a given individual, A2-restricted CTL response tended to be narrow and never dominated the response, and 25/27 epitopes were targeted by at least one person  • Subjects with chronic HIV-1 infection recognized between 2-8 out of 11 B7-restricted epitopes  • An acute seroconvertor homozygous for the B7 allele recognized five B7-restricted epitopes  • The other acute seroconvertor failed to recognize any of the 11 B7-restricted epitopes tested  • The B7-restricted CTL response was highly variable and there was no clearly dominant epitope						
Nef (77–85)	<ul> <li>73 peptides had 81 mo directly related to the r</li> <li>20s proteasome cleava</li> <li>The frequency of recognition</li> </ul>	otifs. 54% bound to the pumber of individuals the ge of the Nef protein pountion may be in part d	HIV-1 infection ed based on putative anchor motifs in the predicted HLA molecule, particularly A2 nat recognized a protein. sitions 66-100 showed a large fraction of ictated by the cleavage step in processin of individuals with HLA B7, and 0/3 (0)	2, B7/35, and B8. The strength of peptides were cleaved ending g.	of HLA-peptide binding was not g at: 87L, 83A, 81Y, 71P, 68F and 67G.		
Nef (77–85)	<ul> <li>One individual, AC-06 interruptions (STI). He restricted by HLA-A3.</li> <li>3/11 HLA-B7 individual</li> </ul>	cutely HIV-infected HL b, was homozygous at all e had only two detectable, 11 by HLA-B7, and 1 alls had detectable B7-r	HIV-1 infection  A-A3 (n=7) or -B7 (n=4) or both -A3 and three class I alleles (A3, B7, Cw7), was the CTL responses during acute infectionable that the HLA-Cw7.  The estricted responses to this epitope during individuals had detectable responses to the serious detectable responses detectable responses to the serious detectable responses detectable responses to the serious detectable responses	as treated during acute infection, but after STI this broadened to g acute infection – 10/15 of HL	n and had supervised treatment to 27 distinct epitopes including 15		
Nef (77–85)	<ul> <li>One individual, AC-06 interruptions (STI). He</li> </ul>	cutely HIV-infected HL 6, was homozygous at al	HIV-1 infection  A-A3 (n=7) or -B7 (n=4) or both -A3 and three class I alleles (A3, B7, Cw7), was the CTL responses during acute infectionable by HLA-Cw7.	as treated during acute infection	and had supervised treatment		

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References		
			cted responses to this epitope duri ividuals had detectable responses t		-B7 epitopes tested were targeted by		
Nef (77–91)	<ul><li>each HIV protein.</li><li>Nef and p24 had the hi</li></ul>	ghest percentage of reactive	e peptides, and p24 had the highes	-	Novitsky2002 rom between 55 and 64 subjects for		
Nef (79–87)	Nef (81–89 HXB3)	MTYKAALDL	Vaccine B3 HIV component: Nef Adju	murine (HLA-A201 transgenic)	Sandberg2000		
	<ul> <li>Ten Nef 9-mer peptides assay, several others be</li> <li>A CTL immune responding DNA under the control</li> </ul>	s were predicted to have a sound weakly use to only 3/10 peptides was of a CMV promotor coated	strong binding affinity with HLA-A	A*0201 – of these, four did bind st y after immunization of HLA-A20 odominal skin by gene gun	rongly by a T2 class I stabilization  1 transgenic mice with either nef		
Nef (82–91)	<ul><li>reducing the antigenic</li><li>Within 7 days of therap</li></ul>	stimulous by, his CTLp frequency dro having an activated effector	pped from 60 to 4 per million PBM		Nixon1999 apy within 90 days of infection, tivated quiescent population (detected		
Nef (82–91)	Nef (82–91 LAI) • C. Brander notes this is	KAAVDLSHFL a C*0802(Cw8) epitope	HIV-1 infection	human (C*0802(Cw8)	) Brander2001		
Nef (82–91)	<ul> <li>C. Brander notes this is a C*0802(Cw8) epitope</li> <li>Nef (82–91 SF2) KAAVDLSHFL HIV-1 infection human (Cw8) Altfeld2001b</li> <li>Therapy provided during acute infection resulted in a narrower CTL response, stronger T help response, and a less diverse viral population than was seen individuals treated during chronic infection</li> <li>The breadth and specificity of the response was determined using ELISPOT by studying 19 individuals with pre-seroconversion therapy (Group 1), 11 individuals with primary infection but post-seroconversion therapy (Group 2), and 10 individuals who responded to HAART given during chronic infection (Group 3), using 259 overlapping peptides spanning p17, p24, RT, gp41, gp120 and Nef</li> <li>Previously described and newly defined optimal epitopes were tested for CTL response</li> <li>Number of HLA-Cw8+ individuals that had a CTL response to this epitope broken down by group: 1/3 group 1, 0/0 group 2, and 0/1 group 3</li> </ul>						
Nef (82–91)	Nef (SF2) • This epitope was mapp an HLA-B60 individua	-	HIV-1 infection identifying new HLA-B60 epitope	human (Cw8) es, and was one of the epitopes pre	Altfeld2000b sented by another HLA molecule in		
Nef (82–96)	each HIV protein.	-	HIV-1 infection ed from 105 HIV-1 positive Botsw e peptides, and p24 had the highes	-	Novitsky2002 rom between 55 and 64 subjects for		

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
	This peptide was amon	g the 8 most reactive C c	lade peptides from among over 350 t	tested spanning all HIV proteins.	
Nef (82–101)	• Three of these 11 had 0	d CTL specific for more L that could recognize veCTL response to this pept	accinia-expressed LAI Nef	human	Lieberman1997a
Nef (82–101)	<ul><li>from 7 proteins, sugges</li><li>Nef peptides PQVPLR</li></ul>	6 was tested for reactive of sting that the breadth of CRMTYKAAVDLSHFL, I	GLEGLI HIV-1 infection overlapping peptides spanning all HITL responses are underestimated if KAAVDLSHFLKEKGGLEGLI and and last share PQVPLRPMTY	accessory proteins are not included	l in the study
Nef (83–91)	73 peptides had 81 mot directly related to the n • 20s proteasome cleavag The frequency of recog	ifs. 54% bound to the pro umber of individuals that ge of the Nef protein posi unition may be in part dic	HIV-1 infection I based on putative anchor motifs in redicted HLA molecule, particularly at recognized a protein. Itions 66-100 showed a large fraction tated by the cleavage step in process individuals with HLA A2. It was a	A2, B7/35, and B8. The strength of of peptides were cleaved ending a ing.	f HLA-peptide binding was not
Nef (83–91)	<ul> <li>Ten Nef 9-mer peptides several others bound w</li> <li>A CTL immune respondent the control of a C</li> <li>AALDLSHFL was prebinder, the other two respondents</li> </ul>	s were predicted to have seakly se to only 3/10 peptides of the control of the co	Vaccine  XB3 HIV component: Nef Adjuventrong binding affinity for HLA-A*0 was detected by a 51Cr-release assay a gold particles delivered to abdomin anding capacity for HLA-A2, and didweak binders injection of Nef peptides in Freund's	201 – of these, four did bind strong  after immunization of HLA-A201  all skin by gene gun  by the performance of the performan	transgenic mice with nef DNA tides recognized that was a strong
Nef (83–92)	HLA-A11 is very command CTL responses were	V-1 exposed persistently a mon in this population, ar re found in 8/8 HIV+ con	HIV-1 infection seronegative (HEPS) female sex word was enriched among the HEPS settrols, and 0/9 HIV- women that were y subjects 053 and 184 who carried	xworkers – weak CTL responses we not exposed	
Nef (83–92)		GAFDLSFFLK ed subtype E in Bond et a	HIV-1 infection al.) epitopes were identified that stin 11 positive	human (A11) nulated CTL from HIV+ female se	Bond2001 x workers (FSW) from Northern

HXB2 Location	<b>Author's Location</b>	Sequence	Immunogen	Species (HLA)	References
	<ul> <li>epitopes for CTL responsible</li> <li>This epitope was predicted that had been previous</li> <li>4/8 tested FSWs recognition</li> </ul>	onses from 8 HLA-A11 p cted by the EpiMatrix maly defined nized this epitope	ed using EpiMatrix, these were screen ositive FSWs, six were novel, six we ethod to be likely to bind to A11, and subtype C, and exact matches were u	ere previously identified I it served as an epitope in the FS	d 26 bound, and 12 of these were Ws, it was one of the six A11 epitopes
Nef (83–94)	Nef (83–94 BRU) • Epitope defined by boo	AAVDLSHFLKEK andaries of overlapping p	HIV-1 infection eptides that stimulate Nef CTL clone	human (A11)	Culmann1991
Nef (84–91)	Nef (84–91 LAI)	AVDLSHFL	HIV-1 infection	human (Bw62)	Culmann-Penciolelli1994
Nef (84–91)	<ul> <li>95 optimally-defined p</li> </ul>	eptides from this databas	HIV-1 infection L that reacted to SLYNTVATL, callir e were used to screen for INFγ respo to SLYNTVATL reacted with seven o	onses to other epitopes	
Nef (84–92)	Nef (84–92 LAI) • C. Brander notes this i	AVDLSHFLK s an A*1101 epitope	HIV-1 infection	human (A*1101)	Brander2001
Nef (84–92)	<ul> <li>cross-reactive and reconspecific manner. Two of AVDLSHFLK was for A) and clade E (aFdIst Japanese subjects, as well as a subject of the subject of</li></ul>	ognized by clade E infector bother HLA A*1101 clade and to elicit clade-specific fflk is most common and was aLdlshflk, and aFdlsF flk to HLA A*1101 was	HIV-1 infection 1101 epitopes were generated for claded individuals. The clade E and B and B defined epitopes were found not to responses in clade B (AVDLSHFLK is also common in clade C). AVDLS Iffik by CTL from 5/7 E clade infected 10-50 times lower than the other variation.	alogs to three more HLA A*1101 to have stimulated a response in cl K is most common, aLdlshflk is a HFLK was strongly recognized but Thai subjects.	epitopes was recognized in a clade ade E infected individuals. common variant also found in clade
Nef (84–92)	Nef (84–92 LAI) • Review of HIV CTL e • C. Brander notes that t		HIV-1 infection in the 1999 database	human (A11)	McMichael1994
Nef (84–92)	<ul> <li>95 optimally-defined p</li> </ul>	eptides from this databas	HIV-1 infection L that reacted to SLYNTVATL, calling e were used to screen for INFγ respo to SLYNTVATL reacted with seven of	onses to other epitopes	
Nef (84–92)			HIV-1 infection uals with appropriate HLA types can hat summarizes this study	human (A11) result in evasion of CTL respons	Couillin1994, Goulder1997a e
Nef (84–92)	Nef (84–92 LAI) • Mutations found in thi	AVDLSHFLK s epitope in HLA-A11 po	HIV-1 infection sitive and negative donors were char	human (A11) racterized	Couillin1995

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References		
Nef (84–92)	Nef (84–92) • Epitope name: AVD	AVDLSHFLK	HIV-1 infection	human (A11)	Oxenius2000		
	CD4 proliferative response	onses and were able to	nfection (three with sustained therapy, two maintain a CTL response even with under we responses and lost their CTL responses	tectable viral load – three patie	ents that had delayed initiation of		
		1/12, B8/44, Cw06/070	gnized this CTL epitope 01, DR3/7, DR52/53, DQ 2/8) had a CTL GGEFFY that declined during therapy ini		GGL, GEIYKRWII,		
	• Patient SC18(HLA A2	/11, B8/44, Cw06/0701	I, DR3/7, DR52/53, DQ2) recognizes the ad brief therapy upon seroconversion and	epitopes ACQGVGGPGHK,			
Nef (84–92)	Nef (82–90) • One of the 51 HIV-1 ep HLA alleles	AVDLSHFLK pitopes selected by Ferr	HIV-1 infection rari et al. as good candidate CTL epitopes	human (A11) for vaccines by virtue of bein	Ferrari2000 g conserved and presented by common		
Nef (84–92)	<ul> <li>individuals treated duri</li> <li>The breadth and specifindividuals with primate (Group 3), using 259 of Previously described a</li> </ul>	ing chronic infection acity of the response wary infection but post-se verlapping peptides spand newly defined opting	HIV-1 infection at the distribution of the dis	g 19 individuals with pre-sero ndividuals who responded to F f	conversion therapy (Group 1), 11 HAART given during chronic infection		
Nef (84–92)			HIV-1 infection, HIV-1 exposeronegative a panel of 54 predefined HIV-1 epitopes		Kaul2001a ently seronegative (HEPS) and 87		
Nef (84–92)	Nef AVDLSHFLK HIV-1 infection human (A11) Oxenius2002b  • Epitope name: AVD  • Using previously defined epitopes [Oxenius2000, Oxenius2001a] in an IFNgamma Elispot assay, 13 chronically HIV-1 infected patients were studied over period including therapy with standard treatment interruptions (STI).  • STIs induced increased recognition of CTL epitopes, but there was no correlation between CTL responses with viral rebound rates, plateau viral loads, or clearance rates.						
Nef (84–92)	<ul> <li>The HIV-1 subtype A f which could direct the conserved, often immu</li> </ul>	ocused vaccine HIVA protein to the cell mem nodominant epitopes tl VA prime-boost vaccin	HIV-1 infection, Vaccine nia MVA boost <i>Strain:</i> subtype A <i>HIV</i> contains p24 and p17, in a reversed order abrane and inhibit efficient peptide proces nat were selected to have particularly goo ation protocol using the HIVA antigen wi 0].	<i>component:</i> p17, p24, polyeprelative to the Gag polyproteinsing and class I presentation, a d cross-reactive potential for the	n to prevent myristylation of p17, as well as a polyepitope string of the A-clade epidemic in Nairobi,		

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References		
	assays after vaccination	n of 5 macaques. The resp	responses to peptide pools were detected ponse to the Mamu A*01 SIV p27 epito atted macaques, possibly because of pro-	ope p11C (CTPYDINQM), in	cluded in the polyepitope region, was		
Nef (84–92)	<ul> <li>73 peptides had 81 mo directly related to the r</li> <li>20s proteasome cleava. The frequency of recognitions.</li> </ul>	tifs. 54% bound to the produmber of individuals that ge of the Nef protein posignition may be in part dic	HIV-1 infection I based on putative anchor motifs in the edicted HLA molecule, particularly A2, t recognized a protein. Itions 66-100 showed a large fraction of tated by the cleavage step in processing individuals with HLA A3. It was a high	, B7/35, and B8. The strength peptides were cleaved ending	of HLA-peptide binding was not		
Nef (84–92)	<ul> <li>One individual, AC-06 interruptions (STI). He restricted by HLA-A3,</li> <li>0/14 HLA-A3 positive</li> </ul>	cutely HIV-infected HLA, was homozygous at all that only two detectable 11 by HLA-B7, and 1 by individuals had detectable	e A3-restricted responses to this epitope	treated during acute infection but after STI this broadened to e during acute infection, but of	n and had supervised treatment o 27 distinct epitopes including 15		
Nef (86–94)	Nef DLSHFLKEK HIV-1 infection, Vaccine human, macaque (A*0301)  Vaccine Vector/Type: DNA prime with vaccinia MVA boost Strain: subtype A HIV component: p17, p24, polyepitope  The HIV-1 subtype A focused vaccine HIVA contains p24 and p17, in a reversed order relative to the Gag polyprotein to prevent myristylation of p17, which could direct the protein to the cell membrane and inhibit efficient peptide processing and class I presentation, as well as a polyepitope string of conserved, often immunodominant epitopes that were selected to have particularly good cross-reactive potential for the A-clade epidemic in Nairobi, Kenya. A DNA and MVA prime-boost vaccination protocol using the HIVA antigen will be used in a phase III clinical trial in Kenya. This epitope is included in the polyepitope string [Hanke2000].  Multiple CD4+ or CD8+ T-cell vaccine-induced responses to peptide pools were detected using intracellular cytokine staining and IFNgamma Elispot assays after vaccination of 5 macaques. The response to the Mamu A*01 SIV p27 epitope p11C (CTPYDINQM), included in the polyepitope region, was not immunodominant in the Mamu A*01 vaccinated macaques, possibly because of processing limitations in context of the artificial polyepitope string						
Nef (86–94)	Nef (86–94)  • ELISPOT was used to HIV-1-infected female		HIV-1 infection, HIV-1 expo seronegative a panel of 54 predefined HIV-1 epitopes		Kaul2001a ently seronegative (HEPS) and 87		
Nef (86–94)	Nef (84–92 LAI) • Review of HIV CTL ep	DLSHFLKEK	HIV-1 infection	human (A3.1)	McMichael1994		

HXB2 Location	<b>Author's Location</b>	Sequence	Immunogen	Species (HLA)	References
Nef (86–100)	Nef (86–100 LAI) • Development of a retro	DLSHFLKEKGGLEGL viral vector (pNeoNef) to generate	HIV-1 infection erate autologous targets	human (A2)	Robertson1993
Nef (86–100)	Nef (86–100 LAI)	DLSHFLKEKGGLEGL	HIV-1 infection	human (B35)	Buseyne1993b
Nef (86–100)		DLSHFLKEKGGLEGL FHIV ranges from 13% to 39%		human (B35 or C4)	Buseyne1993a
	<ul> <li>Epitopes recognized in</li> </ul>	five children were mapped usi	ing synthetic peptides and secon	ted in 70% of infected children ndary cultures ood transfusion after birth and we	nt from CDC stage P2A to P2E
Nef (87–102)	subtype in nef and env	and 7 of the 41 strains were re		-	Jubier-Maurin1999 4 subtypes were classified in the same
Nef (88–100)		SHFLKEKGGLEGL tained from Brazilians to study n most subtype C samples.	HIV-1 infection y epitope diversity in this geogr	human raphic region—most B subtype sec	Guimaráes2002 quences are SHFLKEKGGLEGL, but
Nef (90–97)	• 95 optimally-defined pe	eptides from this database were	e used to screen for INF $\gamma$ respo		Betts2000 unodominant reviously described as presented by
Nef (90–97)	<ul> <li>Optimal expansion of F in the absence of CD4+</li> <li>Those CTL that didn't in the control of the con</li></ul>	IIV-1-specific memory CTL de T cell help to a variable degree respond to CD40LT could exp	ee in most of patients and with IL2 present, and IL15		
Nef (90–97)	• Epitope name: Nef-FL8 • Among HIV+ individua		HIV-1 infection 3 (33%) recognized this epitopo	human (B*08)	Sabbaj2002b
Nef (90–97)	Nef (89–97 LAI) • C. Brander notes this is	FLKEKGGL a B*0801 epitope	HIV-1 infection	human (B*0801)	Brander2001
Nef (90–97)	<ul><li>Most variants appear at</li><li>FLKE(E,N or Q)GGL s</li></ul>	position 5, an anchor residue showed reduced binding efficient	HIV-1 infection HIV-1+ individual, providing e- ency and recognition KGNGGL) completely escaped	•	Price1997

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
	• [Goulder1997a] is a rev	view of immune escap	be that summarizes this study in the conte	ext of CTL escape to fixation	
Nef (90–97)	<ul><li>CTLp (precursors) wer</li><li>B7-FLKEKGGL tetran at 9 months of age</li></ul>	e measured by stimula ner complex was used sponses initially increa	HIV-1 infection stiretroviral therapy (HAART) on HIV-1 ating in culture and assaying using 51Cr for one of the children that was HLA-B' ased in children with complete viral supp	release, against vaccina expressor, and this infant showed a vigor	ed IIIB Env, Gag, Pol, Nef rous response (> 4% of CD8+ T cells
Nef (90–97)	Nef Vaccine Vector/Type: v  This epitope was show carrying 20 HIV-1 epitope	n to be processed and	presented to appropriate CTL clones upo	human (B8) on infection of human target cell	Hanke1998a, Hanke1998b s with vaccinia virus Ankara (VVA)
Nef (90–97)	Nef (88–95)  Natural variants for thi Substitutions Q5, N5, I Substitution I2 binds w	E5 that alter anchor po	osition 5 are not well recognized	human (B8)	Goulder1997g
Nef (90–97)	natural attenuated strai	n of HIV-1 which was	HIV-1 infection a 1.3 to 1.5 year period in members of the Nef-defective evels of CTL effector and memory cells described to the Nef-defector and memory cells describ		Dyer1999 SBBC) who had been infected with a
Nef (90–97)	<ul> <li>Three CTL responses,</li> <li>QASQEVKNW, EIYK</li> </ul>	to epitopes TSTLQEQ RWII, and FLKEKGO	HIV-1 infection  uring acute HIV-1 infection in patient PI  PIGW, ISPRTLNAW, and KAFSPEVIPM  GL were detectable at 5 months post-infe  AC29, in chronic infection	IF, were evident early after infec	Goulder2001a etion; CTL responses to SLYNTVATL
Nef (90–97)	Nef (92–99)  Epitope name: FLK  Characterization of spe HIV-1 infection  CTL activation in respo	FLKEKGGL cific CTL phenotype ponse to increasing vira	HIV-1 infection patterns in response to variation of the vi al load sequential, and co-segregated with tinct CTL sub-populations	-	
Nef (90–97)	CD4 proliferative response	onses and were able to	HIV-1 infection  Infection (three with sustained therapy, two maintain a CTL response even with undive responses and lost their CTL response	letectable viral load – three patie	ents that had delayed initiation of

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References		
	<ul> <li>Patient SC2 (HLA A1 peptides – FLKEKGG FLKENGGI was foun</li> <li>Patient SC9 (HLA A1 SQRRQDILDLWIYH therapy become interm</li> <li>Patient SC19(HLA A1 ACQGVGGPGHK, A' Patient SC10(HLA A1 FLKEKGGL and a rese</li> <li>Patient SC12(HLA A1 immunodominant resp GGKKKYKLK response)</li> <li>Patient SC11(HLA A1 immunodominant resp GGKKKYKLK response)</li> </ul>	p. B7/8, Cw0701/0702, bL tetramer staining ste d in 8/10 clones /2, B8/13, Cw0/0701, ITQGYFPDWQNY, an intent at 1/12, B8/44, Cw06/07 VDLSHFLK, and FNC 1/3, B8/35, DR1/8, DQ sponse to GEIYKRWII bl., B8/39, Cw0701/0702 clonse to FLKEKGGL tinses were stimulated by B8, Cw0201, DR3/1	B8 recognized this early dominant CTL of DR4/53, DQ7) had CTL responsiveness adily declined and at day 1340 the FLKE DR2/11, DQ6/7) had a CTL response agad GEIYKRWII peptides and all response 01, DR3/7, DR52/53, DQ 2/8) had a CTL response 01, DR3/7, DR52/53, DQ 2/8) had a CTL response 01, DR3/7, DR52/53, DQ 2/8) had a CTL response 01, DR3/7, DR52/53, DQ 2/8) had a CTL response 01, DR3/7, DR52/53, DQ 2/8) had a CTL response 01, DR3/7, DR51/52, DQ2/6) had sustained through day 1088 or DR2/3, DR51/52, DQ2/6) had sustained throughout and minor responses to GEIY as a brief period off therapy 1, DR52, DQ2/7) started therapy early, rekQWPL, and GEIYKRWII throughout a	against epitopes FLKEKGGL, de EKGGL stained cells were no localinst epitopes FLKEKGGL, ILF es declined during therapy initial and the state of the s	REPVHGV, ted at day 390 but were restored when GGL, GEIYKRWII, d an immunodominant response to infection and maintained an KYKLK – GEIYKRWII and then reinitiated HAART at day 640		
Nef (90–97)	Nef  HLA tetramers to six of with viral load in patients have hig  In 15 of the patients, the Stimulation with HLA  There were more func	FLKEKGGL epitopes were used to sents with high CD4, but the levels of HIV-specific proportion of IFN grands and Nef epitotional IFN-gamma process.	HIV-1 infection tudy HLA-A2, B8 and B57 CTL in 54 p. t in patients with CD4 T-cells below 400 c T-cell expansions, but many of these comma producing tetramer cells correlated pes significantly increased Nef-specific T-ducing Nef-specific T-cells within the T-one-communication of the term of th	human (B8) atients – HIV-specific tetramer phigh tetramer frequencies were ells aren't functional d with AIDS-free survival F-cell numbers in 2 patients (74) cell population than there were	Kostense2001 positive cells were inversely correlated found despite high viral load  8 and 1113)		
Nef (90–97)	Nef (88–95) • One of the 51 HIV-1 e HLA alleles	FLKEKGGL pitopes selected by Fer	HIV-1 infection rari et al. as good candidate CTL epitopo	human (B8) es for vaccines by virtue of bein	Ferrari2000 g conserved and presented by common		
Nef (90–97)	Nef (88–95 SF2) FLKEKGGL HIV-1 infection human (B8) Altfeld2001b  • Therapy provided during acute infection resulted in a narrower CTL response, stronger T help response, and a less diverse viral population than was seen in individuals treated during chronic infection  • The breadth and specificity of the response was determined using ELISPOT by studying 19 individuals with pre-seroconversion therapy (Group 1), 11 individuals with primary infection but post-seroconversion therapy (Group 2), and 10 individuals who responded to HAART given during chronic infection (Group 3), using 259 overlapping peptides spanning p17, p24, RT, gp41, gp120 and Nef  • Previously described and newly defined optimal epitopes were tested for CTL response  • Number of HLA-B8+ individuals that had a CTL response to this epitope broken down by group: 3/3 group 1, 1/3 group 2, and 1/2 group 3						
Nef (90–97)	• HIV-specific CD8+ T	cells expressed lower le	HIV-1 infection e staining was used to study the function evels of perforin than CMV-specific CD8 esting impaired maturation				

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
	• In most donors, between produce TNF-α	on 50% and 95% of the	e activated virus-specific CD8+ T cells pro	duced IFN- $\gamma$ and MIP-1 $\beta$ wit	h a distinct subset that failed to
Nef (90–97)			HIV-1 infection  The total CTL response in one individual highest response in magnitude compared	human (B8) to all the HLA class I A- and	Day2001  B-restricted epitopes tested in this
Nef (90–97)	Nef • Tetramer assays were correcursor frequency (li	miting dilution assay [	HIV-1 infection nctional assays in 42 people with chronic LDA]) d to be active, and inert CTL were not four		•
Nef (90–97)	<ul> <li>73 peptides had 81 modeliectly related to the n</li> <li>20s proteasome cleavage. The frequency of recognitions.</li> </ul>	ifs. 54% bound to the umber of individuals to ge of the Nef protein punition may be in part of	HIV-1 infection ted based on putative anchor motifs in the predicted HLA molecule, particularly A2, hat recognized a protein. ositions 66-100 showed a large fraction of dictated by the cleavage step in processing of individuals with HLA B8, and it was a	, B7/35, and B8. The strength peptides were cleaved ending	of HLA-peptide binding was not
Nef (90–97)	period including therap	y with standard treatm	HIV-1 infection  000, Oxenius2001a] in an IFNgamma Elis nent interruptions (STI). pitopes, but there was no correlation between		
Nef (90–97)	<ul><li>specific T-cell response</li><li>Nef epitope recognition</li></ul>	es by Elispot and Tetra n was detected in all 4	HIV-1 infection successful anti-viral therapy but with ongo mer staining, maintained for 2-4 years after subjects, gp120, Pol and Gag-specific in 1 nediate maturation phenotype characterized	er initiation of HAART. or 2 subjects – two patients r	ecognized FLKEKGGL.
Nef (90–97)	<ul><li>specific T-cell response</li><li>Nef epitope recognition</li></ul>	es by Elispot and Tetra n was detected in all 4	HIV-1 infection successful anti-viral therapy but with ongo mer staining, maintained for 2-4 years after subjects, gp120, Pol and Gag-specific in 1 and the subject of the	er initiation of HAART. or 2 subjects – two patients r	ecognized FLKEKGGL.
Nef (90–97)	Nef <b>Vaccine</b> Vector/Type: I	FLKEKGGL  ONA prime with vaccin	HIV-1 infection, Vaccine nia MVA boost Strain: subtype A HIV	human, macaque (B8 component: p17, p24, polyep	

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
	which could direct the conserved, often immu Kenya. A DNA and M included in the polyepi  • Multiple CD4+ or CD8 assays after vaccination	protein to the cell memb nodominant epitopes tha VA prime-boost vaccinat tope string [Hanke2000] 8+ T-cell vaccine-induced n of 5 macaques. The res	ntains p24 and p17, in a reversed orderane and inhibit efficient peptide proof twere selected to have particularly gion protocol using the HIVA antigen.  I responses to peptide pools were det ponse to the Mamu A*01 SIV p27 epated macaques, possibly because of	cessing and class I presentation, a cood cross-reactive potential for the will be used in a phase III clinical ected using intracellular cytokine pitope p11C (CTPYDINQM), inc	s well as a polyepitope string of e A-clade epidemic in Nairobi, l trial in Kenya. This epitope is staining and IFNgamma Elispot luded in the polyepitope region, was
Nef (90–100)	<ul> <li>73 peptides had 81 mo directly related to the r</li> <li>20s proteasome cleava. The frequency of recognitions.</li> </ul>	tifs. 54% bound to the produmber of individuals that ge of the Nef protein pos- gnition may be in part dic	edicted HLA molecule, particularly at recognized a protein.	A2, B7/35, and B8. The strength of of peptides were cleaved endinging.	Choppin2001 A2, A3, A24, B7, B8, and B35; these of HLA-peptide binding was not at: 87L, 83A, 81Y, 71P, 68F and 67G.
Nef (92–100)	(LAI) • C. Brander notes this is	KEKGGLEGL s a B*4001,B60 epitope		human (B*4001)	Brander2001
Nef (92–100)	<ul> <li>24 epitopes were descr</li> <li>Serial peptide truncation</li> <li>Patient 01RCH59 was HLA-B*4002 and AEV</li> </ul>	pitope responses in HIV- ibed – 8 were novel, 8 us ons were used to define o Hispanic, not on HAARI WDRVHPV, p24(78-86),		previously defined epitopes, and plated from 12 individuals, assaye	
Nef (92–100)	<ul> <li>individuals treated duri</li> <li>The breadth and specifindividuals with prima (Group 3), using 259 o</li> <li>Previously described a</li> </ul>	ing chronic infection acity of the response was ry infection but post-sero verlapping peptides span and newly defined optima	determined using ELISPOT by study	ying 19 individuals with pre-seroc 0 individuals who responded to H Nef 1se	AART given during chronic infection
Nef (92–100)	exogenous protein and	l by a fusion protein of a allows processing throug	HIV-1 infection es KEKGGLEGL. n HIV protein and anthrax lethal fact the MHC class I pathway. This str using live viral vectors carrying a pro	ategy for CTL detection could all	ow antigen presentation without

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
Nef (92–100)	<ul> <li>This epitope was also B*4002, B*4003, B*4</li> <li>ELISPOT was a rapid</li> </ul>	recognized two expressing 1004, B*4006, and B*4006 an effective method that we	HIV-1 infection y B*4001) response in 6/8 HLA-B60 g HLA-B61 individuals (B61 is usual 8) was used to define five novel B60 epit d population and B60/B61 are very co	ly encoded by B*4002, but this stoopes	
Nef (92–100)			HIV-1 infection o five B61-restricted epitopes tested another subject, and the B60-restrict	human (B60/B61) ed responses together contributed	Day2001 over one-third of the total CTL
Nef (92–112)	an HLA-B60 individua	DL ped by ELISPOT in a stud al	RQDIL- HIV-1 infection  by identifying new HLA-B60 epitopes  t, but the HLA presenting molecule as		•
Nef (92–112)	an HLA-B60 individua	DL ped by ELISPOT in a stud al	RQDIL— HIV-1 infection  by identifying new HLA-B60 epitopest, but the HLA presenting molecule at		•
Nef (93–106)	Nef (93–106 BRU) • HIV-1 specific CTLs d	EKGGLEGLIHSQRR	HIV-1 infection ns of HIV-1 infected patients	human (A1, B8)	Hadida1992
Nef (97–111)	<ul><li>each HIV protein.</li><li>Nef and p24 had the hi</li></ul>	ighest percentage of react	HIV-1 infection ined from 105 HIV-1 positive Botswa ive peptides, and p24 had the highest clade peptides from among over 350	magnitude of HIV-1 responses.	Novitsky2002 om between 55 and 64 subjects for
Nef (102–115)	<ul> <li>One had a strong response</li> </ul>	onse to this peptide, the ot	nfected with the same batch of factor	human (B7) VIII	Goulder1997e, Goulder1997a
Nef (102–121)	<ul><li> Eleven subjects had C</li><li> Two of these 11 had C</li></ul>	ad CTL specific for more	accinia-expressed LAI Nef de	human	Lieberman1997a

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References					
Nef (103–127)	Nef (103–127 PV22)	SQRRQDILDLWIYHTQGYF- PDWQNY	HIV-1 infection	human (B13)	Jassoy1993					
	• HIV-1 specific CTLs re	lease $\gamma$ -IFN, and $\alpha$ - and $\beta$ -TNF								
Nef (103–127)	Nef (103–127)	SQRRQDILDLWIYHTQGYF- PDWQNY	HIV-1 infection	human (B13)	Oxenius2000					
	<ul> <li>Epitope name: SQR</li> <li>Patients who started therapy at acute HIV-1 infection (three with sustained therapy, two with limited therapy upon early infection) had strong HIV specific CD4 proliferative responses and were able to maintain a CTL response even with undetectable viral load – three patients that had delayed initiation of HAART had no HIV specific CD4 proliferative responses and lost their CTL responses when HAART was eventually given and their viral loads became undetectable</li> <li>The only study subject out of eight that was HLA B13+ recognized this epitope</li> </ul>									
	<ul> <li>Patient SC9 (HLA A1/2, B8/13, Cw0/0701, DR2/11, DQ6/7) had a CTL response against epitopes FLKEKGGL, ILKEPVHGV, SQRRQDILDLWIYHTQGYFPDWQNY, and GEIYKRWII peptides and all responses declined during therapy initiated at day 390 but were restored when therapy become intermittent</li> </ul>									
Nef (105–114)	• HLA-B*2705 is associa	RRQDILDLWI ope from within reactive peptide I ated with slow HIV disease progre ing motif includes R at position 2		human (B*2705) ef(102-121 LAI)]	Goulder1997c					
Nef (105–114)	Nef (105–114 LAI) • C. Brander notes this is	RRQDILDLWI a B*2705 epitope	HIV-1 infection	human (B*2705)	Brander2001					
Nef (105–114)	<ul> <li>individuals treated during</li> <li>The breadth and specification individuals with primar (Group 3), using 259 or</li> <li>Previously described ar</li> </ul>	ng chronic infection city of the response was determine y infection but post-seroconversion verlapping peptides spanning p17, and newly defined optimal epitopes	ed using ELISPOT by studying 19 on therapy (Group 2), and 10 individually p24, RT, gp41, gp120 and Nef	individuals with pre-seroco luals who responded to HA	ART given during chronic infection					
Nef (105–114)	Nef (105–114) • B27-restricted CTL res	RRQDILDLWI ponse was strongest to this epitop	HIV-1 infection e in one individual	human (B27)	Day2001					
Nef (105–114)	<ul><li>Epitope name: Nef-RII</li><li>Among HIV+ individua</li></ul>	RRQDILDLWI 0 als who carried HLA B27, 1/2 (50	HIV-1 infection %) recognized this epitope	human (B27)	Sabbaj2002b					
Nef (105–115)	Nef (105–115) • Epitope name: Cw7-RY	RRQDILDLWIY 711	HIV-1 infection	human (Cw7)	Yu2002a					

HXB2 Location	<b>Author's Location</b>	Sequence	Immunogen	Species (HLA)	References
	He had only two detect		infection, but after STI thi		rvised treatment interruptions (STI). including 15 restricted by HLA-A3,
Nef (106–115)	(LAI)	RQDILDLWIY		(B7)	Brander2001, Goulder1999a
Nef (108–115)	• Epitope name: Nef-DY		HIV-1 infection	human (Cw*0701)	Sabbaj2002b
	<ul> <li>24 epitopes were descr</li> <li>Serial peptide truncation</li> <li>Subject 03RCH40 was RT(449-457), A*2601</li> </ul>	ons were used to define optimal ep	estricting elements but we itopes for CTL cell lines id of 2500, CD4 count of 3	are previously defined epitopes, and isolated from 12 individuals, assayed 372, was not on HAART, and also reference to the control of the co	
Nef (112–126)	<ul><li>each HIV protein.</li><li>Nef and p24 had the hi</li></ul>	ghest percentage of reactive peption	les, and p24 had the highe	human wanans; Elispot data was obtained f est magnitude of HIV-1 responses. 50 tested spanning all HIV proteins.	Novitsky2002 from between 55 and 64 subjects for
Nef (112–133)	Nef (111–132)	LWIYHTQGYFPDWQNYTPG- PGV		human	Lieberman1995
Nef (112–133)	Nef (111–132 SF2)	developed by ex vivo stimulation  LWIYHTQGYFPDWQNYTPG- PGV	• •	human	Lieberman1997a
	<ul><li>Eleven subjects had CT</li><li>Four of these 11 had CT</li></ul>	d CTL specific for more than 1 H L that could recognize vaccinia-e TL response to this peptide s were HLA-A2, B21; HLA-A1,	xpressed LAI Nef	26, B7, B38	
Nef (112–133)	Nef (111–132 SF2)	LWIYHTQGYFPDWQNYTPG- PGV	HIV-1 infection	human	Lieberman1997b
	CTL expanded ex vivo	were later infused into HIV-1 infe	ected patients		
Nef (113–125)	Nef (113–125 BRU) • Nef CTL clones from F	WIYHTQGYFPDWQ HIV+ donors	HIV-1 infection	human (B17)	Culmann1989
Nef (113–127)		WIYHTQGYFDPWQNY tained from Brazilians to study ep n Nef-gene subtype C samples, an		human graphic region – WIYHTQGYFDP'n found in other subtypes tested.	Guimaráes2002 WQNY displayed an (H) to (N)
Nef (113–128)	Nef (113–128 BRU) • HIV-1 specific CTLs de	WIYHTQGYFPDWQNYT etected in lymphoid organs of HIV	HIV-1 infection 7-1 infected patients	human (A1)	Hadida1992

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References		
Nef (113–128)	Nef (113–128 LAI) • Epitope name: N2	WIYHTQGYFPDWQNYT	HIV-1 infection	human (A1)	Mollet2000		
	CD8+ cell IFNgamma	production to measure respon	ses	om an unselected Caucasian popul	_		
	specificities that were r HIV-specific responses	not previously detectable were diminished	newly detected, as were CMV	of HIV-specific CTL tripled and be specific CD8+ PBL – but with co sting response, new specificities, of	ntinued viral suppression,		
Nef (114–127)	Nef	VYHTQGYFPDWQNY	HIV-1 infection	human	Jubier-Maurin1999		
Nef (115–125)	Nef (115–125 BRU) • Nef CTL clones from H	YHTQGYFPDWQ HIV+ donors	HIV-1 infection	human (B17)	Culmann1991		
Nef (116–125)	Nef (116–125 BRU)  • C. Brander notes this is  • Subtype of B57 not det		HIV-1 infection	human (B*5701)	Brander2001		
Nef (116–125)	• 95 optimally-defined p	eptides from this database we	HIV-1 infection t reacted to SLYNTVATL, calli re used to screen for INF $\gamma$ responded to four B57		Betts2000 nunodominant		
Nef (116–125)	Nef (116–125 BRU) • Nef CTL clones from I	HTQGYFPDWQ HIV+ donors, optimal peptide	HIV-1 infection mapped	human (B57)	Culmann1991		
Nef (116–125)	Nef (116–125) • Epitope name: HTQ	HTQGYFPDWQ	HIV-1 infection	human (B57)	Oxenius2000		
	<ul> <li>Patients who started therapy at acute HIV-1 infection (three with sustained therapy, two with limited therapy upon early infection) had strong HIV specific CD4 proliferative responses and were able to maintain a CTL response even with undetectable viral load – three patients that had delayed initiation of HAART had no HIV specific CD4 proliferative responses and lost their CTL responses when HAART was eventually given and their viral loads became undetectable</li> <li>None of the 8 study subjects recognized this epitope but none were HLA B57+</li> </ul>						
Nef (116–125)	<ul><li>Epitope name: Nef-HQ</li><li>Among HIV+ individu</li></ul>	<u>.</u>	HIV-1 infection  6 (0%) recognized this epitope	human (B57)	Sabbaj2002b		
Nef (117–127)	<ul><li>95 optimally-defined p</li><li>1/11 of the A2+ individ</li></ul>	eptides from this database we duals was HLA A*0205/A*02	re used to screen for INF $\gamma$ respo	ed to HLA Bw62 epitope TQGYI			

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
Nef (117–127)	Nef (117–127 LAI) • C. Brander notes this is	TQGYFPDWQNY a B*1501 epitope	HIV-1 infection	human (B*1501)	Brander2001
Nef (117–127)	Nef (117–127) • No immunodominant re	TQGYFPDWQNY sponses were detected to four B6	HIV-1 infection 2-restricted epitopes tested	human (B62)	Day2001
Nef (117–127)	Nef (117–127 LAI)  Optimal peptide defined	TQGYFPDWQNY by titration	HIV-1 infection	human (Bw62)	Culmann1998
Nef (117–128)	Nef (117–128 BRU) • Nef CTL clones from H	TQGYFPDWQNYT IV+ donors	HIV-1 infection	human (B17, B37)	Culmann1991
Nef (117–147)	<ul> <li>Anti-HIV lipopeptide va administered in a phase</li> <li>A CD4+ T cell prolifera</li> </ul>	I trial tive response to at least one of the	peptides o acid peptides derived from Nef, C e six peptides was observed in 9/10	vaccinees – 1/10 reacted to	this Nef peptide
	<ul><li>9/12 tested mounted a C</li><li>10/12 tested had an IgG</li></ul>		six peptides; each of the six peptide	es elicited a CTL response	in at least one individual
Nef (118–127)	Nef (118–127 LAI) • Review of HIV CTL epi	QGYFPDWQNY		human (Bw62)	McMichael1994
Nef (120–128)	<ul><li>95 optimally-defined pe</li><li>1/11 of the A2+ individual</li></ul>	ptides from this database were usuals was HLA A*0205/A*0208, A	HIV-1 infection cted to SLYNTVATL, calling into qued to screen for INFγ responses to cA30, B27, B44 but responded to HL ed with seven epitopes including the	other epitopes A B37 epitope IYKRWIIL0	Betts2000 nodominant GL, and one of the other individuals
Nef (120–128)	<ul> <li>individuals treated durin</li> <li>The breadth and specific individuals with primary (Group 3), using 259 ov</li> <li>Previously described an</li> </ul>	g chronic infection bity of the response was determined infection but post-seroconversion erlapping peptides spanning p17, d newly defined optimal epitopes	ed using ELISPOT by studying 19 in therapy (Group 2), and 10 individ p24, RT, gp41, gp120 and Nef	ndividuals with pre-serocor uals who responded to HAA	ART given during chronic infection
Nef (120–128)	Nef (120–128 LAI) • C. Brander notes this is	YFPDWQNYT a B*3701 and B*5701 epitope	HIV-1 infection	human (B*3701)	Brander2001
Nef (120–128)	Nef (120–128 LAI)  C. Brander notes this is  Subtype of B57 not dete		HIV-1 infection	human (B*5701)	Brander2001

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
Nef (120–128)		be mutants in the mother was	HIV-1 infection context of mother-to-infant trar associated with transmission, b		Wilson1999a ne virus tended to be found in infected
Nef (120–128)	Nef (120–128 LAI) • Nef CTL clones from H	YFPDWQNYT IIV+ donors – optimum pept	HIV-1 infection ide mapped by titration	human (B37, B57)	Culmann1998
Nef (120–128)	<ul><li> Epitope name: Nef-YT9</li><li> Among HIV+ individual</li></ul>		HIV-1 infection 5 (20%) recognized this epitope	human (B57)	Sabbaj2002b
Nef (120–144)	Nef (120–144 SF2)  • Epitope recognized by (	YFPDWQNYTPGPGIRYP FGWCYK CTL clone derived from CSF		human (A24)	Jassoy1992
Nef (122–136)	<ul><li>each HIV protein.</li><li>Nef and p24 had the high</li></ul>	ghest percentage of reactive p	peptides, and p24 had the highes	human vanans; Elispot data was obtained f st magnitude of HIV-1 responses. tested spanning all HIV proteins.	Novitsky2002 From between 55 and 64 subjects for
Nef (122–141)	<ul><li> Eleven subjects had CT</li><li> Three of these 11 had C</li></ul>	PDWQNYTPGPGVRYPLT d CTL specific for more than L that could recognize vacci TL response to this peptide s were HLA-A2, B21; HLA-	n 1 HIV-1 protein nia-expressed LAI Nef	human	Lieberman1997a
Nef (123–137)	• FFPDYTPGPGTRFPL	and FFPDYKPGPGTRFPL,	naturally occurring variants, we	human mother-infant HIV transmission stu ere found in mother and are not rece ere found in infant and are not rece	cognized
Nef (126–135)	73 peptides had 81 motidirectly related to the motion 20s proteasome cleavage. The frequency of recognition of the frequency	ifs. 54% bound to the predic umber of individuals that rec e of the Nef protein position nition may be in part dictated	ted HLA molecule, particularly ognized a protein. s 66-100 showed a large fractio d by the cleavage step in process	A2, B7/35, and B8. The strength on of peptides were cleaved ending	at: 87L, 83A, 81Y, 71P, 68F and 67G.
Nef (126–138)	Nef (126–138 BRU) • Nef CTL clones from H	NYTPGPGVRYPLT IIV+ donors	HIV-1 infection	human (B7)	Culmann1991

HXB2 Location	<b>Author's Location</b>	Sequence	Immunogen	Species (HLA)	References		
Nef (127–141)	<ul><li>each HIV protein.</li><li>Nef and p24 had the hig</li></ul>	hest percentage of reactive per	otides, and p24 had the highest	human mans; Elispot data was obtained f magnitude of HIV-1 responses. ested spanning all HIV proteins.	Novitsky2002 from between 55 and 64 subjects for		
Nef (128–135)	<ul> <li>All five could be transpo</li> <li>Both TPGPGVRYPL an and both peptides seem</li> </ul>	rted by TAP, and 4/5 had N-te d TPGPGVRY are naturally p to be the direct product of a pr	rmini that were major cleavage rocessed ligands that can be el oteasomal digest	uted from HLA-B7 molecules, bo	Lucchiari-Hartz2000 en 123-152 one had extended precursor fragment oth are recognized by the same CTL, a major cleavage site between the Y		
Nef (128–136)	<ul><li>Epitope name: Nef-TP9</li><li>Among HIV+ individua</li></ul>	TPGPGVRYP  Is who carried HLA B07, 4/9 (	HIV-1 infection 44%) recognized this epitope	human (B07)	Sabbaj2002b		
Nef (128–137)	Nef TPGPGIRYPL HIV-1 infection human Kaul2001c  This study examines CTL responses in HIV exposed, persistently seronegative individuals, HEPS, who eventually seroconverted – 11/114 HEPS Nairobi sex workers eventually seroconverted, and for six of these HIV CTL reactive epitopes had been defined while seronegative  The epidemiological factor associated with seroconversion was stopping sex work and HIV-specific CTL activity declines when HEPS sex workers stop working for a period or retire  This epitope was recognized by 1/22 HEPS control sex workers, ML851						
Nef (128–137)	Nef (128–137 LAI) • C. Brander notes this is	TPGPGVRYPL a B*0702 epitope	HIV-1 infection	human (B*0702)	Brander2001		
Nef (128–137)	<ul> <li>All five could be transpo</li> <li>Both TPGPGVRYPL an and both peptides seem</li> </ul>	rted by TAP, and 4/5 had N-te d TPGPGVRY are naturally p to be the direct product of a pr	rmini that were major cleavage rocessed ligands that can be el oteasomal digest	uted from HLA-B7 molecules, bo	Lucchiari-Hartz2000 en 123-152 one had extended precursor fragment oth are recognized by the same CTL, a major cleavage site between the Y		
Nef (128–137)	Nef (128–137 LAI) • C. Brander notes this is	TPGPGVRYPL a B*4201 epitope		human (B*4201)	Brander2001		
Nef (128–137)	<ul><li>73 peptides had 81 motion</li><li>directly related to the nu</li><li>20s proteasome cleavage</li></ul>	fs. 54% bound to the predicted mber of individuals that recog e of the Nef protein positions 6	I HLA molecule, particularly A nized a protein.	A2, B7/35, and B8. The strength of peptides were cleaved ending a	Choppin2001 A2, A3, A24, B7, B8, and B35; these of HLA-peptide binding was not at: 87L, 83A, 81Y, 71P, 68F and 67G		

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
	TPGPGVRYPL was rec	cognized in 8/16 (50%) of	individuals with HLA B7, and 1/9 (11	1%) of individuals with HLA E	335. It was a high affinity HLA binder.
Nef (128–137)	CD8+ T cells were four viral load was also four  • All three patients were  • ELISPOT was used to the state of the state o	nd prior to seroconversion ad B*2705, with HLA alleles test a panel of CTL epitop	HIV-1 infection fic CTL responses were studied during , and there was a close temporal relation s: A1, A30/31, B*2705, B35; A1, A*0 es that had been defined earlier and we 705 epitope KRWIILGGLNK	onship between the number of 0301, B7, B*2705; and A*020	1, A*0301, B*2705, B39
	<ul> <li>Weak responses were o B*2705</li> <li>No acute response was</li> </ul>	bserved to A*301-RLRPC detected to the following	response to SLYNTVATL GGKKK, A*301-QVPLRPMTYK, and epitopes: A*201-ILKEPVHGV, A*30 PVGEIY, B35-NSSKVSQNY, B35-VP	1-KIRLRPGGK, A*301-AIFQ	QSSMTK, A*301-TVYYGVPVWK,
Nef (128–137)	Nef (128–137 LAI)  There was a high degre variants, indicating imm The epitope position was	nune selection	HIV-1 infection Lepitopes in Nef in four slow and non	human (B7) -progressors, and variant speci	Haas 1996, Haas 1997 ffic CTLs arose over time to eliminate
Nef (128–137)		oss-reactivity could protectus is identical to the B cla	HIV-1 exposed seronegative exted prostitutes from Nairobi using pr t against both A and D and confer prot de epitope	eviously-defined B clade epito	
Nef (128–137)	<ul><li>Seroprevalence in this of</li><li>Most isolated HIV strain</li></ul>	cohort is 90-95% and their ins are clade A in Nairobi, y observed using A or D c ed among B and D clade v	viruses	CTL may confer protection in the world	Rowland-Jones1998b cross-reactive, however stronger
Nef (128–137)	<ul><li>donors</li><li>Th1-biasing cytokines I within</li></ul>	IL-12 or IFN alpha enhand	in vitro stimulation cell responses – DCs can stimulate aut ce CTL responses in vitro whether the his epitope, although it had been immu	epitope is delivered by pulsing	g from peptide, or expressed from
Nef (128–137)	Nef (128–137 SF2) • Therapy provided during individuals treated during the state of		HIV-1 infection in a narrower CTL response, stronger	human (B7) T help response, and a less div	Altfeld2001b verse viral population than was seen in

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References				
	individuals with primar (Group 3), using 259 o • Previously described as	ry infection but post-ser verlapping peptides spa nd newly defined optima	s determined using ELISPOT by studying oconversion therapy (Group 2), and 10 in ning p17, p24, RT, gp41, gp120 and Neal epitopes were tested for CTL respons TL response to this epitope broken down	individuals who responded to l ef e	HAART given during chronic infection				
Nef (128–137)	Nef (128–137)	TPGPGVRYPL	HIV-1 infection, HIV-1 exp seronegative		Kaul2001a				
	HIV-1-infected female • Responses in HEPS we reduced risk of infection	Nairobi sex workers omen tended to be lower	a panel of 54 predefined HIV-1 epitope c, and focused on different epitopes with in the response in the HEPS women up	HLA presenting molecules the	at have previously been associated with				
	<ul> <li>43/91 HEPS women ha</li> <li>Among HLA-B7 wome</li> <li>The dominant response</li> <li>Subject ML 1203 starte</li> </ul>	<ul> <li>43/91 HEPS women had CD8+ responses and detection of HIV-1-specific CTL in HEPS women increased with the duration of viral exposure</li> <li>Among HLA-B7 women, 4/5 HEPS and 5/6 HIV-1 infected women recognized this epitope</li> <li>The dominant response to this HLA allele was to this epitope in 3 of the 4/5 HEPS cases and in 2 of the 5/6 HIV-1 infected women</li> <li>Subject ML 1203 started with CTL responses to A*6802 DTVLEDINL and to B7 FPVTPQVPLR prior to seroconversion, and upon seroconversion acquired additional responses to A*6802 ETAYFILKL which became dominant, B7 TPGPG(V/I)RYPL, B7 IPRRIRQGL, and B7 SPRTLNAWV</li> </ul>							
Nef (128–137)	• HIV-specific CD8+ T of CD27 expression on H	ells expressed lower lev IV-specific cells, sugges	HIV-1 infection staining was used to study the function of the staining was used to study the function of the staining was used to study the function activated virus-specific CD8+ T cells proceed the staining that the staining was activated virus-specific CD8+ T cells proceed to stain the staining was activated virus-specific CD8+ T cells proceed to stain the staining was activated virus-specific CD8+ T cells proceed to stain the staining was used to study the function of the staining was used to study the function of the staining was used to study the function of the staining was used to study the function of the staining was used to study the function of the staining was used to study the function of the staining was used to study the function of the staining was used to study the function of the staining was used to study the function of the staining was used to study the function of the staining was used to stain the stain the staining was used to stain the stain the staining was used to stain the stain the stain the staining was used to stain the st	+ T cells from the same donor,	and this was associated with persistent				
Nef (128–137)	studied in eight HIV-1- • 2 to 17 epitopes were repitopes were targeted • Subjects with chronic I • An acute seroconvertor • The other acute serocon	infected subjects, two vecognized in a given incomplete by at least one person HIV-1 infection recognize homozygous for the B'nvertor failed to recognize	HIV-1 infection pitopes restricted by HLA class I A and with acute infection, five with chronic, as dividual, A2-restricted CTL response ter zed between 2-8 out of 11 B7-restricted fallele recognized five B7-restricted ep ize any of the 11 B7-restricted epitopes uriable and there was no clearly dominar	nd one long-term non-progress nded to be narrow and never do epitopes itopes tested	sor (LTNP)				
Nef (128–137)	<ul><li>73 peptides had 81 mod directly related to the n</li><li>20s proteasome cleavag</li><li>The frequency of recog</li></ul>	tifs. 54% bound to the plumber of individuals the ge of the Nef protein pognition may be in part displayed.	HIV-1 infection ed based on putative anchor motifs in the predicted HLA molecule, particularly A2 at recognized a protein. sitions 66-100 showed a large fraction of actated by the cleavage step in processin of individuals with HLA B7, and 1/9 (1)	2, B7/35, and B8. The strength of peptides were cleaved ending g.	of HLA-peptide binding was not g at: 87L, 83A, 81Y, 71P, 68F and 67G.				

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
Nef (128–137)	<ul> <li>One individual, AC-06 interruptions (STI). He restricted by HLA-A3,</li> <li>0/11 HLA-B7 individu</li> </ul>	cutely HIV-infected HLA-, was homozygous at all the had only two detectable of 11 by HLA-B7, and 1 by als had detectable B7-rest	HIV-1 infection  A3 (n=7) or -B7 (n=4) or both -A3 and B hree class I alleles (A3, B7, Cw7), was tre CTL responses during acute infection, but HLA-Cw7. ricted responses to this epitope during acute dividuals had detectable responses to this	eated during acute infection a after STI this broadened to 2 atte infection – 10/15 of HLA	nd had supervised treatment 27 distinct epitopes including 15
Nef (128–137)	Nef • Four HIV patients with specific T-cell response • Nef epitope recognition	TPGPGVRYPL  n prolonged clinically success by Elispot and Tetramen n was detected in all 4 sub-	HIV-1 infection ressful anti-viral therapy but with ongoing rataining, maintained for 2-4 years after injects, gp120, Pol and Gag-specific in 1 or ate maturation phenotype characterized by	human (B7) g evidence of replication and nitiation of HAART. 2 subjects.	•
Nef (128–137)	<ul> <li>The HIV-1 subtype A f         which could direct the         conserved, often immu         Kenya. A DNA and M         included in the polyepi</li> <li>Multiple CD4+ or CD8         assays after vaccination</li> </ul>	Focused vaccine HIVA corprotein to the cell membra nodominant epitopes that VA prime-boost vaccination tope string [Hanke2000]. 3+ T-cell vaccine-induced n of 5 macaques. The resp	HIV-1 infection, Vaccine MVA boost <i>Strain:</i> subtype A <i>HIV co</i> atains p24 and p17, in a reversed order relatane and inhibit efficient peptide processing were selected to have particularly good or protocol using the HIVA antigen will be responses to peptide pools were detected bonse to the Mamu A*01 SIV p27 epitope atted macaques, possibly because of processing	ative to the Gag polyprotein of g and class I presentation, as pross-reactive potential for the ne used in a phase III clinical using intracellular cytokine of p11C (CTPYDINQM), included	to prevent myristylation of p17, well as a polyepitope string of A-clade epidemic in Nairobi, trial in Kenya. This epitope is staining and IFNgamma Elispot aded in the polyepitope region, was
Nef (128–137)	<ul><li>Seroprevalence in this</li><li>Most isolated HIV stra responses are frequentl</li></ul>	cohort is 90-95% and thei ins are clade A in Nairobi y observed using A or D of	HIV-1 exposed seronegative gative prostitutes from Nairobi – these CT r HIV-1 exposure is among the highest in , although clades C and D are also found-clade versions of epitopes clade D version: TPGPGIRYPL	the world	Rowland-Jones1998b cross-reactive, however stronger
Nef (128–137)	<ul><li>CD8+ T cell responses</li><li>Low risk individuals di</li><li>CD8+ T cell epitopes:</li></ul>	osed but persistently seron tended to be to the same id not have such CD8+ ce	als), SLYNVATL (4 individuals), LSPRTI	cervical CD8+ T cell respon	ises

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
Nef (130–139)	73 peptides had 81 motif directly related to the nu  • 20s proteasome cleavage The frequency of recogn	s. 54% bound to the predimber of individuals that read of the Nef protein position may be in part dictated.	cted HLA molecule, particularly Accognized a protein. ons 66-100 showed a large fraction ed by the cleavage step in processi	A2, B7/35, and B8. The strength of peptides were cleaved endinging.	Choppin2001 A2, A3, A24, B7, B8, and B35; these of HLA-peptide binding was not at: 87L, 83A, 81Y, 71P, 68F and 67G 55, although it was a high affinity HLA
Nef (130–143)	Nef (130–143 LAI)  CTL response to this epi Peptide defined on the ba		HIV-1 infection rm survivors otif, yet not cross-restricted except	human (B*57)	Goulder1996b
Nef (130–143)	Nef (121–141) • One of the 51 HIV-1 epit HLA alleles	GPGVRYPLTFGWCY topes selected by Ferrari e	HIV-1 infection t al. as good candidate CTL epitop	human (B57) bes for vaccines by virtue of being	Ferrari2000 g conserved and presented by commor
Nef (132–144)	subtype in nef and env a	nd 7 of the 41 strains were		_	Jubier-Maurin1999 4 subtypes were classified in the same
Nef (132–147)	Nef (132–147 BRU) • HIV-1 specific CTLs det	GVRYPLTFGWCYKLVP ected in lymphoid organs	HIV-1 infection	human (A1, B8)	Hadida1992
Nef (132–147)	Nef (132–147 BRU) • Nef CTL clones from HI	GVRYPLTFGWCYKLVPIV+ donors	HIV-1 infection	human (B18)	Culmann1991
Nef (132–147)	<ul> <li>DNA vaccinated BALB/ immunization</li> <li>Strong but non-lasting H protein boost</li> <li>Immunization with eithe</li> </ul>	c mice primed and boosted IV-specific CTL response r the multiepitopic DNA of	A with recombinant protein boost d with the multiepitopic vaccine w	rith IL18 showed lymphoprolifera say and DNA prime/DNA boost v duced HIV-1 specific Th1 cytokin	was more effective than DNA prime
Nef (133–148)	Nef (133–148 LAI) • P. Goulder, pers. comm.	VRYPLTFGWCYKLVPV		human (B57)	Brander1996b
Nef (134–141)	Nef (138–147 LAI) • C. Brander notes this is a	RYPLTFGW an A*2402 epitope	HIV-1 infection	human (A*2402)	Brander2001
Nef (134–141)	Nef (138–147 SF2)  • Therapy provided during individuals treated during		HIV-1 infection n a narrower CTL response, strong	human (A24) ger T help response, and a less div	Altfeld2001b verse viral population than was seen in

HXB2 Location	<b>Author's Location</b>	Sequence	Immunogen	Species (HLA)	References
	individuals with prima (Group 3), using 259 c • Previously described a	ry infection but post-ser overlapping peptides spa nd newly defined optim	s determined using ELISPOT by study coconversion therapy (Group 2), and 10 nning p17, p24, RT, gp41, gp120 and al epitopes were tested for CTL respon CTL response to this epitope broken d	0 individuals who responded to H Nef nse	IAART given during chronic infection
Nef (134–141)	<ul> <li>CTL epitopes (http://h</li> <li>60 epitope responses v magnitude of the responses v magnitude of the responses.</li> <li>1 year post-HAART tr in PB, and 13/25 epito.</li> <li>Treatment interruption become undetectable i</li> <li>Breakdowns of epitope.</li> </ul>	and lymph node (LN) Coiv-web.lanl.gov/content. were detected in both PE onse was similar in LN at in the LN. eatment in five patients pe responses in the PB I following HAART indenthe PB, and the additional responses were shown	HIV-1 infection  2D8+ T-cell responses were compared /hiv-db/REVIEWS/brander2001.html) and LN samples of the 15 patients, and PB, but the percentage of CD8+ T studied, the magnitude of the CD8 T-coecame undetectable, in contrast to 5/2 uced resulted in increased viremia according of 9 novel epitope responses. for 4 individuals. Patient C displayed A24-RL9(gp41), A24-YL8(gp41), and	of for each person's class I HLA all and an additional 8 responses were cells in the LN is lower so the nuclear response was decreased in both 26 in the LN.  The companied by the restoration of the the greatest response to B27-KK	leles. detected only in LN. The total umber of HIV-specific cells per million th LN and PB, but more dramatically e detection of 13 epitopes that had
Nef (134–141)	Nef (134–141 LAI) • Optimal peptide define	RYPLTFGW ed by titration		human (B27)	Culmann1998
Nef (134–143)	Phe, Leu or Ile at the C  This peptide induced C	C term) – 53 of the 59 pc CTL in 3/4 HIV-1+ peop	eptides bound A*2402		Ikeda-Moore1997 anchors in HIV proteins (Tyr at 2, and specific CTL clones were obtained
Nef (134–143)	<ul> <li>Epitope name: Nef138</li> <li>A Sendai virus vector responses and has the</li> <li>MHC class I/peptide to</li> </ul>	-10 system (SeV) was devel potential to elicit immun etramers could be made	Vaccine em (SeV) HIV component: class I/pe oped that expressed HLA-A*2402-res ne responses. using this system that bound to epitop ss A*2402-HIV epitope complexes inc	stricted class I/peptide complexes: be-specific CTLs in PBMCs.	
Nef (134–143)	<ul> <li>73 peptides had 81 mo directly related to the r</li> <li>20s proteasome cleava</li> <li>The frequency of recognition</li> </ul>	tifs. 54% bound to the p number of individuals the ge of the Nef protein pognition may be in part d	HIV-1 infection ed based on putative anchor motifs in a predicted HLA molecule, particularly a part recognized a protein. sitions 66-100 showed a large fraction dictated by the cleavage step in process of individuals with HLA A24. It was	A2, B7/35, and B8. The strength of peptides were cleaved endinging.	of HLA-peptide binding was not at: 87L, 83A, 81Y, 71P, 68F and 67G.

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
Nef (134–144)	Nef (134–144 LAI)  • Mutational variation in  • [Goulder1997a] is a rev		HIV-1 infection als with appropriate HLA types can resululat summarizes this study	human (B18) t in evasion of CTL response	Couillin1994, Goulder1997a
Nef (134–144)	CD4 proliferative responsive HAART had no HIV spundetectable	onses and were able to ma pecific CD4 proliferative	HIV-1 infection  ction (three with sustained therapy, two waintain a CTL response even with undetected responses and lost their CTL responses watope but none were HLA B18+	table viral load – three patie	nts that had delayed initiation of
Nef (135–143)	<ul><li>All five could be transp</li><li>YPLTFGWCY is the n</li></ul>	orted by TAP, and 4/5 ha aturally processed ligand	in vitro stimulation ere identified in Nef in the conserved imm d N-termini that were major cleavage poir for B7, and this epitope is the only one of the cell, possibly due to a predominant p	nts for the proteasome, only f the five that may require tri	one had extended precursor fragments mming at the N-termini
Nef (135–143)	Nef (135–143 LAI) • C. Brander notes this is	YPLTFGWCY s a B*1801 epitope	HIV-1 exposed seronegative	human (B*1801)	Brander2001
Nef (135–143)	<ul> <li>24 epitopes were descr</li> <li>Serial peptide truncatio</li> <li>Subject 00RCH33 was A*3002; AETFYVDG</li> <li>Among HIV+ individu</li> </ul>	pitope responses in HIV- ibed – 8 were novel, 8 us ons were used to define of on HAART had a viral lo A, RT(437-445), HLA B als who carried HLA B5	HIV-1 infection  1 infected minority women living in the Used new restricting elements but were prevotimal epitopes for CTL cell lines isolated and of 2900 and CD4 count of 727 and alse 4501; and RSLYNTVATLY, p17(76-86), 8, 8/15 (53%) recognized this epitope – or 5, 13/19 (68%) recognized this epitope	iously defined epitopes, and from 12 individuals, assaye to recognized the epitopes H HLA A*3002	8 were previously described d by a Cr-release IGPGRAFY, gp160(310-318), HLA
Nef (135–143)	Nef (subtype D)  11/16 heavily HIV exp CD8+ T cell responses Low risk individuals di CD8+ T cell epitopes:	YPLTFGWCF osed but persistently sero tended to be to the same d not have such CD8+ ce	HIV-1 exposed seronegative negative sex-workers in Nairobi had HIV-epitopes but at generally lower levels that lls nals), SLYNVATL (4 individuals), LSPRT	n cervical CD8+ T cell respo	onses
Nef (135–143)	Nef (135–143 LAI)  • Nef CTL clones from F	YPLTFGWCY	HIV-1 exposed seronegative	human (B18)	Culmann1991, Culmann-Penciolelli1994
Nef (135–143)	Nef (135–143 SF2)	YPLTFGWCY ng acute infection resulted	HIV-1 infection d in a narrower CTL response, stronger T	human (B18) help response, and a less div	Altfeld2001b terse viral population than was seen in

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
	individuals with prima (Group 3), using 259 c • Previously described a	ry infection but post-se overlapping peptides sp and newly defined opting	as determined using ELISPOT by study eroconversion therapy (Group 2), and 10 anning p17, p24, RT, gp41, gp120 and N nal epitopes were tested for CTL response CTL response to this epitope broken do	individuals who responded to I lef se	HAART given during chronic infection
Nef (135–143)	<ul><li>T-cells, detected by int</li><li>Ghonorrhea caused the</li></ul>	tracellular cytokine pro e weaker HIV-1 specific	HIV-1 infection yan sex workers caused a functional defi duction and tetramer assays, while not a c CTL responses in 4 HIV-1 exposed per ic CTL in 2 HEPS subjects were shown	ffecting the total number of epi- sistently seronegative (HEPS)	tope-specific CTLs.  women to become undetectable by
Nef (135–143)	<ul> <li>CTL epitopes (http://h</li> <li>60 epitope responses v magnitude of the responses v magnitude of the responses v magnitude of the response v magnitude v</li></ul>	and lymph node (LN) of iv-web.lanl.gov/content were detected in both Plonse was similar in LN in the LN. eatment in five patients pe responses in the PB is following HAART into the PB, and the addition in the PB is the properties of the properties and the properties are shown in the PB.	HIV-1 infection  CD8+ T-cell responses were compared in t/hiv-db/REVIEWS/brander2001.html) for B and LN samples of the 15 patients, and and PB, but the percentage of CD8+ T constructed in the contract to 5/26 duced resulted in increased viremia according of 9 novel epitope responses.  In for 4 individuals. Patient D displayed to 1(RT), A32-RW10(gp120), and B18-YY	for each person's class I HLA and an additional 8 responses were ells in the LN is lower so the number of the LN.  If the LN is lower so the number of the LN is lower so the number of the LN in the LN.  If the greatest response to B27-KK is the greatest respons	Iteles.  e detected only in LN. The total umber of HIV-specific cells per million oth LN and PB, but more dramatically ne detection of 13 epitopes that had
Nef (135–143)	<ul> <li>HIV-1-infected female</li> <li>Responses in HEPS we reduced risk of infection women</li> <li>43/91 HEPS women he</li> <li>Among HLA-B18 wor respond to FRDYVDR</li> <li>The dominant response</li> </ul>	study CTL responses to Pairobi sex workers omen tended to be lowed on, and there was a shift and CD8+ responses and men, 1/4 HEPS and 8/9 RF(Y/F)K, while infector to this HLA allele was specificity were only s	er, and focused on different epitopes with in the response in the HEPS women up did detection of HIV-1-specific CTL in HE HIV-1 infected women recognized this ed women tended to respond to YPLTFC is to this epitope for the one reactive HE een for responses restricted by class I HI	es in 91 HIV-1-exposed, persistent HLA presenting molecules that on late seroconversion to epito PS women increased with the depitope, likelihood ratio 5.3, p. v. WC(Y/F) PS case and in all 8/9 HIV-1 inf	at have previously been associated with pes recognized by the HIV-1 infected duration of viral exposure value 0.04, and HEPS women tended to fected women
Nef (135–143)	Nef (139–147 SF2)  • Binds HLA-B*3501	YPLTFGWCF	HIV-1 infection	human (B35)	Shiga1996

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
Nef (135–143)	73 peptides had 81 mot directly related to the n • 20s proteasome cleavas The frequency of recog	ifs. 54% bound to the pumber of individuals that the of the Nef protein position may be in part di	HIV-1 infection and based on putative anchor motifs in the redicted HLA molecule, particularly AZ at recognized a protein. Sitions 66-100 showed a large fraction of ctated by the cleavage step in processin of individuals with HLA B7, and 11/14	2, B7/35, and B8. The strength of peptides were cleaved ending g.	of HLA-peptide binding was not at: 87L, 83A, 81Y, 71P, 68F and 67G
Nef (135–143)	responded to Gag, 8/11 CD8+ T-cells in one wo T-cells in breast milk frepitope YPLTFGWCY. The frequencies of resp	responded to Pol, 7/11 oman, and another wom om a volunteer who wa onses in the two compa	HIV-1 infection HIV-1 infected women from the US ar women to Nef, and 2/5 women to Env pan had cytolytic responses measured by sHLA A3, A11, B35, B51 induced IFN rtments differed, and 2/4 women that reconses in peripheral blood cells.	peptide pools. These responses Cr-release.  Igamma after stimulation with	were shown to be primarily due to a peptide that carries known B35
Nef (135–143)		oss-reactivity could prot us is identical to the B o	HIV-1 exposed seronegative infected prostitutes from Nairobi using peet against both A and D and confer proclade epitope	previously-defined B clade epite	
Nef (135–143)	<ul> <li>Seroprevalence in this c</li> <li>Most isolated HIV strainersponses are frequentl</li> <li>This epitope is conserv</li> </ul>	cohort is 90-95% and the ns are clade A in Nairo y observed using A or E ed among A and B clade	HIV-1 exposed seronegative prostitutes from Nairobi – these eir HIV-1 exposure is among the highest bi, although clades C and D are also for D clade versions of epitopes e viruses  VCF, was preferentially recognized by C	e CTL may confer protection st in the world and – B clade epitopes are often	Rowland-Jones1998b n cross-reactive, however stronger
Nef (135–143)	<ul><li>sex workers eventually</li><li>The epidemiological fa working for a period or</li></ul>	seroconverted, and for sector associated with servetire	HIV-1 infection posed, persistently seronegative individ six of these HIV CTL reactive epitopes oconversion was stopping sex work and ed in 1/22 HEPS sex worker controls (N	had been defined while serones HIV-specific CTL activity dec	gative
Nef (135–143)		ifs. 54% bound to the p	HIV-1 infection and based on putative anchor motifs in the redicted HLA molecule, particularly A2 at recognized a protein.		

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
	The frequency of recog	gnition may be in part d	ositions 66-100 showed a large fraction of ictated by the cleavage step in processing of individuals with HLA B7, and 11/14	ng.	
Nef (136–144)	73 peptides had 81 more directly related to the notation 20s proteasome cleavage. The frequency of recognitions are supported by the frequency of the freq	tifs. 54% bound to the plumber of individuals the ge of the Nef protein pognition may be in part d	HIV-1 infection ed based on putative anchor motifs in the predicted HLA molecule, particularly A nat recognized a protein. esitions 66-100 showed a large fraction of ictated by the cleavage step in processir of individuals with HLA A3. It was a lo	2, B7/35, and B8. The strength of peptides were cleaved ending ng.	of HLA-peptide binding was not
Nef (136–145)	<ul><li>donors</li><li>Th1-biasing cytokines within</li></ul>	IL-12 or IFN alpha enh es were studied and the HHVAREL	in vitro stimulation g T cell responses – DCs can stimulate a ance CTL responses in vitro whether th relative binding affinity of A2 epitopes be A*0201	e epitope is delivered by pulsing	g from peptide, or expressed from
Nef (136–145)	Nef (136–145 LAI)  • C. Brander notes this is	PLTFGWCYKL s an A*0201 epitope		human (A*0201)	Brander2001
Nef (136–145)	All five could be transp	oorted by TAP, and 4/5 led PLTFGWCYKL also	in vitro stimulation were identified in Nef in the conserved had N-termini that were major cleavage be recognized PLTFGWCYKLV, and bot the in low copy number	points for the proteasome, only	one had extended precursor fragments
Nef (136–145)	<ul><li>Epitope name: Nef-PL</li><li>Among HIV+ individu</li></ul>		HIV-1 infection 02, 3/29 (10%) recognized this epitope	human (A02)	Sabbaj2002b
Nef (136–145)	<ul> <li>one A subtype infectio</li> <li>Pol reactivity: 8/8 had</li> <li>Gag reactivity: 7/8 reac</li> <li>Nef reactivity: 7/8 reac</li> <li>Env reactivity: 3/8 reac</li> </ul>	n from a person living in CTL to A subtype, and cated with A or B subtype, and the with A subtype, and the with A subtype, and the with A subtype, 1/8	HIV-1 infection ermining the CTL activity in seven patie in France originally from Togo, to differ 7/8 to B subtype, and HIV-2 Pol was no be gag, 3/8 with HIV-2 Gag d 5/8 with B subtype, none with HIV-2 8 with B subtype, none with HIV-2 Env sity of response, and recognized Gag SI	rent antigens expressed in vaccir of tested	nia

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
Nef (136–145)	<ul> <li>A polyepitope vaccine of HHD mice have a transfer expressed in the mice</li> <li>CTL responses to Gag (observed in HIV polyto)</li> <li>No CTL immune response 180-189 (VLEWR)</li> <li>Sixteen HLA A2+ paties the polytope – one individual control of the polytope – one individ</li></ul>	was generated in a vaccing gene of HLA A2 linked (77-85) SLYNTVATL, P pe HHD-vaccinated microses were generated again FDSRL) onts were tested for their vidual recognized all sever than one epitope, but the	en of these epitopes; 7 patients had C hey were not able to test all peptides	ded seven epitopes, all presented domains of H-2D <sup>d</sup> – this transger 120-128) KLTPLCVTL, and Nef d with vaccinia boost s Nef 157-166 (PLTFGWCYKL), eptide restimulation in culture wit CTL cultures able to recognize at	(190-198) AFHHVAREL were Pol 346-354 (VIYQYMDDL), and the epitopes selected for inclusion in least one of the epitopes, and 6 of
Nef (136–145)	epitopes in this group, a	ort of HIV+ female sex although E clade version ized the E clade version	HIV-1 infection workers (FSW) from Northern Thaila s of previously defined B-clade A2 a of this epitope PLCFGWCFKL, white	nd A24 epitopes were also tested	
Nef (136–145)	studied in eight HIV-1-	infected subjects, two wi ecognized in a given indi	HIV-1 infection itopes restricted by HLA class I A ar th acute infection, five with chronic, vidual, A2-restricted CTL response t	and one long-term non-progresso	
Nef (136–145)	73 peptides had 81 mot directly related to the m • 20s proteasome cleavag The frequency of recog	ifs. 54% bound to the prumber of individuals that e of the Nef protein posinition may be in part dic	edicted HLA molecule, particularly at recognized a protein.	A2, B7/35, and B8. The strength of peptides were cleaved endinging.	Choppin2001 A2, A3, A24, B7, B8, and B35; these of HLA-peptide binding was not at: 87L, 83A, 81Y, 71P, 68F and 67G.
Nef (136–146)	<ul><li> All five could be transp</li><li> The CTL that recognize</li></ul>	orted by TAP, and 4/5 ha	recognized PLTFGWCYKLV, and bo	e points for the proteasome, only	Lucchiari-Hartz2000 en 123-152 one had extended precursor fragments ally processed and both seem to be the

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References	
Nef (137–145)	for the A3 supertype) v • Progressors had memore • A positive correlation be observed, which may c	while the effector cells or ry resting CD8+ T-cells between effector CD8+ ontribute to the inability	HIV-1 infection g memory resting CD8+ T-cell respons of long-term nonprogressors recognized that recognized far fewer epitopes that T-cells and plasma viremia and a negative of LTNPs to clear virus pes alleles (A*0201, A*0202, A*0203	d far fewer epitopes n LTNPs tive correlation between CD8+ e	ses tested, (18 for the A2 supertype, 16	
Nef (137–145)	<ul> <li>Ten Nef 9-mer peptides assay, several others be</li> <li>A CTL immune respon DNA under the control</li> <li>LTFGWCFKL was also vaccination did elicit a</li> </ul>	s were predicted to have bund weakly use to only 3/10 peptides of a CMV promotor, co tested by subcutaneous response		*0201 – of these, four did bind after immunization of HLA-A2 ominal skin by gene gun – LTFC adjuvant, because it bound stro	01 transgenic mice with either nef GWCFKL did not elicit a CTL response ngly to HLA-A*0201, and the peptide	
Nef (137–146)	Nef (221A)  • Epitope name: Nef-221  • HIV was scanned for a criteria, and 30 of these  • Three additional previor recognized at least one maximum of 2)  • 1/22 individuals with comparison of 2/12 acutely infected in	LTFGWCFKLV  a Il peptides which carrie be bound to HLA-A*020 busly described HLA-A of the 23 peptides (med	HIV-1 infection  d the A2-supermotif pattern conserved 1 – 20/30 bound to at least 3/5 of HLA 2 epitopes were added to the set of 20, lian of 2 and maximum of 6), while 6/ recognized this epitope in ELISPOT its epitope	human (A2) in more than 50% of B clade section—A2 supertype alleles tested and 18/22 chronically infected 12 acute infected individuals recommends.	Altfeld2001c equences – 233 peptides met this HLA-A2 individuals had CTL that eognized at least 1 (median of 1 and	
Nef (137–146)	<ul> <li>LTFGWCFKLV binds to five HLA-A2 supertype alleles:A*0203, A*0201 (highest affinity), A*0206, A*6802 and A*0202</li> <li>Nef (158–167) LTFGWCFKLV HIV-1 infection human (A2 supertype) Propato2001</li> <li>Long-term nonprogressors (LTNPs) had strong memory resting CD8+ T-cell responses against the majority of epitopes tested, (18 for the A2 supertype, 16 for the A3 supertype) while the effector cells of long-term nonprogressors recognized far fewer epitopes</li> <li>Progressors had memory resting CD8+ T-cells that recognized far fewer epitopes than LTNPs</li> <li>A positive correlation between effector CD8+ T-cells and plasma viremia and a negative correlation between CD8+ effector T-cells and CD4+ T-cells was observed, which may contribute to the inability of LTNPs to clear virus</li> <li>This epitope can bind all five HLA-A2 supertypes alleles (A*0201, A*0202, A*0203, A*0206 and A*6802)</li> <li>Tetramer staining with A2, beta2microglobulin, and either SLYNTVATL, KLVGKLNWA, or LTFGWCFKL revealed that tetramers detected more HIV-specific sells in LTNP than in progressors, activated effector cells were the minority population, and ELISPOT correlated better with the effector cell subpopulation than the total tetramer stained population</li> </ul>					
Nef (162–181)	Nef (161–180)  • HIV-specific CTL lines	TSLLHPVSLHGMD	DPEREVL HIV-1 infection	human	Lieberman1995	

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
Nef (162–181)	Eleven subjects had CT	TSLLHPVSLHGMDDPEREVL d CTL specific for more than 1 H L L that could recognize vaccinia-e L response to this peptide	IV-1 protein	human	Lieberman 1997a
Nef (162–181)	Nef (101–120 SF2) • CTL expanded ex vivo	TSLLHPVSLHGMDDPEREVL were later infused into HIV-1 infe		human	Lieberman1997b
Nef (162–181)	<ul> <li>Eleven subjects had CT</li> </ul>	TSLLHPVSLHGMDDPEREVL d CTL specific for more than 1 H. L. that could recognize vaccinia-e L. response to this peptide	IV-1 protein	human	Lieberman1997a
Nef (166–177)	<ul> <li>individuals treated duri</li> <li>The breadth and specification individuals with primare (Group 3), using 259 or</li> <li>Previously described an</li> </ul>	ng chronic infection lecity of the response was determin ry infection but post-seroconversion verlapping peptides spanning p17, and newly defined optimal epitopes	ed using ELISPOT by on therapy (Group 2), a p24, RT, gp41, gp120 were tested for CTL re		nversion therapy (Group 1), 11 ART given during chronic infection
Nef (172–191)	• Eleven subjects had CT	GMDDPEREVLEWRFDSRLAF d CTL specific for more than 1 H. L that could recognize vaccinia-e FL response to this peptide was HLA-A2, B21	IV-1 protein	human	Lieberman1997a
Nef (175–184)	non-progressor  Three additional sub-dohighlighted 2078 possil	ominant HLA B7 epitopes were de	efined using EpiMatrix. V-1 derived from the stu	human (B7) onal approach used to predict epitopes i , a non-anchor based strategy for definin dy subject, followed by B7 anchor resid	g potential epitopes, which
Nef (180–189)	variants, indicating imr			human (A*0201) and non-progressors, and variant specific	Haas1996, Haas1997 c CTLs arose over time to eliminate
Nef (180–189)	Nef (180–189 LAI) • C. Brander notes this is	VLEWRFDSRL s an A*0201 epitope		human (A*0201)	Brander2001

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
Nef (180–189)	Nef (180–189 LAI)	VLMWQFDSRL	Vaccine	murine (transgenic) (A*0201)	Boissonnas2002
	<ul> <li>Ten naturally occurring functions through vacc</li> <li>Only two variants coul</li> <li>In vivo priming with N vlQwRfdsKl, vlVwrfd</li> </ul>	g variants of this epitope wination of HLA-A*0201 t d induce vaccine response lef peptide VLMWQFDSI Trl, and vlAwKLdsrl but r	ransgenic mice. ss: VLMWQFDSRL, a high affinity RL induced cross-reactive CTL to 6 tot the LAI peptide vlEwrfdsrl)	djuvant: CFA 1-A*0201 and for their ability to industry binder, and VLQWRFDSRL a me 6/7 peptides tested (AlmwKfdsKl, v 8/6 variant Nef peptides (vlMwQfds	edium affinity binder to A*0201. elmwKfdsrl, vlmwKfdsKl,
Nef (180–189)	<ul> <li>C3H (H-2k) transgenic epidermal gene gun withe proteasome.</li> <li>A single immunization</li> <li>Immunodominant epitresponses and stimulat</li> <li>The presence of multip</li> </ul>	mice carrying a fused HI th an ubiquitin expression with the UB-HIV-1 librar opes SLYNTVATL (Gag), ed CTL that were function ble plasmids HLA-A*0201	library of 32 plasmids that spannery vaccine induced potent, stable at ILKEPVHGV(Pol), RIQRGPGRA all in a Cr-release assay and agains	H-2Dk alpha3 hybrid class I molected the HIV-1 genome. Ubiquitin target and multivalent CTL responses again AFVTIGK(P18) and AFHHVAREK at wild type antigen. ecrease CTL immunogenicity, and 0	gets the expressed HIV-1 peptides to ast all library members.  (Nef) elicited strong CD8+/IFN-
Nef (180–189)	<ul><li>donors</li><li>Th1-biasing cytokines within</li></ul>	IL-12 or IFN alpha enhan	ce CTL responses in vitro whether	human (A2) e autologous CTL responses from T the epitope is delivered by pulsing es for A2 was: PLTFGWCYKL gre	-
Nef (180–189)	<ul> <li>A polyepitope vaccine</li> <li>HHD mice have a transexpressed in the mice</li> <li>CTL responses to Gag observed in HIV polyto</li> <li>No CTL immune responses to Table 180-189 (VLEWR)</li> <li>Sixteen HLA A2+ pating the polytope – one indicates the polytope – one ind</li></ul>	was generated in a vaccin segene of HLA A2 linked to (77-85) SLYNTVATL, Pope HHD-vaccinated mice onses were generated again (FDSRL) ents were tested for their a ividual recognized all seve	o the transmembrane and cytotoxic of (476-484) ILKEPVHGV, gp120 c, and these responses were enhanced that HLA A2-restricted HIV epitoperability to make CTL responses by perior of these epitopes; 7 patients had ey were not able to test all peptides	oded seven epitopes, all presented by domains of H-2D <sup><math>d</math></sup> – this transgend (120-128) KLTPLCVTL, and Nef (ed with vaccinia boost es Nef 157-166 (PLTFGWCYKL), I	e is the only MHC molecule 190-198) AFHHVAREL were Pol 346-354 (VIYQYMDDL), and the epitopes selected for inclusion in east one of the epitopes, and 6 of

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
Nef (180–189)	Nef (180–189 LAI) • Epitope name: N3	VLEWRFDSRL	HIV-1 infection	human (A2)	Mollet2000
	CD8+ cell IFNgamma	production to measure re	•		_
	specificities that were r HIV-specific responses	not previously detectable diminished	iral load decreased and frequencies of were newly detected, as were CMV see: increases or decreases in pre-exist	specific CD8+ PBL – but with cont	inued viral suppression,
Nef (180–189)	Nef (179–188 93TH25		HIV-1 infection	human (A2)	Bond2001
	epitopes in this group,	although E clade versions nized the E clade version	workers (FSW) from Northern Thaila s of previously defined B-clade A2 at of this epitope VLIWKFDSAL, whi	nd A24 epitopes were also tested.	•
Nef (180–189)	studied in eight HIV-1-	infected subjects, two wi ecognized in a given indi	HIV-1 infection itopes restricted by HLA class I A an th acute infection, five with chronic, vidual, A2-restricted CTL response t	and one long-term non-progressor	(LTNP)
Nef (182–198)	Nef (182–198 BRU) • HIV-1 specific CTLs de	EWRFDSRLAFHHVA: etected in lymphoid organ	REL HIV-1 infection ns of HIV-1 infected patients	human (A1, B8)	Hadida1992
Nef (182–198)	Nef (182–198 LAI) • The C-terminal region	EWRFDSRLAFHHVA. of Nef (182-205) contain	REL HIV-1 infection s multiple CTL epitopes with 5 distin	human (A2, A25(10)) act HLA restrictions	Hadida1995
Nef (182–198)	Nef (182–198 BRU) • CTL isolated in childre	EWRFDSRLAFHHVA: en born to HIV-1 positive		human (A25)	Cheynier1992
Nef (182–198)	Nef (182–198 LAI) • The C-terminal region	EWRFDSRLAFHHVA: of Nef (182-205) contain	REL HIV-1 infection s multiple CTL epitopes with 5 distinguished	human (B35) nct HLA restrictions	Hadida1995
Nef (182–198)	Macaca mulatta did nor	t have a detectable response to this epitor	REL Vaccine  Strain: LAI HIV component: Nef use to Rec Mengo virus-HIV-1 Nef 6 use in the Mengo virus construct – in		VanderRyst1998  ng CTL response in mice when
Nef (182–201)	Nef (191–205 SF2) Of 25 patients, most ha Eleven subjects had CT One of these 11 had CT The responding subject	nd CTL specific for more TL that could recognize v. TL response to this peption	accinia-expressed LAI Nef	human	Lieberman1997a

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
Nef (182–205)	Nef (182–205 LAI)	EWRFDSRLAFHHVARI EYFKN	ELHP- Vaccine	human	Gahery-Segard2000
	<ul> <li>Anti-HIV lipopeptide v administered in a phase</li> <li>A CD4+ T cell prolifer</li> <li>9/12 tested mounted a 0</li> </ul>	e I trial ative response to at least or	ng amino acid peptides derived from ne of the six peptides was observed ne of the six peptides; each of the six	in 9/10 vaccinees – 4/10 reacted	
Nef (183–191)	<ul> <li>24 epitopes were descri</li> <li>Serial peptide truncatio</li> <li>This epitope was newly</li> <li>Subject 01RCH50 also</li> <li>960 and CD4 count of</li> </ul>	pitope responses in HIV-1 libed – 8 were novel, 8 used in swere used to define option of defined in this study recognized the epitope RM 728		previously defined epitopes, and lated from 12 individuals, assayed 002 – she was African American,	
	Among HIV+ individual	als who carried HLA B15,	3/17 (18%) recognized this epitope	;	
Nef (186–193)	Nef (186–193 LAI) • The C-terminal region	DSRLAFHH of Nef (182-205) contains	HIV-1 infection multiple CTL epitopes with 5 distir	human (B35) act HLA restrictions	Hadida1995
Nef (186–194)	Nef (186–194)  • ELISPOT was used to s HIV-1-infected female		HIV-1 infection, HIV-1 ex seronegative panel of 54 predefined HIV-1 epitop		Kaul2001a ntly seronegative (HEPS) and 87
Nef (186–194)	Nef (186–194 BRU) • Resulted in the assemble	DSRLAFHHV ly of HLA-B51		human (B51)	Connan1994
Nef (188–196)	Nef (188–196 LAI) • The C-terminal region	RLAFHHVAR of Nef (182-205) contains	HIV-1 infection multiple CTL epitopes with 5 distir	human (B52) act HLA restrictions	Hadida1995
Nef (188–201)	<ul><li>Primary assays showed</li><li>Epitopes recognized in</li></ul>	five children were mapped	HIV-1 infection 39% at least one HIV protein was detected using synthetic peptides and seconspitopes in Nef, was infected via blooming the secons of the sec	ndary cultures	Buseyne1993a  nt from CDC stage P2A to P2E
Nef (190–198)	sex workers eventually	seroconverted, and for six ctor associated with seroco	HIV-1 infection sed, persistently seronegative indivi of these HIV CTL reactive epitope: onversion was stopping sex work an	s had been defined while seronega	

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
	• This epitope was in 1/2	2 HEPS controls, ML17	749		
Nef (190–198)	Nef • Epitope name: Nef AL	AFHHVAREL 9	HIV-1 infection	human (A*0201)	Altfeld2001c
	<ul> <li>HIV was scanned for al criteria, and 30 of these</li> <li>Three additional previo</li> </ul>	ll peptides which carried bound to HLA-A*020 ously described HLA-A2 at recognized at least or	the A2-supermotif pattern conserved in 1 – 20/30 bound to at least 3/5 of HLA-A2 epitopes were added to the set of 20, in the of the 23 peptides (median of 2 and median).	A2 supertype alleles tested acluding Nef AL9, and 18/22 c	hronically infected HLA-A2
			ILA-A2 patients with chronic HIV-1 info	ection or the 13 HLA-A2 patie	ents with acute HIV-1 infection
Nef (190–198)	Nef	ALKHRAYEL	HIV-1 infection, Vaccine	human, macaque (A*0201)	Hanke2000, Wee2002
	<ul> <li>The HIV-1 subtype A f which could direct the p conserved, often immun Kenya. A DNA and M included in the polyepin</li> <li>Multiple CD4+ or CD8 assays after vaccination</li> </ul>	ocused vaccine HIVA coprotein to the cell membrodominant epitopes that VA prime-boost vaccina tope string [Hanke2000] + T-cell vaccine-induced of 5 macaques. The re	a MVA boost <i>Strain:</i> subtype A <i>HIV</i> ontains p24 and p17, in a reversed order brane and inhibit efficient peptide process at were selected to have particularly goo tion protocol using the HIVA antigen with a responses to peptide pools were detect sponse to the Mamu A*01 SIV p27 epite inated macaques, possibly because of pro-	relative to the Gag polyprotein ssing and class I presentation, and cross-reactive potential for the ill be used in a phase III clinicated using intracellular cytokine ope p11C (CTPYDINQM), income	n to prevent myristylation of p17, as well as a polyepitope string of the A-clade epidemic in Nairobi, al trial in Kenya. This epitope is e staining and IFNgamma Elispot cluded in the polyepitope region, was
Nef (190–198)	<ul> <li>A CTL response was for and D clades – such crown the A subtype consens</li> <li>The D subtype consens</li> <li>[Hunziker1998] sugges [Brander1998b]</li> <li>[Hunziker1998] maintat position of Hunziker et</li> </ul>	ound in exposed but universelved in exposed but universelved in a LKHRAYEL us is AfEHKAREM that HLA-A2 does not that HLA-A2 does al., Rowland-Jones and	HIV-1 exposed seronegative A-B52 and A2.1, A2.2 and A2.4 infected prostitutes from Nairobi using prectagainst both A and D and confer proof of the fact present this epitope, and notes that the present this epitope contrary to an earl colleagues are confident that this epitope	reviously-defined B clade epitotection in Nairobi where both that it does not promote A2 as: rlier report [Hadida1995], (also be in its A clade form is presen	subtypes are circulating sembly [Connan1994] – also see o see [Brander1998a])—despite the tted by HLA-A*0201 and A*0202, and
N. C (100, 100)			both seropositive and exposed-uninfect		
Nef (190–198)	donors		in vitro stimulation T cell responses – DCs can stimulate au ance CTL responses in vitro whether the		_

<b>HXB2</b> Location	<b>Author's Location</b>	Sequence	Immunogen	Species (HLA)	References				
	B7 and A2 Nef epitopo much greater than AFI		relative binding affinity of A2 epitopes f	for A2 was: PLTFGWCYKL gr	eater than VLEWRFDSRL which was				
Nef (190–198)	Nef (190–198) Vaccine Vector/Type:	AFHHVAREL vaccinia HIV compon	Vaccine nent: polyepitope	human (A2)	Woodberry 1999				
	<ul> <li>HHD mice have a tran expressed in the mice</li> </ul>	sgene of HLA A2 links	cinia construct that contiguously encode ed to the transmembrane and cytotoxic do	omains of $H-2D^d$ – this transger	ne is the only MHC molecule				
	<ul><li>observed in HIV polyt</li><li>No CTL immune responsef 180-189 (VLEWR)</li></ul>	ope HHD-vaccinated nonses were generated agreement (properties of the properties of	Pol (476-484) ILKEPVHGV, gp120 (12 nice, and these responses were enhanced gainst HLA A2-restricted HIV epitopes I	with vaccinia boost Nef 157-166 (PLTFGWCYKL).	, Pol 346-354 (VIYQYMDDL), and				
	the polytope – one ind	ividual recognized all sore than one epitope, bu	eir ability to make CTL responses by pep seven of these epitopes; 7 patients had CT t they were not able to test all peptides for tients	ΓL cultures able to recognize at	least one of the epitopes, and 6 of				
Nef (190–198)	<ul> <li>individuals treated dur</li> <li>The breadth and specifindividuals with prima (Group 3), using 259 c</li> <li>Previously described a</li> </ul>	ing chronic infection ficity of the response w ry infection but post-se overlapping peptides sp and newly defined optin	HIV-1 infection  Ited in a narrower CTL response, stronge as determined using ELISPOT by studyic proconversion therapy (Group 2), and 10 anning p17, p24, RT, gp41, gp120 and N and epitopes were tested for CTL response CTL response to this epitope broken dow	ng 19 individuals with pre-sero individuals who responded to E lef	conversion therapy (Group 1), 11 IAART given during chronic infection				
Nef (190–198)	Nef (190–198)  • Variants ALKHRAYE				Kaul2001a				
	<ul> <li>ELISPOT was used to HIV-1-infected female</li> </ul>	•	o a panel of 54 predefined HIV-1 epitope	es in 91 HIV-1-exposed, persiste	ently seronegative (HEPS) and 87				
Nef (190–198)	Nef (subtype B)	AFHHVAREL	HIV-1 exposed seronegativ	human (A2, A*0202, A*0201)	Rowland-Jones1998b				
	• Seroprevalence in this	<ul> <li>HIV-specific CTL were found in exposed seronegative prostitutes from Nairobi – these CTL may confer protection</li> <li>Seroprevalence in this cohort is 90-95% and their HIV-1 exposure is among the highest in the world</li> <li>Most isolated HIV strains are clade A in Nairobi, although clades C and D are also found – B clade epitopes are often cross-reactive, however stronger</li> </ul>							
	<ul><li>responses are frequent</li><li>Clade A version of the</li></ul>	ly observed using A or epitope: ALKHRAYE	obt, although clades C and D are also for D clade versions of epitopes L, Clade D epitope: AFEHKAREM exposed and uninfected prostitutes	und – B clade epitopes are ofter	n cross-reactive, nowever stronger				
Nef (190–198)	Nef (190–198 LAI) • Naturally occurring L	AFHHVAREK to K anchor substitutio	HIV-1 infection n abrogates A2 binding, but permits HLA	human (A3) A-A3 binding	Hadida1995				

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
Nef (192–206)	Nef (192–206 BRU) • HIV-1 specific CTLs d	HHVARELHPEYFKNC etected in lymphoid organs of	HIV-1 infection HIV-1 infected patients	human (A1)	Hadida1992
Nef	infants  No HIV+ infants had n disease, and not in rapi	o demonstrable CTL at birth, d progressors	but Th1 responses accompanie	human sed production of beta-chemokine d by CTL responses developed in fected with vaccina/HIV construc	children with slowly progressive
Nef	Anti-NKR IgM MAb r	nasked this inhibitory function			De Maria1997 nin-activated PBMC cultured in the ectable levels
Nef	standard method, lytic	units (LU20)	•		Lubaki 1999 ion (LR) of net specific lysis, and the s observed using ACU and LR, but no
Nef	<ul><li>The vaccine used was r</li><li>In vitro inducible CTL</li></ul>	ec canarypox expressing HIV activity against HIV-1 Env, G	-1 env, gag, pol, nef and protea ag, Pol, and Nef antigens was	human  HIV component: Env, Gag, Pro, Notes (vCP300) with or without admobserved in 79% (15 of 19) of vac CTL induction and detection sense.	inistration of HIV-1 SF-2 rgp120 ccine recipients
Nef	responses to Gag, Pol, <ul><li>Data suggests that the</li></ul>	Env or Nef antigens	y of the CD8 T cell repertoire (		Gamberg1999 d six individuals showed HIV-specific etic diversity) remains intact through
Nef	<ul><li>9/9 HIV-1+ subjects we</li><li>The nef DNA immuniz</li><li>Highly active antiretro</li></ul>	ation induced the highest and viral treatment (HAART) did	accinations for nef, rev or tat, a most consistent CTLp activity not induce new HIV-specific C	human  nd novel proliferative and CTL re , IFN-gamma production, and IL- TL responses but reduced viral log plementary and promising combin	6 and IgG responses ad, while DNA vaccination induced
Nef		orrelation between strong CTL CD4 and CD8 cells, and lowe		human nse in 7-12 month old infants, and	Buseyne1998a I remaining AIDS-free for the first year

HXB2 Location	Author's Location Sequence	Immunogen	Species (HLA)	References
Nef	Nef (LAI) • In infants with positive CTL responses, mo subtypes	HIV-1 infection st responses showed cross-clade reactivity	human y with somewhat diminished reco	Buseyne1998b ognition of epitopes from different
Nef	Nef (LAI)  Vaccine Vector/Type: canarypox HIV con  A Canarypox vaccine expressing gp120, gp responses to Gag, Env, Nef and Pol were de	41, Gag, Protease, Nef and Pol CTL epito	opes gave rise to CTL that could	Evans1999 be detected in 61% of the volunteers
Nef	Nef • CTL dense regions of Nef tend to lie in con adaptation to infection that focuses the CTI			
Nef	Nef (LAI)  Seventeen recently infected patients were to An early response (within a month followir Early responses to Pol, Rev, Vif and Tat we	g PI) was noted in 87% of the subjects to		
Nef	Nef (LAI)  CTL responses to Env, Gag, Nef and RT was all proteins, 10 ARC patients responded we			
Nef	Nef  • A correlation between conserved regions of biological reasons such as the one described epitope definition such that conserved epitope both p17 and Nef show a correlation betwee known epitopes are evenly distributed across	d above [daSilva1998], or due to epitope pes would tend to be identified because the epitope density and conserved regions	processing, or may possibly be a ney would be more likely to be c	n artifact of experimental strategy for ross-reactive with the test reagents
Nef	Nef (BRU)  • In vitro measurements of CTL-activity by C disease progression as measured by viral lo		human o correlation between CTL-activi	Aladdin1999 ity (gp120, Gag, Pol and Nef) and
Nef	Nef (SF2) • CTL precursor frequencies were determine found in non-transmitting mothers than in t (Lazuriaga95);			
Nef	<ul> <li>(subtype C)</li> <li>This study is provides a survey of CTL resp</li> <li>37 of 45 subjects (82%) demonstrated Nef</li> <li>Two Nef-immunodominant regions were id corresponded to amino acid positions 122 to</li> </ul>	specific ELISPOT CTL responses of more entified, one spanned amino acid position	e than 100 SFC/106 PBMC	

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
	probed with ELISPOT	using peptides derived m subtype B peptides, a	from the same subtype (a median of the and ELISPOT results with a median of	ree Nef epitopes recognized wit	
Nef	cross-reactive CTL resp HIV-1 clades A, B, and • Proteins corresponding	ponses in HIV infected ID to the subtype of the in	HIV-1 infection an epidemic, and a vaccine trial using B Ugandans to A, D, and B clade recomb infecting strains tended to trigger higher ith B clade proteins and the co-circulati	inant vaccinia viruses expressional levels of CTL response measur	ng Gag, Env, Pol, RT or Nef from
Nef		he cellular immune res			Calarota2001  HIV-1 DNA vaccines can boost the CTL
Nef	• 6/24 HIV uninfected in • Reviewed in [Kuhn200		HIV-1 exposed seronegatiths) born to HIV+ mothers had HIV-1 s		De Maria1994, Kuhn2002 nia-expressed Nef, Gag/Pol, Env.
Nef	variable regions found  While the uneven distriused to probe the immuto not be found in C-tervirus where variation is and turn regions in the	in Nef, Env and p17. ibution of epitopes may ane response and autolorminal positions of epits best tolerated traces o proteins.	HIV-1 infection ture and included in this database tend to be in part due to a limited cross-recogn regous strains, regions with a paucity of the opes, and had lower cleavage prediction of immune escape have left an imprint of the open and Protease, epitopes are more even	nition of specific responses beca defined epitopes also had highe a scores for epitope processing. In the viral population. Epitopes	ause of differences between peptides r frequencies of amino acids that tend This suggests that in the regions of the
Nef	cells in BALBc mice. I	LFn causes exogenous	HIV-1 infection n proteins are candidate HIV vaccines t protein to be taken up and processed in late gag-specific CD4 proliferation and	a class I pathway. Expressed pr	oteins from Gag p24 and nef fragments
Nef	<ul><li> Nef and/or Pol CTL res</li><li> The magnitude and bre</li><li> Pol and Int CTL respor</li></ul>	sponses were detected is adth of Gag and p24 Tenses correlated positive	HIV-1 infection ted patients elicited gamma-IFN CD8+ in 86% of the subjects -cell responses correlated with absolute ly with absolute CD4+ T-cell count either CD4 counts or viral load		Edwards2002 related with viral load

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
Nef	patients on successful	HAART treatment, rela	HIV-1 infection ccinia expressing Gag, Pol, Nef and Env of tive to autologous monocytes. Some weak letection of low frequency memory cells.		
Nef	was measured in an El proteins.  • All 22 patients targeted recognized Nef. Robus  • Despite high HCV vira strong anti-HCV response.	d at least one protein. 20 at CTL activity was indeal loads, very few HCV onses were mounted.	HIV-1 and HCV co-infection ied in 22 individuals who were co-infected cells using targets expressing either Gag, 0/22 patients recognized RT, 17/22 patient ependent of disease progression or viral locable CD8+ T-cell Elispot responses were detected in 9/17 coinfected patients, but	ed with HIV-1 and hepatitis C or RT, Env and Nef in a vaccinia ats recognized Gag, 13/22 subjected. In a control HCV infected	construct, or one of seven HCV ects recognized Env and 11/22 patients d person who did not have HIV-1,
Nef	<ul> <li>Before ART 2/13 infar became undetectable a</li> <li>One older infant, at 23 group. 3/4 infants older</li> </ul>	nts <6 months of age shafter successful therapy- months, had CTL respert than 6 months of age	HIV-1 infection ART were studied in 13 HIV-1 vertically in owed IFNgamma Elispot CD8+ T-cell resection of the state of the	sponses, one to Nef and one to d all 3 had CMV-specific CD8- Pol, Nef and Env, and had the	Env and Nef, and these responses + T-cell responses. lowest plasma viremia of the study
Nef	boosted HIV-1 specific rebound to pretreatment	CTL responses and ele	HIV-1 infection infected patients undergoing HAART the evated CTL responses were maintained up I count decline was observed. CD8 responses vaccinia.	p to 22 weeks after the last trea	tment interruption, but viral load
Nef	<ul> <li>Vpr can cause cells to mice with recombinan HIV antigens.</li> <li>Vpr compromised CD:</li> </ul>	go into G2 arrest, and i t adenovirus expressing 8+ T-cell lytic response	Vaccine onent: Vpr, Nef, Gag/Pol t surpresses immune cell activation and in Vpr and HIV-1 antigens Nef or Gag/Pol s and T-helper proliferative responses in r on of IL-12 and TNFalpha, indicative of V	was tested to see if Vpr reduce mice co-immunized with Vpr a	ed the immune response to the other and Nef or Gag/Pol.
Nef			HIV-1 infection illing was detected in duodenal and rectal ed CTL was different in the peripheral ble		
Nef	Nef		HIV-1 infection r3503, B*3504, and B*5301 tend to proce	human (B*35)	Jin2002

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References			
	<ul> <li>Of 32 patients with HLA-B*35 alleles CD8+ CTL responses were quantified using an intracellular cytokine staining assay – 75% had responses to Pol, 69% to Gag, 50% to Nef, and 41% to Env.</li> <li>The overall magnitude of CTL responses did not differ between those bearing B*3501 and the others. A higher percentage of Gag responses was observed</li> </ul>							
	in those that had lowe	r RNA levels that carried I	B*3501, and there was a negative a	association with viral load and CTL a out not in B*3502, B*3503, B*3504,	activity. The data is consistent with			
Nef	Nef (BRU)		Vaccine	murine (H-2D $^d$ )	Collings1999			
	<ul><li>A comparison of DNA (non-replicating).</li><li>CTL immune respons</li></ul>	Vector/Type: DNA Strain: BRU HIV component: nef rison of DNA vaccination with HIV-1 Nef expression vectors pBN-CMV-NEF and pBN-RSV-NEF (self-replicating), pCGE2-NEF licating). nune responses were detected using all three expression vectors, while a humoral immune response to Nef was only observed in the sel on vectors; possibly antibody responses require higher levels of protein expression						
Nef	Nef (SIV)		SIV infection	Rhesus macaque (Mamu-A*11, -B*03, -B*04, and -B*17)	Dzuris2000			
	• Cell binding assays for Mamu molecules were employed to describe the peptide binding motifs for Mamu-A*11, -B*03, -B*03, -B*04, and -B*17 CTL epitopes – a similarity for Mamu-A*11 and -B*03 and human HLA-B*44 and -B*27, respectively, was observed – all epitopes studied were SIV epitopes, so not specifically listed here							

# II-B-21 HIV-1 CTL Epitopes

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
HIV-1			HIV-1 infection with acute or recent HIV-1 infection in al T-cell receptor repertoire	human mplies that HAART treatment a	Schito2001 alone can not completely conserve
HIV-1		V responses of CD8+ T of ion steps through integra	HIV-1 infection cells cultured with CD4 infected HIV c tion of provirus	human ells are mediated be blocking e	Mackewicz2000 xpression of viral RNA, and do not
HIV-1	counter-balancing effe virus had a low replica reduce viral set point v	cts in a new infection: a ration rate, then CTLp and with observed replication	CD4 helper cells could control an infe	elp but also more target cells. Tection. Only a vaccine that could	he model indicates that if the infecting
HIV-1	(EBV) presented by 11	l common HLA class I m 14/20 (70%) HIV+ indiv			Currier2002b lovirus (CMV), and Epstein Bar Virus from these individuals were capable of
HIV-1			HIV-1 infection dea that T-helper cell dysfunction resul TL memory through therapy and imp		
HIV-1	parasites, and the author	or suggests this is associa	HIV-1 infection, Vaccine ared with to other pathogens. We do not ted with the need for a strong T-cell rentrolled but persists may be required to	sponse to these diseases. Vacci	ne strategies that achieve a
HIV-1		tions of the potential adv	Vaccine quence for vaccine design is discussed, antages of the strategy based on C-clackao2003]		Gaschen2002 odel ancestor sequence or a consensus
HIV-1	<ul><li>infection and multiple</li><li>Vigorous CTL respons</li></ul>	animals with the same H ses are made despite class	HIV-1 infection pes in natural human infections, and in LA molecules can be tracked. I down-regulation by the Nef protein, ness advantage of this function of Nef 1	but it may delay cytolysis of in	
HIV-1	Vaccine HIV compone	nt: polyepitope	HIV-1 infection, Vaccine	human	Newman2002

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
	polyepitope vaccine ap constructs are discusse • The C-terminal flankir C, G, A, T, S (small) > cleavage is the likely r	pproach. Strategies conceed.  ng residue (C1) was foun  > F, W, Y (aromatic) > I,  reason for this observatio  lue from F to K for an Hi	L, M, V (aliphatic) > D (negative). As	nctional epitopes and use of linl ance of epitopes, such that R or this position is outside and pro-	Kers to enhance processing of such  K (positive charge) > N or Q (amide) > ximal to the epitope, processing and
HIV-1			HIV-1 infection, Vaccine	human	Johnston2001
		ate of HIV vaccine approfound in HEPS studies.	paches, and discusses the role of CTL	induced immunity in protection	or partial protection in animal studies,
HIV-1			HIV-1 infection	human	Klenerman2002
			responses is discussed, as narrowly for		
			ion may be associated with a better dis and class I specific induction of more		are considered, including NK cell
HIV-1	асичну, срноре анин	ty, epitope conservation,	HIV-1 infection	human	Kuhn2002
ПІ V-1	Intrauterine exposure of	of infants to HIV from th	neir mothers results in HIV-1 specific T		
	babies, and HIV-1 spec	cific CTL in some. Such	responses are evident, but it is unknown	wn whether they are associated v	with lack of infection, but there is some ed of CD4 and CD8 responses detected
HIV-1			HIV-1 infection	human	Kuhn2002, Levy1998
		n approximately 16/31 (5 ive response.	d CD8+ T-cell non-cytotoxic anti-HIV (2%) of uninfected children born of inf		sion of acute viral infection of CD4 nonly detected in those <1 year old, and
HIV-1			Vaccine	human	Altes2001
		0 00	CTL vaccine response exceeds the lequickly to protect from infection.	vel of response seen in chronic i	infection, that a memory CTL
HIV-1			Vaccine	human	Copeland2002
	• This review summariz	es cytokines and chemol	kines produced by CD8+ T-cells that ca	an interfere with HIV's infection	n and replication.
HIV-1			Vaccine		Edgeworth2002
	This review summarize	es HIV vaccine strategie	s, adjuvants, current clinical trials and	animal models.	
HIV-1			Vaccine		Graham2002
	This review summarize	es HIV vaccine approach	nes and clinical trials.		
HIV-1	Env (HXB2)		Vaccine	murine, guinea pig	Chakrabarti2002
	Vaccine Vector/Type:	DNA Strain: HXB2	HIV component: gp140deltaCFI, gp16	60 deletions	

HIV-1 CTL Epitopes HIV-1 CTL Epitopes

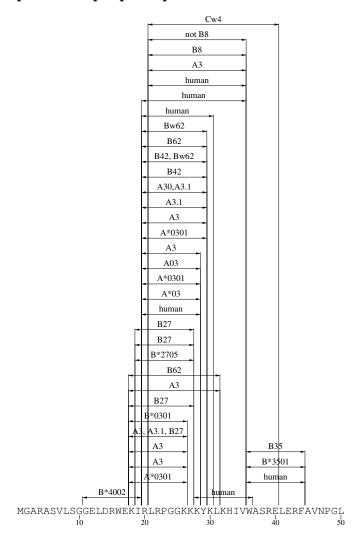
HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
	<ul> <li>envelopes – modificati</li> <li>The mutant envelope g response.</li> </ul>	included eliminations included eliminations included eliminations included the part of the	used to vaccinate BALB/c or Huntley on of glycosylation sites, deletions, and most promising result, enhancing antite, fusogenic domain and spacing of t	l exchange of the V3 loop to chan body responses while retaining th	ge from a X4 or R5 phenotype. e ability to stimulate a strong CTL
HIV-1		hepatitis B surface antigombinant HIV1 V3/HE	Vaccine gen lipoprotein particles HsBAg Stra BsAg hybrid particles into rabbits or m		Michel1993 or several months anti-V3 or HIV-1
HIV-1	CD8+ T-cell IFN-gam • Different peptides can	ma induction to HIV an	GF-beta1 or IFN-gamma from CD8+	-	-
HIV-1	CD8+ T-cell IFN-gam • Different peptides can	ma induction to HIV an	GF-beta1 or IFN-gamma from CD8+	-	-
HIV-1	<ul><li>CD8+ T-cell IFN-gam</li><li>Different peptides can</li></ul>	ma induction to HIV an	GF-beta1 or IFN-gamma from CD8+	•	
HIV-1	assay are prohibitive for Thailand – over 30% of	or a Phase III study, Elic carry the HLA-A11 alle	Vaccine meeting held to discuss options for de spot shows interlaboratory variation by le. Predominant strains may be evolving differ in vaccinees and infected indiv	nt could be extended to many saming to evade recognition of A11 res	ples. HLA-A11 is very common in
HIV-1	<ul><li>described, and the imp</li><li>Interesting specific exa</li></ul>	pact of breadth of CTL ramples are given concer	Vaccine  The natural epitope interactions with esponses and diversity considered in a ming anchor chain residues. For B27, an fit in the B pocket, but the substituti	vaccine context. the B pocket fits Arg (R) but not I	Lys (K), so even this conservative
HIV-1	gp120 (V3) and p24 (IIIB, MN, BH10) <b>Vaccine</b> Vector/Type:	virus-like particle Stra	Vaccine  ain: gp120 A clade UG5.94UG018, ar	murine (H-2 <sup>d</sup> ) ad B clade IIIB HIV component:	Buonaguro2002 gp120 and Pr55gag

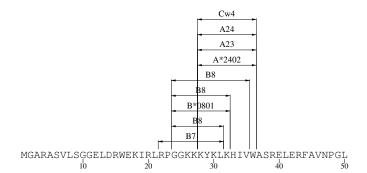
HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References	
	• BALB/c mice were given intraperitoneal immunization with virus-like particle (VLPs) expressing recombinant subtype A gp120 and Pr55gag in the absence of adjuvants.					
<ul> <li>High dose-independent humoral responses against both gp120 and p24 peptides were detected. Antibodies able to elicit 50% neutral IIIB and the autologous clade a virus were obtained.</li> <li>Recombinant rgp120 (clade B, MN) induced T-cell proliferative responses in vitro from vaccinated animals.</li> <li>CTL activity was observed against splenocytes expressing Env (clade A) and Gag (clade B, BH10) from a vaccinia construct.</li> </ul>					-	
HIV-1	Vaccine Vector/Type:	Listeria monocytogenes H	Vaccine IV component: Gag	murine (MHC H2d)	Lieberman2002	
	21	onocytogenes vectors elicit st	1 0	s in vaccinations of BALB/c mice and	can protect mice from a	

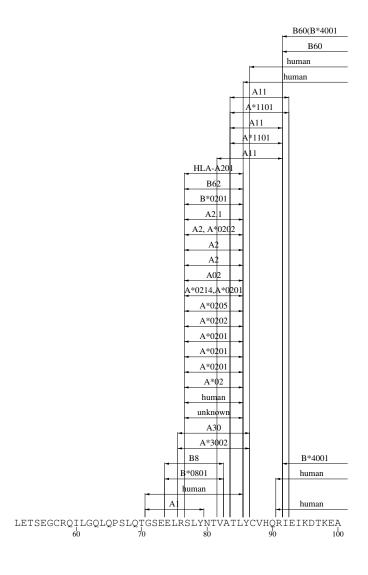
# **II-C** Maps of CTL Epitope Locations Plotted by Protein

Linear CTL epitopes less than twenty-two amino acids long are shown.

II-C-1 p17 CTL Epitope Map





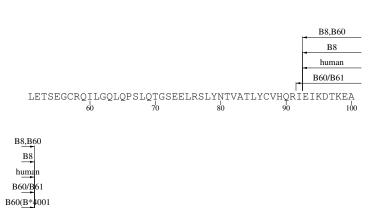


B60

B\*4001

humar

human



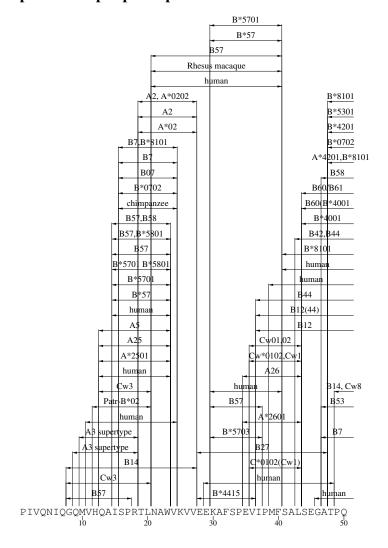
B35

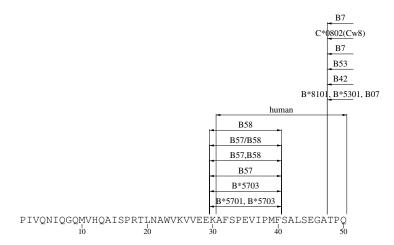
B\*3501

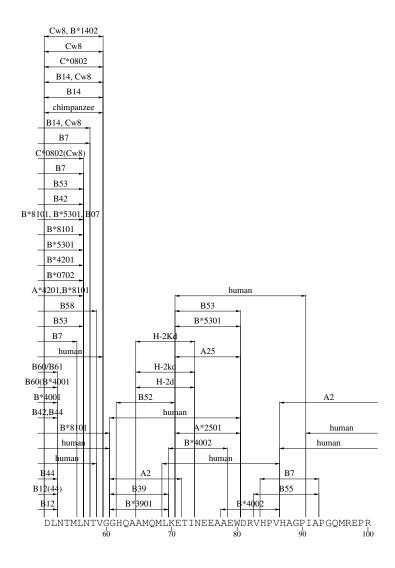
A33

LDKIEEEQNKSKKKAQQAAADTGHSNQVSQNY

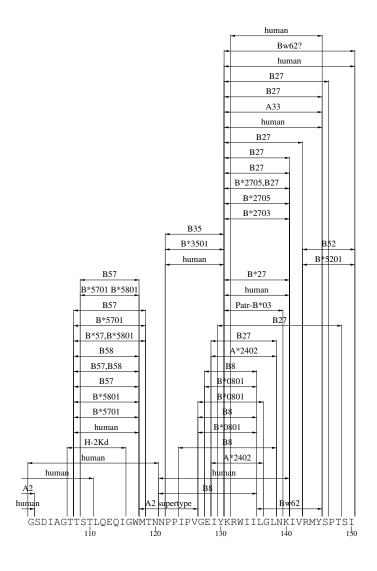
II-C-2 p24 CTL Epitope Map

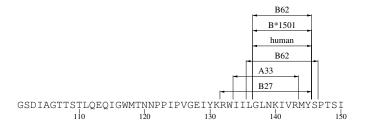


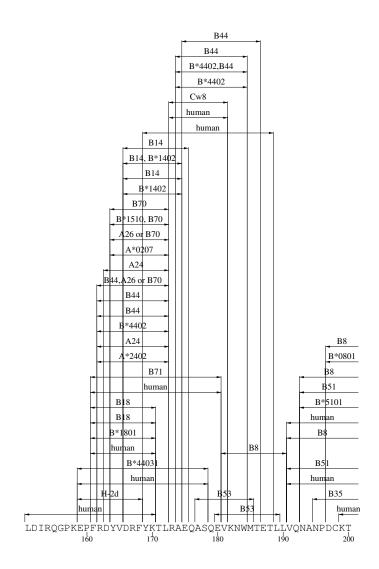


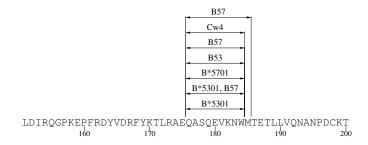


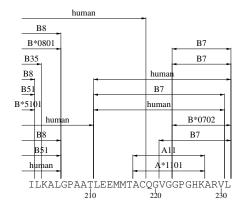






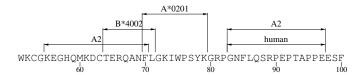


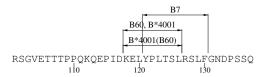




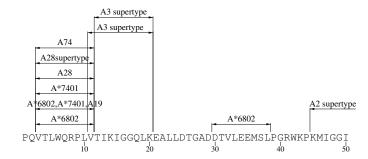
## II-C-3 p2p7p1p6 CTL Epitope Map





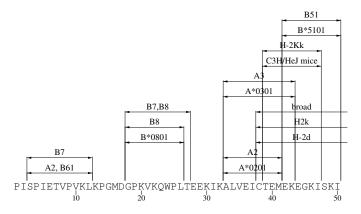


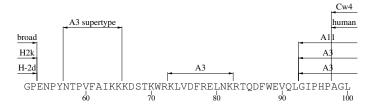
## **II-C-4** Protease CTL Epitope Map

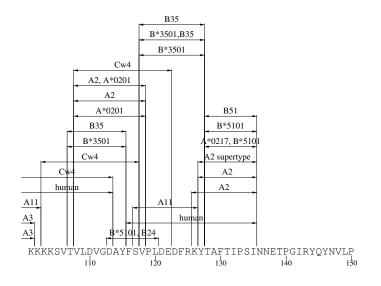


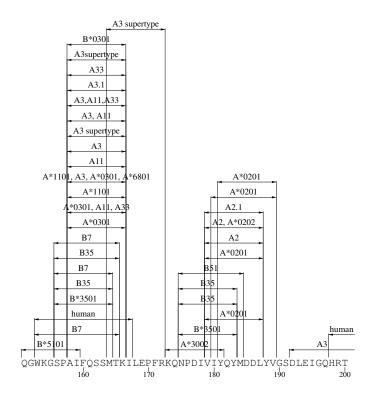


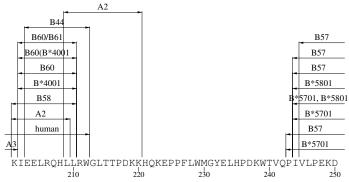
#### II-C-5 RT CTL Epitope Map



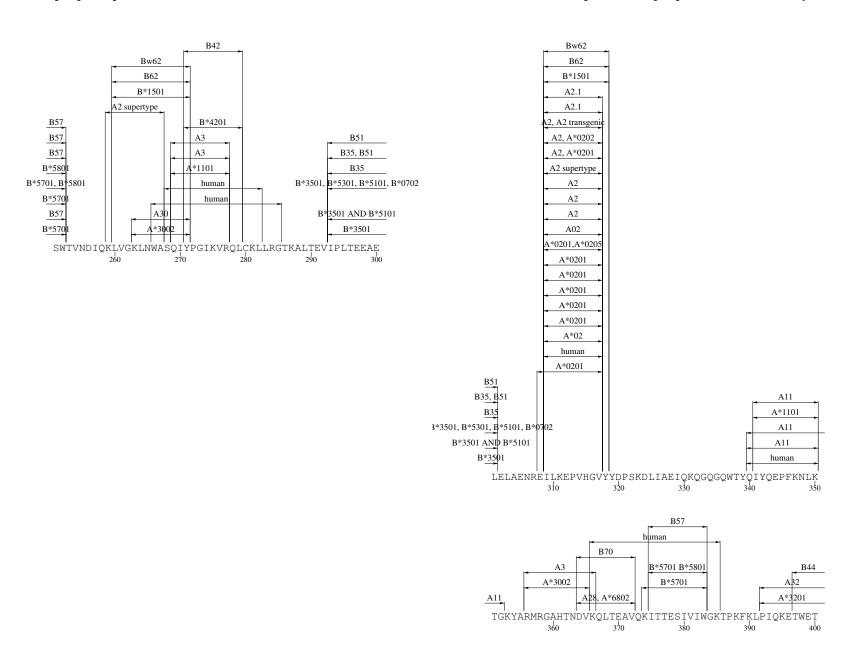


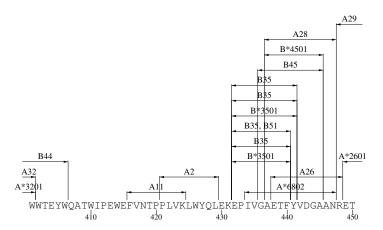


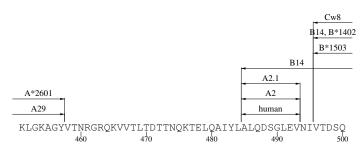


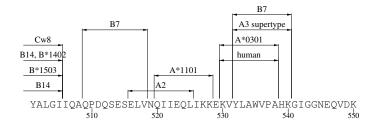


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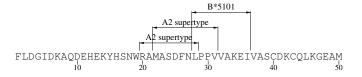


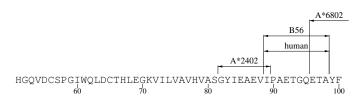


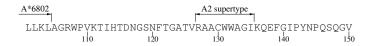


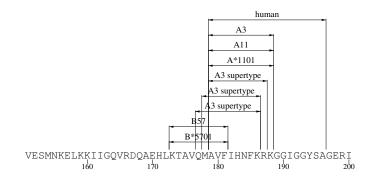
LVSAGIRKVL 560

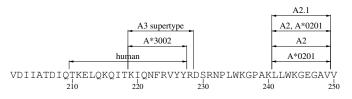
#### II-C-6 Integrase CTL Epitope Map





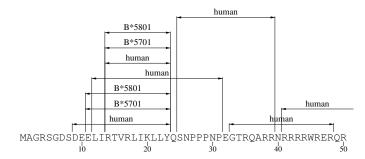


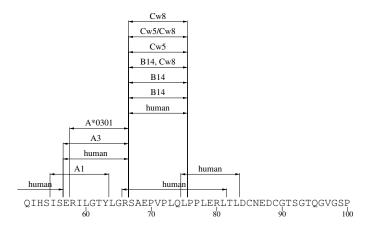




IQDNSDIKVVPRRKAKIIRDYGKQMAGDDCVASRQDED 260 270 280

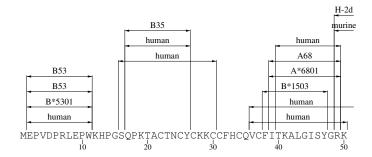
## II-C-7 Rev CTL Epitope Map





QILVESPTVLESGTKE

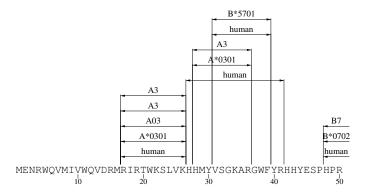
## II-C-8 Tat CTL Epitope Map

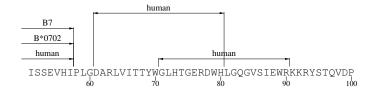




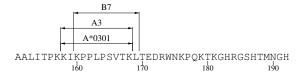
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## II-C-9 Vif CTL Epitope Map

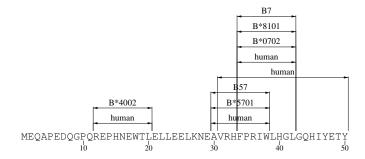


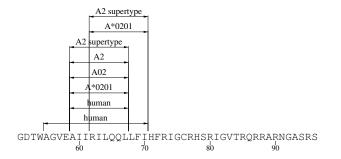




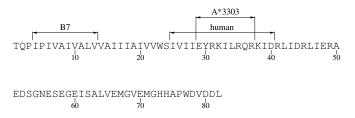


#### II-C-10 Vpr CTL Epitope Map

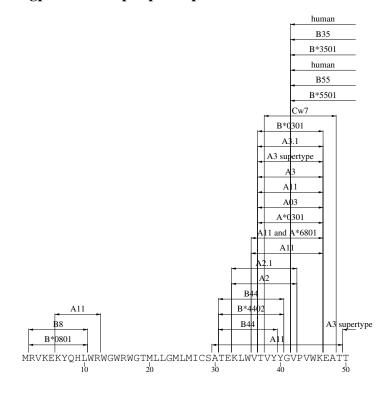


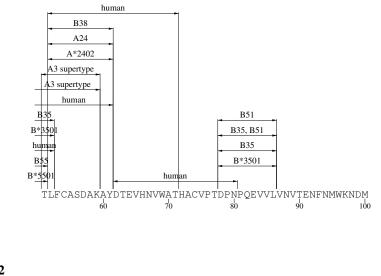


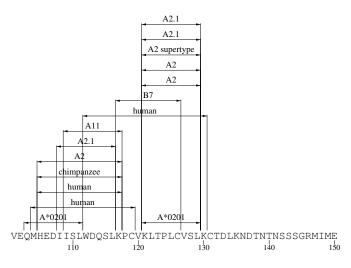
## II-C-11 Vpu CTL Epitope Map

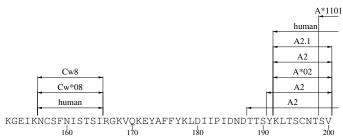


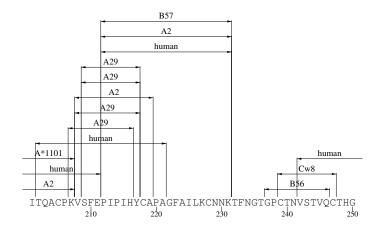
## II-C-12 gp160 CTL Epitope Map

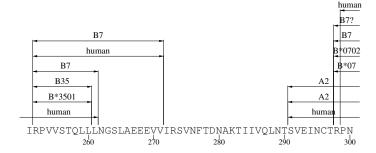




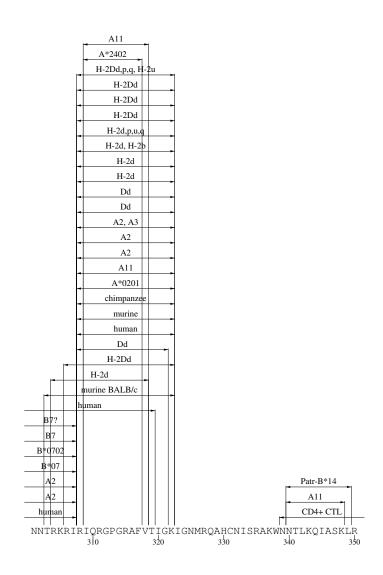


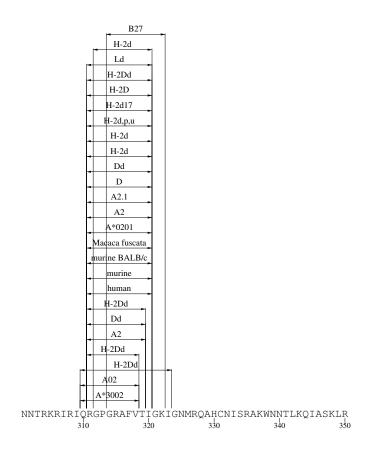


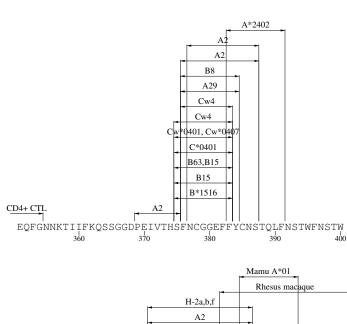


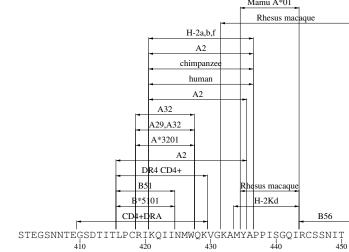


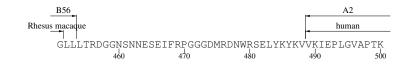
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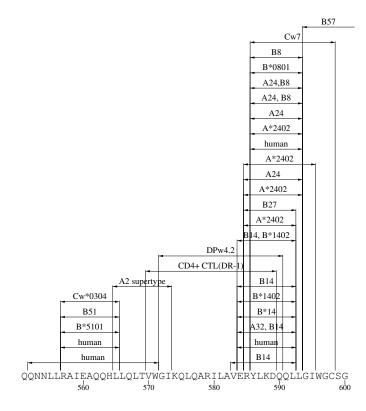




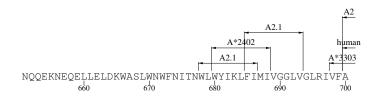


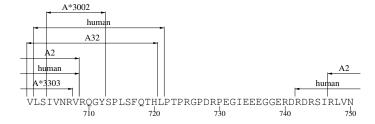


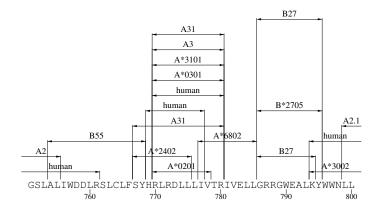


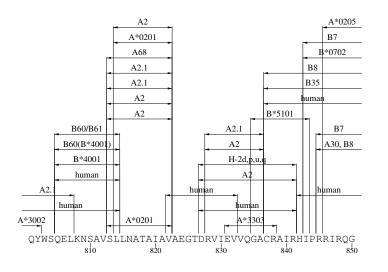


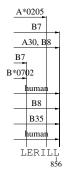




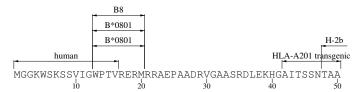


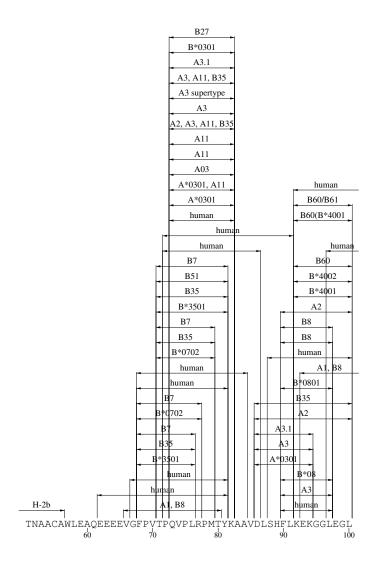


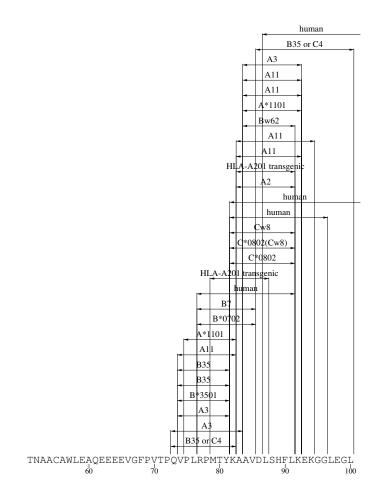


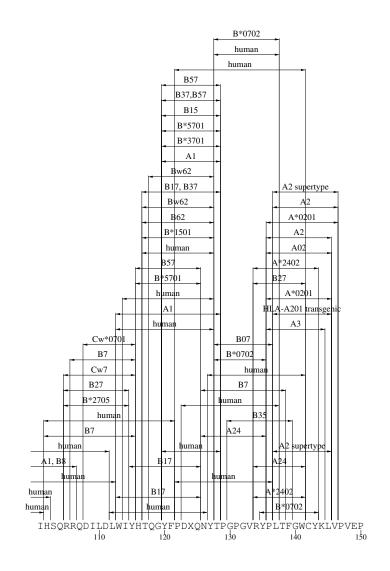


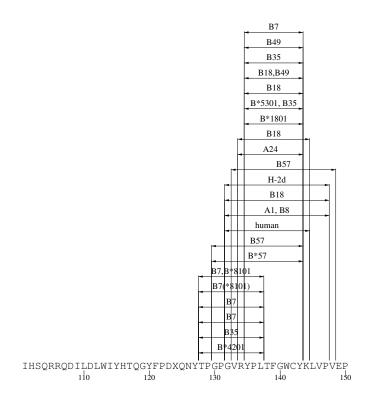
#### II-C-13 Nef CTL Epitope Map

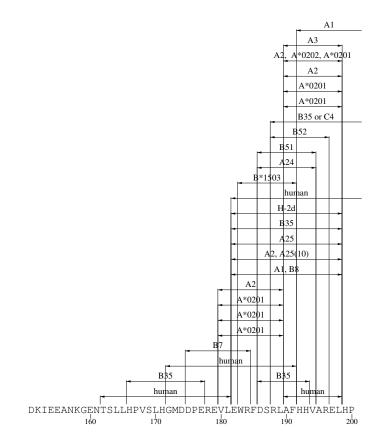














# Part III HIV Helper T-Cell Epitopes

## **III-A Summary**

Part III includes tables and maps of HIV-specific helper T-cell (Th) epitopes arranged sequentially according to the location of the proteins in the HIV-1 genome. This section parallels the organization of the CTL section. We attempted to make this section as comprehensive as possible, requiring that the epitope be contained within a region of 30 amino acids maximum, but not that the precise boundaries be defined. The HLA specificity is usually not determined for Th epitopes. For more recent updates, epitope sequence alignments, and useful searching capabilities, please see our web site: http://hiv-web.lanl.gov/immunology. The same epitope can have multiple entries, as each entry represents a single publication. Helper T-cell responses to proteins with no defined epitope are described at the end of each protein section.

Recent studies utilize multiple functions attributed to T cells to define responses, and the simple distinctions of cytotoxic T-cell and helper T-cells have become blurred as more is learned about the range of responses triggered in CD4 and CD8 positive T-cells responding to antigenic stimulus. When adding the most recent studies to the database, we have tried to place T cell responses in a reasonable manner into our traditional helper T cell and CTL sections, and to specify the assay used to measure the response in each study.

#### III-A-1 Tables

Each Th epitope has a six-part basic entry:

HXB2 Location: The viral strain HXB2 (GenBank Accession Number K03455) is used as a reference strain throughout this publication. The position of the defined epitope location relative to the sequence of the HXB2 protein is indicated. The numbering in this table corresponds to the protein maps. Because of HIV-1 variation the epitope may not actually be present in HXB2, rather the position in HXB2 indicates the position aligned to the epitope. HXB2 was selected as the reference strain because so many studies use HXB2, and because crystal structures for HXB2-related proteins are often available. The precise positions of an epitope on the HXB2 reference strain can be readily obtained using the interactive position locator at our web site: http://hiv-web.lanl.gov/content/hiv-db/LOCATE\_SEQ/locate.html.

**Author Location:** The amino acid positions of the epitope boundaries and the reference sequence are listed as given in the primary publication. Frequently, these positions as published are imprecise, and do not truly correspond to the numbering of the sequence, but they provide a reasonable guide to the peptide's approximate location in the protein. Also, in many cases the reference sequence identification was not provided, and in such cases it is not possible to use these numbers to specify precise locations.

Epitope Sequence: The amino acid sequence of the epitope of interest as defined in the reference, based on the reference strain used in the study defining the epitope. On occasions when only the position numbers and not the actual peptide sequence was specified in the original publication, we tried to fill in the peptide sequence based on the position numbers and reference strain. If the sequences were numbered inaccurately by the primary authors, or if we made a mistake in this process, we may have misrepresented the binding site's amino acid sequence. Because of this uncertainty, epitopes that were not explicitly written in the primary publication, that we determined by looking up the reference strain and the numbered location, are followed by a question mark in the table.

**Immunogen:** The antigenic stimulus of the Th response to the defined epitope. Often this is an HIV-1 infection. If a vaccine was used as the original antigenic stimulation, not a natural infection, this is noted on a separate line, and additional information about the vaccine antigen is provided as available.

**Species(HLA):** The species responding and HLA specificity of the epitope, when known.

**Reference:** The primary reference (sometimes two or more directly related studies are included). Details for some of the earlier references are in Part V.

Following the entry for a given Th epitope are brief comments explaining the context in which the epitope was studied and what was learned about the epitope in a given study.

#### **III-A-2** HIV Protein Epitope Maps

All HIV Th epitopes mapped to within a region of 21 amino acids or less are indicated on the HIV protein epitope maps. The location and HLA restriction elements of Th epitopes are indicated on protein sequences of HXB2. These maps are meant to provide the relative location of defined epitopes on a given protein, but the HXB2 sequence may not actually carry the epitope of interest, as it may vary relative to the sequence for which the epitope was defined. Epitopes with identical boundaries and HLA fields are included in the maps only once. If one laboratory determines HLA presenting molecules at the serotype level (example: A2) and another at the genotype level (example: A\*0201) both will be included in the map. MHC specificities are indicative of the host species; when no MHC presenting molecule is defined, the host species is noted.

#### **III-A-3** Alignments

To conserve space, no epitope alignments are provided in this book, but they can be generated using the T helper epitope search tool at http://hiv-web.lanl.gov/immunology. All epitopes are aligned to the HXB2 sequence, with the sequence used to define the epitope indicated directly above it. Sequences are sorted by their subtype and country of origin.

The master alignment files from which the epitope alignments were created are available at our web site (http://hiv-web.lanl.gov/ALIGN\_CURRENT/ALIGN-INDEX.html). The alignments were modified in some cases to optimize the alignment relative to the defined epitope and minimize insertions and deletions; epitope alignments are generated by anchoring on the C-terminal residue. A dash indicates identity to the consensus sequence, and a period indicates an insertion made to maintain the alignment. Stop codons are indicated with a \$, and frameshifts by a #, or ambiguous codons (nucleotide was r, y, or n) by an x; they are inserted to maintain the alignments. In consensus sequences an upper case letter indicates the amino acid was present in all sequences, a lower case letter indicates the amino acid was present in most sequences in a given position, and a question mark indicates two or more amino acids were represented with equal frequency.

# **III-B HIV Helper T-Cell Epitope Tables**

All HIV Helper T-Cell epitopes arranged by protein position. The table entries are sorted in a nested way—first by protein, then by HXB2 start location within the protein and finally by HLA presenting molecule. Epitopes for which the HXB2 location is unknown appear at the end of the listing of the protein in which they are located.

#### III-B-1 p17 Helper T-Cell Epitopes

HXB2 Location	<b>Author's Location</b>	Sequence	Immunogen	Species (HLA)	References
p17 (18–42)	p17 (18–42 PV22)	KIRLRPGGKKKYKLKHIVW- ASRELE	HIV-1 infection	human (DRB1*13)	Lotti2002
	6 months after initiation	of HAART. There was no different	ence in level of response in those wi	th or without a detectable p	
	terms of HLA restrictio		5 responding clones were generated nes had a Th1 cytokine secretion pro es could also induce cytotoxicity.		
	-	.1 to p55, 90.6 to peptide) secrete	using overlapping peptides. Clone 6 d IFNgamma, indicative of a Th1 re		quence restricted by DRB1*13. This ha. Clone 6 was highly cytotoxic,
p17 (21–35)	<ul><li>individuals, one in p24</li><li>Patient 024's naturally o</li><li>Naturally occurring var</li></ul>	and one in p17 occurring variant LRPGGKKKY0	HIV-1 infection Differative responses to HIV – 12 sho QLKHIV also elicited a strong prolif within the individual who made this in pe	ferative response.	
p17 (22–29)	-	RPGGKKKY? eration in HIV-infected donors. e as p24(22-29), but it appears to	HIV-1 infection be in p17.	human	Schrier1989
p17 (33–47)	p17 (33–47 IIIB, B10) • Peptides were identified	HIVWASRELERFAVN? i that commonly evoke T-cell resp	HIV-1 infection conses – 57% of 90 HIV+ people ha	human d a T-cell response to this p	Wahren1989b, Wahren1989a peptide
p17 (35–59)	<ul><li>6 months after initiation</li><li>For one individual, patieterms of HLA restriction</li></ul>	n of HAART. There was no different F45 CDC stage A2, CD4+ p5.	ag-specific CD4+ T cell responses pence in level of response in those wib responding clones were generated neshad a Th1 cytokine secretion pro-	th or without a detectable p . Her response was consiste	ently strong and heterogeneous in

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References			
	• 4/10 clones from patient F45 had their epitopes mapped using overlapping peptides. Clone 25 recognized this peptide sequence restricted by DRB1*13 using TCR Vbeta 5.1. This clone had a SI of 4.9 to p55, 13.7 to peptide, secreted low levels of IFNgamma, indicative of a Th1 response. Clone 25 had cytotoxic activity, mediated through both a perforin and a Fas-based pathway.							
p17 (93–107)		) EIKDTKEALDKIEEE tides were identified that cou	HIV-1 infection ald commonly evoke T-cell response	human onses.	Wahren1989b, Wahren1989a			
p17 (118–132)		0) AAADTGHSSQVSQNY tides were identified that cou	HIV-1 infection ald commonly evoke T-cell respo	human onses.	Wahren1989b, Wahren1989a			

## III-B-2 p24 Helper T-Cell Epitopes

HXB2 Location	<b>Author's Location</b>	Sequence	Immunogen	Species (HLA)	References
p24 (1–11)	<ul><li>individuals, one in p24 a</li><li>Out of five truncated ver</li><li>Nine naturally occurring</li></ul>	and one in p17 sions of peptide PIVQNLQGQN variants of this epitope were fo	HIV-1 infection roliferative responses to HIV – 1: MVHQAISPRTL, only p24(1-11 and within the individual who mappetide, suggestive of immune of	) elicited a proliferative respons nade this response – all bound to	
p24 (1–15)	p24 (133–147 IIIB, B10) • Peptides were identified		HIV-1 infection ponses – 62% of 90 HIV+ peopl	human e had a T-cell response to this p	Wahren1989b, Wahren1989a eptide
p24 (1–22)	correlated with low viral	load in 10 chronically infected	undetectable in chronic infectio		Rosenberg1997 tive responses were inversely
p24 (7–21)	responses from multiple This epitope binds to nin and DRB4*0101 with ar This epitope sequence is 7/22 HIV infected indivi	HIV-infected donors ne HLA-DR alleles: DRB1*010 n IC <sub>50</sub> threshold below 1,000 nM conserved in 52% of clade B is	A solates (13/22 responded to some of the	RBI*0405, DRB1*1302, DRB1	
p24 (7–21)	<ul> <li>Epitope name: Gag 171</li> <li>Four Th HIV epitopes provaccine strategies of in F</li> <li>Responses to pooled perpromotor were compared</li> </ul>	resented by HLA-DR molecules H-2b mice. otides, polyepitope peptides in a d. A linear arrangement in polye epitope construct with the GPGI	linear construct or in a branched	be presented my murine class II  I MAP construct, and a DNA potential epitope that could be disru	pted with the addition of GPGPG
p24 (11–26)		VHQAISPRTLNAWVKC  r proliferative response in PBMC dues for HLA DR: VHQAISPR'		human	Bedford1997

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
p24 (11–30)	<ul> <li>Listeria moncytogenes</li> <li>Listeria moncytogenes</li> <li>BALB/c(H-2d) and C5</li> </ul>	Listeria moncytogenes is an intracellular bactor vaccine expressing HI i7BL/6(H-2b) mice	IVKVVEEK Vaccine  Strain: SF2 HIV component: p24 erium that lives in the cytoplasm and ge V-1 p24 protein (Lm-Gag) was used to	stimulate gag specific CD4+ T cel	l proliferative responses in
	in C57BL/6 mice and a	also can stimulate a BA	overlapping peptides that span p24) wer LB/c response N-gamma producing cells, a Th1 respor		ns – this epitope is immunodominan
p24 (11–30)	<ul> <li>BALB/c and C57BL/6</li> <li>L. monocytogenes is a are processed and pres</li> <li>The class II T helper re</li> </ul>	Listeria monocytogenes mice were immunized gram-positive bacteria ented by both class I ar esponse was probed usi	WKVVEEK Vaccine  S Strain: HXB2 HIV component: Ga with rec Listeria monocytogenes (Lm-C) that enters the macrophage on phagocy and class II pathways  ng 20 mer peptides that overlapped by inized in H-2 <sup>b</sup> and H-2 <sup>d</sup> mice	Gag) expressing HIV-1 HXB2 Gag tosis and lives in the cytoplasm –	secreted L. monocytogenes antigens
p24 (21–36)	p24 (153–167) • Epitope elicits a prima	NAWVKVVEEKAFS ry proliferative respons	EPEC in vitro stimulation e in PBMC from uninfected donors	human	Bedford1997
p24 (31–46)	<ul> <li>Peptide contains a CTI</li> </ul>	L epitope identified in F A*0201 and causes reg	BMC from uninfected donors HIV-positive patients ulation of class I expression on T2 cells	human (A*0201)	Bedford1997
p24 (31–52)		QDL ted with strong HIV-1-s	SEGATP – HIV-1 infection specific proliferative response etected in two long term survivors	human	Rosenberg1997
p24 (41–56)	p24 (173–187) • Epitope elicits a prima	SALSEGATPQDLN ry proliferative respons	ITMC in vitro stimulation e in PBMC from uninfected donors	human	Bedford1997
p24 (48–62)	<ul><li>Homology to an SIV e</li><li>T-cells from 8 of 19 H</li></ul>	pitope recognized by m IV+ individuals respond	in study of proliferative response to p24 nacaque T-cells		Adams1997 proliferative response
p24 (51–66)	p24 (183–197) • Epitope elicits a prima	DLNTMLNTYGGHÇ ry proliferative respons	DAAC in vitro stimulation te in PBMC from uninfected donors	human	Bedford1997

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
p24 (51–82)	Gag (183–214 LAI)	DLNTMLNTVGGHQAAMQML- KETINEEAAEWDR	Vaccine	human	Gahery-Segard2000
	<ul><li>administered in a phase</li><li>A CD4+ T cell prolifera</li><li>9/12 tested mounted a C</li></ul>	accine consisting of six long pepties I trial ative response to at least one of the	e six peptides was observe the six peptides, each of the	g and Env HIV-1 proteins modified d in 9/10 vaccinees – 2/10 reacted t six peptides elicited a CTL respons	o this peptide
p24 (69–88)	Gag (p24) (201–220 IIIB)  Epitope name: P21  PBMC from a seronega Gag-specific CD4+ T-cdilution. All reacted wi  Clone 85 recognized the	LKETINEEAAEWDRVHPVHA ative donor, the healthy brother of ell clones by in vitro immunization the p24 except one which recognize	in vitro stimulation a pair of monozygotic twir n with HIV-1 overlapping ed a p24 peptide and a p6 p 18; the two TCR receptors	human (DR)  as discordant for HIV-1 infection, we 20mer peptides spanning p55. Six opeptide. All CD4+ T cell clones we indicates this limiting dilution repeag-infected B-LCL.	clones were generated by limiting re HLA clas II DR restricted.
p24 (71–86)	p24 (203–217) • Epitope elicits a primar	ETINEEAAEWDRVHPC  ry proliferative response in PBMC	in vitro stimulation from uninfected donors	human	Bedford1997
p24 (73–97)	p24 (205–229 PV22)	INEEAAEWDRVHPVHAGPI- APGQMR	HIV-1 infection	human (DRB1*03)	Lotti2002
	<ul> <li>6 months after initiation</li> <li>For one individual, patiterms of HLA restriction</li> <li>profile (high IL-4 and II)</li> <li>4/10 clones from patient using TCR Vbeta 22. T</li> </ul>	n of HAART. There was no differe ent F45 CDC stage A2, CD4+ p55 on and Vbeta usage, and some clor L-5 production). 5/10 CD4+ clone at F45 had their epitopes mapped u	ence in level of response in 5 responding clones were goes had a Th1 cytokine sec- es could also induce cytotousing overlapping peptides 49.6 to peptide, secreted lo	those with or without a detectable generated. Her response was consist retion profile (high IFNgamma prod	ently strong and heterogeneous in duction) while some had a Th2 sequence restricted by DRB1*03
p24 (76–85)	• T-cells from 11 of 24 H	EAAEWDRVHP  nic Gag peptides used in study of s  IIV+ individuals responded to this  (increase in culture time to 8 days	epitope	human o p24 ultures) gave increased detection of	Adams1997 proliferative response
p24 (76–90)		0) EAAEWDRVHPVHAGP ides were identified that could con	HIV-1 infection nmonly evoke T-cell respo	human nses.	Wahren1989b, Wahren1989a
p24 (81–95)		DRVHPVHAGPIAPGQ rirus-like particle Strain: SF2 Ind multiple linear B-cell epitopes		macaque macaques	Mills1990

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
p24 (81–102)	p24 (213–234 SF2)	DRVHPVHAGPIAPGQMREP- RGS	HIV-1 infection	human	Rosenberg1997
	correlated with low vira	Th responses are characteristically to all load in 10 chronically infected p tive response in one of two long te	•	rong p24-specific proliferat	ive responses were inversely
p24 (86–94)	p24 (NY5)  Gag-specific CD4+ hel acute infection, two being perforin-mediated cyto  3/23 p24-derived peptic peptide DRVHPVHAG	VHAGPIAPG per T-cell clones were derived from fore (AC-01 and AC-36) and one attoxicity in all CD4+ T-cell clones in the destered induced proliferative p2-2PIAPGQMREPRGS (81-102), and	HIV-1 infection m one long-term non-progressor (LT ffter (AC-25) STI. Gag peptide recog	the LTNP CDT-01. The imition it. One was characterize	n, IFNgamma production and munodominant response was to the
p24 (87–101)	p24 (219–233 BRU) • Peptide G2: could prim	HAGPIAPGQMREPRG ne for in vitro immunoproliferative	in vitro stimulation responses and for subsequent IgG re	murine (H-2 <sup>b</sup> )	Vaslin1994
p24 (96–103)	p24 (228–235 LAI) • Stimulates T-cell prolif	MREPRGSD eration in HIV-infected donors	HIV-1 infection	human	Schrier1989
p24 (96–110)	± '	0) MREPRGSKIAGTTST ides were identified that could con	HIV-1 infection nmonly evoke T-cell responses.	human	Wahren1989b, Wahren1989a
p24 (99–118)	Gag-specific CD4+ T-c dilution. All reacted wi  Clone 6 recognized three	th p24 except one which recognized the petition in pet	in vitro stimulation  a pair of monozygotic twins discorda  n with HIV-1 overlapping 20mer per  ed a p24 peptide and a p6 peptide. A  a Th1 response using TCR Vbeta 6  sing different peptide concentrations	otides spanning p55. Six clot ll CD4+ T cell clones were (6s5A1N1). Sequencing T0	ones were generated by limiting HLA clas II DR restricted. CR Vbeta regions of colonies from
p24 (101–115)		GSDIAGTTSTLQEQI virus-like particle Strain: SF2 I nd multiple linear B-cell epitopes	Vaccine Wive component: p24 were found in vaccinated macaques	macaque  epitope response defined	Mills1990 by T-cell clone
p24 (101–116)	p24 • Epitope elicits a primar	GSDIAGTTSTLQEQIC ry proliferative response in PBMC	in vitro stimulation from uninfected donors	human	Bedford1997
p24 (109–128)	Gag-specific CD4+ T-c	ell clones by in vitro immunization	in vitro stimulation a pair of monozygotic twins discorda n with HIV-1 overlapping 20mer per ed a p24 peptide and a p6 peptide. A	otides spanning p55. Six clo	ones were generated by limiting

administered in a phase I trial

HXB2 Location	<b>Author's Location</b>	Sequence	Immunogen	Species (HLA)	References
					esponses were stimulated), using TCR ein from vaccinia virus Gag-infected
p24 (111–132)	p24 (243–264 SF2)	LQEQIGWMTNNPPIPVGEI- YKR	HIV-1 infection	human	Rosenberg1997
		ed with strong HIV-1-specific prole to this epitope was detected in tw			
p24 (119–133)	<ul> <li>but only 3/14 (21%) of</li> <li>PBMC from individuals weeks post treatment</li> <li>DRB1*13-DQB1*06 w population)</li> <li>This epitope was mapped</li> <li>Two distinct DRB1*13</li> </ul>	those who did not have DRB1*13-Do was also found to be enriched amored with truncated peptides using the	3-DQB1*06, maintained vir QB1*06 displayed increase ing long-term non-progresso the Elispot assay de region spanning 251 to 2	ral suppression for 18 months d IFN $\gamma$ secretion and stronger propris (LTNPs) (it was in 9/18 versus, 270, and this 20-mer bound with v	Blankson2001b, Malhotra2001 DRB1*13-DQB1*06 positive people, differative responses against p24 80 eversus 21% of the general every high affinity to DRB1*1302 –
p24 (121–136)	p24 (253–267)	NPPIPVGEIYKRWIIC y proliferative response in PBMC	in vitro stimulation	human	Bedford1997
p24 (121–140)	<ul> <li>Listeria moncytogenes</li> <li>Listeria moncytogenes</li> <li>BALB/c(H-2d) and C5'</li> <li>Two of three reactive p' in BALB/c mice and di</li> </ul>		ives in the cytoplasm and g tein (Lm-Gag) was used to peptides that span p24) we se	stimulate gag specific CD4+ T ce	
p24 (121–140)	<ul> <li>BALB/c and C57BL/6</li> <li>L. monocytogenes is a gare processed and prese</li> <li>The class II T helper re</li> </ul>	NPPIPVGEIYKRWIILGLNK isteria monocytogenes Strain: He mice were immunized with rec Li gram-positive bacteria that enters ented by both class I and class II p sponse was probed using 20 mer ponse for the H-2 <sup>d</sup> haplotype, but we	HXB2 HIV component: G steria monocytogenes (Lm- the macrophage on phagocy athways peptides that overlapped by	Gag) expressing HIV-1 HXB2 Gay ytosis and lives in the cytoplasm – 10, and the peptide MPPIPVGEI	- secreted L. monocytogenes antigens
p24 (121–152)	Gag (183–214 LAI)  Vaccine Vector/Type: li  Anti-HIV lipopeptide v	NPPIPVGEIYKRWIILGLN- KIVRMYSPTSILD ipopeptide accine consisting of six long pepti		human and Env HIV-1 proteins modified	Gahery-Segard2000 by a palmitoyl chain was

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HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
	<ul> <li>9/12 tested mounted a 0 peptide was particularly</li> </ul>	CTL responses to at least or	ne of the six peptides, each of the CTL response in four vaccinees	d in 9/10 vaccinees – 9/10 reacted six peptides elicited a CTL respon	
p24 (127–141)	responses from multipl This epitope binds ten DRB5*0101 and DRB4 This epitope sequence 6/22 HIV infected indiv	dentified that had the HLA- e HIV-infected donors HLA-DR alleles: DRB1*0 4*0101 with an IC <sub>50</sub> thresh is conserved in 95% of clac	old below 1,000 nM le B isolates pitope (13/22 responded to some of	human (DR supermotiful bind to MHC class II DR molecul DRB1*1101, DRB1*1302, DRB1* of the DR supermotif epitopes, the	es and all elicted proliferative
p24 (128–137)	<ul> <li>but only 3/14 (21%) of</li> <li>PBMC from individual weeks post treatment</li> <li>DRB1*13-DQB1*06 w</li> <li>The truncated peptide t</li> <li>This region, shared by DRB1*1302</li> <li>Two distinct epitopes w</li> </ul>	those who did not have DRs with the haplotype DRB1 was also found to be enriched hat gave the optimal prolife 2 overlapping peptides, was	RB1*13-DQB1*06, maintained vi *13-DQB1*06 displayed increase ed among long-term non-progresse erative response for a Th1 phenoty is the reactive region for clones fro region spanning 251 to 270, and the	ral suppression for 18 months ed IFN $\gamma$ secretion and stronger proors (it was in 9/18 versus, versus 2 ype clone was this nine-mer om two DRB1*13 patients, one car	
p24 (129–148)	Gag-specific CD4+ T-c dilution. All reacted wi  Clone 74 recognized tw	ative donor, the healthy bro cell clones by in vitro immu th p24 except one which re two peptides including this o	nization with HIV-1 overlapping ecognized a p24 peptide and a p6 ne with a Th1 response using TC	peptide. All CD4+ T cell clones we R Vbeta 13 (13s1); it required 200	clones were generated by limiting ere HLA clas II DR restricted.
p24 (131–145)	* *	•	Vaccine SF2 HIV component: p24 bitopes were found in vaccinated i	macaque macaques – epitope response define	Mills1990 ed by T-cell clone
p24 (131–145)	Gag (298–312) • Epitope name: Gag 298	KRWIILGLNKIVRMY	HIV-1 infection	human (DR supermoti	if) Wilson2001

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
	responses from multipl This epitope binds thirt DRB1*0405, DRB1*0 This epitope sequence 8/22 HIV infected indiv	e HIV-infected donors teen HLA-DR alleles: DRB4*01 401, DRB*0301, DRB1*1501 a is conserved in 94% of clade B	101, DRB5*0101, DRB1*09 nd DRB1*0101, with an IC <sub>5</sub> isolate e (13/22 responded to some of	0 threshold below 1,000 nM	les and all elicited proliferative  RB1*1302, DRB1*1201, DRB1*1101,  9 non-responder peptides tended to
p24 (131–152)		KRWIILGLNKIVRMYSPTS ILD ed with strong HIV-1-specific p	roliferative response	human	Rosenberg1997
	A proliferative respons	e to this epitope was detected in	two long term survivors		
p24 (135–154)	• 8 of 24 HIV+ individua	ILGLNKIVRMYSPTSILDI nic Gag peptides used in study on als responded to this epitope (increase in culture time to 8 do	of the proliferative response	human to p24 ultures) gave increased detection of	Adams1997  f proliferative response
p24 (139–157)	Gag-specific CD4+ T-c dilution. All reacted wi Clone 6 recognized thre clone 6 suggested this of this clone. Upon act Clone 6 was activated i Clone 37 recognized th activated by peptide, no Clone 97 recognized th	tell clones by in vitro immunization p24 except one which recognee peptides including this one was a clonal population. Assays ivation, clone 6 was observed to no response to vaccinia virus Gaguis peptide sequence with a Th2 of by processed protein from vaccis peptide sequence with a using	of a pair of monozygotic twittion with HIV-1 overlapping nized a p24 peptide and a p6 with a Th1 response using TC using different peptide concest induce a cytopathic effect in g-infected B-LCL, so could be response using TCR Vbeta 3 ceinia virus Gag-infected B-Lg TCR Vbeta 9 and 14; the two	peptide. All CD4+ T cell clones wark Vbeta 6 (6s5A1N1). Sequencin entrations suggest that this peptide the adherent layer of fibroblasts of ecognize naturally processed epitor, and was a homogeneous T-cell pLCL.	clones were generated by limiting there HLA clas II DR restricted.  g TCR Vbeta regions of colonies from the colonies, 271-290, contains the main epitope expressing HLA DR4W14 and -W15.  sopes.  opulation. This clone was only this limiting dilution represents a mixed
p24 (141–156)		IVRMYSPTSILDIRQC ry proliferative response in PBM idues for HLA DR: IVRMYSP		human	Bedford1997
p24 (146–160)		0) SPTSILDIRQGPKEP ides were identified that could c	HIV-1 infection commonly evoke T-cell response	human nses.	Wahren1989b, Wahren1989a
p24 (149–168)	Gag (p24) (281–300 IIIB) • Epitope name: P29	SILDIRQGPKEPFRDYVDF	RF in vitro stimulation	human (DR4)	Venturini2002

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
	Gag-specific CD4+ T-c dilution. All reacted wi  Clone 6 recognized three	ell clones by in vitro immunization the p24 except one which recognize peptides including this one with	a pair of monozygotic twins discord on with HIV-1 overlapping 20mer per ed a p24 peptide and a p6 peptide. As the a Th1 response using TCR Vbeta of sing different peptide concentrations	ptides spanning p55. Six c All CD4+ T cell clones we 6 (6s5A1N1). Sequencing	clones were generated by limiting re HLA clas II DR restricted. TCR Vbeta regions of colonies from
p24 (150–169)	p24 (282–301) • Stimulates T-cell prolife	ILDIRQGPKEPFRDYVDRFY eration in HIV-infected donors	HIV-1 infection	human	Schrier1989
p24 (151–166)	p24 (283–297) • Epitope elicits a primar	LDIRQGPKEPFRDYVC y proliferative response in PBMC	in vitro stimulation From uninfected donors	human	Bedford1997
p24 (155–177)			e responses, CTLs and antibodies	murine	Nakamura1997
p24 (156–170)		O) GPKEPFRDYVDRFYK ides were identified that could co	HIV-1 infection mmonly evoke T-cell responses.	human	Wahren1989b, Wahren1989a
p24 (156–174)	• T-cells from 5 of 21 HI	QPKEPFRDYVDRFYKTLRA nic Gag peptides used in study of V+ individuals responded to this (increase in culture time to 8 day		human ave increased detection of	Adams 1997 proliferative response
p24 (161–180)	<ul> <li>Listeria moncytogenes</li> <li>Listeria moncytogenes</li> <li>BALB/c(H-2d) and C5'</li> <li>Two of three reactive poresponse in both BALB</li> </ul>	vaccine expressing HIV-1 p24 pro 7BL/6(H-2b) mice 24 peptides (out of 22 overlapping	F2 HIV component: p24 lives in the cytoplasm and generates otein (Lm-Gag) was used to stimulat g peptides that span p24) were recog	te gag specific CD4+ T cel	l proliferative responses in
p24 (161–180)	<ul> <li>BALB/c and C57BL/6</li> <li>L. monocytogenes is a are processed and prese</li> <li>The class II T helper re</li> </ul>	gram-positive bacteria that enters ented by both class I and class II p	HXB2 HIV component: Gag isteria monocytogenes (Lm-Gag) expenses the macrophage on phagocytosis and pathways peptides that overlapped by 10, and the state of the	d lives in the cytoplasm –	secreted L. monocytogenes antigens

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
p24 (163–177)	<ul> <li>but only 3/14 (21%) of</li> <li>PBMC from individuals weeks post treatment</li> <li>DRB1*13-DQB1*06 w</li> </ul>	those who did not have DRB1 s with the haplotype DRB1*13 was also found to be enriched a	*13-DQB1*06, maintained viral 3-DQB1*06 displayed increased	I suppression for 18 months IFN $\gamma$ secretion and stronger prolices (it was in 9/18 versus, versus 21)	Blankson2001b, Malhotra2001 PRB1*13-DQB1*06 positive people, ferative responses against p24 80 % of the general population)
p24 (175–199)	<ul> <li>6 months after initiation</li> <li>For one individual, patiterms of HLA restriction</li> <li>profile (high IL-4 and I</li> <li>4/10 clones from patient</li> </ul>	n of HAART. There was no dift ent F45 CDC stage A2, CD4+ on and Vbeta usage, and some L-5 production). 5/10 CD4+ c at F45 had their epitopes mapp	5-Gag-specific CD4+ T cell resp fference in level of response in the p55 responding clones were gen clones had a Th1 cytokine secret lones could also induce cytotoxi ed using overlapping peptides. C	hose with or without a detectable perated. Her response was consist tion profile (high IFNgamma prodicity.  Clone 26 recognized this peptide s	ently strong and heterogeneous in luction) while some had a Th2
p24 (181–196)		VKNWMTETLLVQNANC  ry proliferative response in PB  idues for HLA DR: VKNWM'		human	Bedford1997

## III-B-3 p2p7p1p6 Helper T-Cell Epitopes

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
p2p7p1p6 (30–44)	p15 (393–407 IIIB, B10) • 12 gag and 18 env peptide	FNCGKEGHTARNCRA es were identified that could con	HIV-1 infection nmonly evoke T-cell responses.	human	Wahren1989b, Wahren1989a
p2p7p1p6 (55–69)	p15 (418–432 IIIB, B10) 12 gag and 18 env peptide	KEGHQMKDCTERQAN es were identified that could con	HIV-1 infection nmonly evoke T-cell responses.	human	Wahren1989b, Wahren1989a
p2p7p1p6 (60–74)	p15 (423–437 IIIB, B10) • 12 gag and 18 env peptide	MKDCTERQANFLGKI es were identified that could con	HIV-1 infection nmonly evoke T-cell responses.	human	Wahren1989b, Wahren1989a
		PSYKGRPG ation in HIV-infected donors as p24(439-446), but because of	HIV-1 infection the numbering used for Gag epitopes	human s, we placed it in p2p7p1p6	Schrier1989
p2p7p1p6 (83–97)	p15 (446–460 BRU) • Peptide G4: could prime	GNFLQSRPEPTAPPA for in vitro immunoproliferative	in vitro stimulation responses and for subsequent IgG re	murine (H-2 <sup>b</sup> )	Vaslin1994
p2p7p1p6 (98–112)	p15 (473–487 IIIB, B10) • Peptides were identified t		HIV-1 infection onses – 50% of 90 HIV+ people had	human a T-cell response to this pe	Wahren1989b, Wahren1989a eptide
	•	REETTTPS ation in HIV-infected donors as p24(466-473), but it is in p2p2	HIV-1 infection 7p1p6.	human	Schrier1989
	<ul> <li>PBMC from a seronegative Gag-specific CD4+ T-cell dilution. All reacted with</li> <li>Clone 74 recognized two for stimulation by peptide</li> </ul>	clones by in vitro immunization p24 except one which recognize peptides, including this one, wit es 480-500 and 261-280, respect	in vitro stimulation  a pair of monozygotic twins discorda n with HIV-1 overlapping 20mer pep ed a p24 peptide and a p6 peptide. A th a Th1 response using TCR Vβ 13 ively. Sequencing TCR Vbeta region a virus Gag-infected B-LCL, so coul	tides spanning p55. Six clo Il CD4+ T cell clones were (13s1); it required 200 ng/r is of colonies from clone 74	ones were generated by limiting HLA class II DR restricted. In (100 nM) and 1 $\mu$ g/ml (0.5 $\mu$ M) 4 suggested this was a clonal

## III-B-4 Gag Helper T-Cell Epitopes

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
Gag		virus-like particle HIV o		human	Kelleher1998b
			virus-like particle did not significantly imp short-lived increased proliferative response		nt, viral load, or p24 antibody titre
Gag	• 18 HIV-1-seropositive 10 units of native p24	e patients with a low freque and 100 ug of HZ321, a g	HIV-1 infection, Vaccine frus HZ321 (REMUNE(TM)) Strain: Z3: ency or no detectable CD4+ T cell response p120 depleted antigen CD4+ T cells were shown to increase in re	e to HIV-1 antigen receive	d an HIV-1 immunogen consisting of
	enhancement was obs	erved after a single immur		•	
Gag	in 2/12 patients		HIV-1 infection infected patients allowed recovery of p24 Tak viremia in one patient, while in the second		
Gag	normalization of imm  A vigorous HIV-specionly 1/5 controls treat  Vigorous Th response	une parameters  fic Th response (stimulation and after seroconversion as were detected as early as to seroconversion had no le	HIV-1 infection -1 infections were treated with didanosine, on index greater than 8) was observed in 7/2 -34 days after treatment begin oss of naive CD4 T lymphocytes, recovery	8 patients treated before co	omplete WB seroconversion, but in
Gag	• The magnitude of the	Th1 response correlated we tude of the CD8+ CTL res	HIV-1 infection CD4+ T-cell IFN-gamma producing Th1 re rith previous interruptions in HAART, sugg ponse did not correlate with interruptions i	gesting the interruptions pr	
Gag	<ul> <li>Immunization of HIV p24 and p17 and a train</li> </ul>	nsient elevation in viral loa	7/p24 Ty virus-like particle (p24-VLP) resu	_	Klein1997 ved increased proliferative response t
Gag	p24 <b>Vaccine</b> Vector/Type:	gp120 depleted virus HZ3	Vaccine 21 (REMUNE(TM)) Strain: Z321 HIV	human // component: gp120 deple	Moss1998 ted virus

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
			rus (REMUNE $^{TM}$ ) triggered an increas in env and clade G in gag. [Moss1998]	e in lymphocyte proliferative resp	ponse to native p24, a clade B virus
Gag			HIV-1 infection control and HIV disease outcome	human	Rosenberg 1999
	<ul><li>syndrome</li><li>This suggests that Th c</li></ul>	cells are part of the nor	es were found in seven persons who wer mal response to HIV-1 infection, but the ath – if peak viremia can be controlled,	eir numbers are rapidly diminishe	d by either being infected during the
Gag			HIV-1 infection individuals who effectively maintain lowerior to sero-conversion, strong helper re-		Rosenberg1998
Gag	p17 Vaccine Vector/Type: 1  Different p17 genes de their H-2 type.		Vaccine HIV component: p17 assispecies and expressed and purified i	murine n E. coli primed different Th 1 an	Birk1998a d Th 2 subsets in mice, depending on
Gag	<ul><li>HIV-1 replication in vi</li><li>Gag proteins including</li></ul>	tro is unlikely to influe p17 and possibly p7 a	HIV-1 infection performance or reproducibility of clinic ence the assay s well as p24 perform better than p24 al e assays, but with lower radiolabled thyr	lone	Schiller2000
Gag	paper shows using flow subjects	v cytometric detection	HIV-1 infection HIV-1 specific Th responses were elimin of antigen-induced cytokines that Th-1 ency of these cells, presumably due to re	CD4+ memory gag-specific Th co	
Gag	Gag • Patients from later stag	ges of infection given I	HIV-1 infection IAART do not show restoration of HIV-	human -1 specific Th proliferative respon	Plana1998 ses
Gag		•	HIV-1 infection ed to test Th proliferative responses afte specific proliferative responses	human r IL2 therapy – while IL2 therapy	Kelleher1998a causes an increase in CD4+
Gag	<ul><li>Priming with an HIV-I</li><li>The proliferative respo</li></ul>	ONA vaccine and boosnse to Env and Gag afan SI for HIV Gag and	Vaccine nia boost Strain: LAI HIV compone ting with a vaccinia construct induced g ter the DNA vaccination had a mean SI I Env – The Th response happened desp hanced	reater levels of HIV T-cell immur of 1.5-4, but after boosting with r	HIV-fowlpox virus, there was a 6-17

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
Gag	• Ten different vaccine		Vaccine ke particle, ISCOM ed for their ability to protect from infect NAb responses, beta-chemokines, and a		Heeney1999 sing a non-pathogenic SHIV challenge
	• DNA, protein+adjuvar	nt, VLP and ISCOM va the highest NAb titers,		-	detectable CTL response, and gave
Gag	Gag/Pol (MN)		Vaccine	chimpanzee	Kim1998
	Co-stimulatory molec	ules co-expressed with	HIV component: GAG, POL, ENV Ac an HIV-1 immunogen in a DNA vaccin Env and Gag/Pol specific CTL and Th p	ne used to enhance the immune re	
Gag			Vaccine IN, LAI HIV component: gp120, gp41 g MN gp120 and LAI gp41/gag/proteas		Salmon-Ceron1999 oproliferative response in healthy
Gag	<ul><li>detected in ten patient</li><li>Untreated patients sho</li></ul>	s, but an Env specific rowed a negative correla	HIV-1 infection p24, p55 and gp120 were tested in 27 pa esponse was detected in only one patier tion between plasma viral load and HIV below the detection limit	nt	-
Gag	CD4+ Th1 responses • Kinetics suggest that	concurrently with viral viral replication leads to	HIV-1 infection ptions (STI) in 3 chronically HIV infect rebound, as measured by proliferation a o rapid destruction of the HIV-specific 1 layed relative to the Th1 responses and	assays and by IFN $\gamma$ production by $\Gamma$ h1 cell response	
Gag	and p66 T-helper CD4 treatment	proliferative response	HIV-1 infection ow CD4+ counts who received HAAR1 s, in contrast to 0/8 chronically HIV inf  CD4 nadir patients being more likely t	ected patients with high CD4+ co	ounts at the initiation of antiretroviral
Gag	patients	%) subjects had a prolif	HIV-1 infection otent anti-retroviral therapy allowed a T ferative response to Gag p24, and 7/41 (		• •

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
Gag		, alloantigen, and PHA di	HIV-1 infection ent anti-retroviral therapy did not allo d develop in many HIV+ patients, an		Blazevic2000 p24 or gp160, but Th proliferative ronger and more frequent Th response
Gag	<ul> <li>individuals treated dur</li> <li>The breadth and specifindividuals with prima (Group 3), using 259 c</li> </ul>	ing chronic infection ficity of the CTL response ry infection but post-sero overlapping peptides span	e was determined using Elispot by stu	udying 19 individuals with pre- 0 individuals who responded to Nef	Altfeld2001b diverse viral population than was seen in seroconversion therapy (Group 1), 11 HAART given during chronic infection uses than individuals who were
Gag	CD4 proliferative resp	onses and were able to m pecific CD4 proliferative	aintain a CTL response even with un responses and lost their CTL respons	detectable viral load – three pat	Oxenius2000  Ily infection) had strong HIV-specific tients that had delayed initiation of ly given and their viral loads became
Gag	Freund's adjuvant  • Lewis rats simultaneou	usly immunized with HIV		ory sequences CpG had increas	Moss2001  mponent: whole virus Adjuvant: CpG  ed Th proliferative responses, but when
Gag	Freund's adjuvant  • Lewis rats co-immuniz	zed with HIV-1 antigen in			Moss2000  mponent: whole virus Adjuvant: CpG, ncreased IFN $\gamma$ expressing CD4+ and
Gag	<ul><li>IFNγ producing. Prolif</li><li>Gag specific CTL leve</li></ul>	ferative responses against ls were correlated with G	HIV-1 infection esponses (SIs) were inversely correla t gp160 were rarely observed (only 4 ag proliferative responses but were no any HIV-1 antigen tested.	cases).	Kalams1999a aive patients. The responses were Th1, subjects lacked p24 specific Gag
Gag			HIV-1 infection lp in many viral infections, and cover ion to prevent the early decimation or		
Gag	p24 • Dysfunction of HIV-1	specific proliferative resp	HIV-1 infection conses, but not responses to other anti-	human igens, is evident in HIV-1 progr	Wilson2000b

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References				
	<ul><li>borderline responses.</li><li>None of the progressor</li></ul>	IL-2 production was see rs (0/5) had HIV-1 spec	of and gp120 with SI between 8-99 we en in all cases, and IL-4 production wa ific proliferative responses, or IL-2 or aphylococcus enterotoxin B, tetanus t	as also evident many responses. IL-4 induction.	ressors (LTNP), the seventh had a HIV-1+ LTNP, progressors, and HIV-1				
Gag			HIV-1 infection I higher frequencies of Th1 response to the were inversely correlated with viral left.		Alatrakchi2002 ens.				
Gag	<ul> <li>The fractions of naive proliferation responses suggesting that ongoin</li> <li>DTH responses to reca</li> </ul>	· · · · · · · · · · · · · · · · · · ·							
Gag	eight patients received T cell responses for up No induction of drug e 34 UK infected patient the rest were B. Recombinant HIV-1 de ELISPOT assays. The 6/8 of the untreated ine at baseline, but this na Post-therapy, the avera	four ART drugs. Initia to 64 weeks after there escape mutations was of the trived gp120, p24, p66 strongest preservation of dividuals were tested for prowed to p24 and gp12 uge spot forming cells for	apy. bserved, although two individuals had 1. 11/45 subjects had non-UK acquired and overlapping peptide pools spanning of T helper responses 12 weeks off SC	escape mutations in their infecting HIV infection, 2 were clade A, 1 and Nef were employed to CART was seen for p24-specific Cotectable response. 1 had detectable eeks. 3 had detectable and persiste weeks of follow up had not decline	ks in all patients and preserving CD4+ g virus at baseline. was A/E, 1 was C, 1 was "untypable", measure CD4 T-cell frequencies in cD4+ T-cell responses. e responses to all HIV-1 proteins tested ent responses, but only to p24.				
Gag	• HIV-1 p17/p24:Ty viru	s-like particles therape	Vaccine  ain: IIIB HIV component: p17, p24  utic vaccination of 56 HIV-1 infected evidence suggesting it can enhance Th	patients had no effect on disease J	progression, AIDS and CD4+ T-cell				
Gag	<ul><li>acute infection, two be</li><li>The immunodominant were obtained from the</li></ul>	efore (AC-01 and AC-30 response in LTNP CTS e three patients given th	HIV-1 infection derived from one long-term non-prog 6) and one after (AC-25) STI. 6-01 was to peptide 9, and 9/10 clones derapy. These six clones all reacted wi xic responses. The implications of cyt	derived from this patient reacted th different p24 peptides, and all l	with it. Three, two, and one clones had peptide induced proliferative				

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
Gag	<ul><li>(HAART failures and patient groups with act</li><li>No differences in the f</li></ul>	HAART naive). Patient tive HIV-1 replication,	HIV-1 infection HIV-1 infected patients with HAART sup as with HAART suppression showed strong suggesting active viral replication in vivo fic CD4+ T-cells that were positive for cy a viral replication.	nger p24- and p66-specific prol o specifically reduces proliferati	iferative responses compared to on responses.
Gag	<ul> <li>viremia but had progre</li> <li>SF2 p24 20mer peptid proliferative response nonprogressors. IL-4 (were see per peptide. I</li> <li>The results taken toget</li> <li>One immunologically</li> </ul>	essive CD4+ T-cell decl es overlapping by 10 w with every one of the 2. (Th2) responses were st In contrast, only 1/10 puther suggest that a balar	HIV-1 infection 10 clinical non-progressors, and 3 immurine) were analyzed for their T-helper cell ere used to assess the response in the diff 2 p24 overlapping peptides. All peptides rong, but somewhat less comprehensive a rogressors had a clear proliferative and II need Th1/Th2 response to HIV is importance became symptomatic while on the study. It conse.	responses to p24 and cytokine ferent groups. At least 1/10 and produced an IL-2 (Th1) responses 6/22 peptides elicited no IL-2 response to 2/22 peptides, a ant for viral control in long-term	profile.  I up to 7/10 nonprogressors had a use in at least one of the 10  I production, and fewer IL-4 responses nd neither one made an IL-4 response.  In non-progression.
Gag	<ul> <li>Of 5 mouse inbred line proliferative responses</li> </ul>	es tested: DBA/2 (H-2d s to HIV proteins (gp16	Vaccine in: BRU HIV component: whole virus , Ad, Ed), B10.A(4R) (H-2h4, Ak) and B 0, gp120, p17, p24, Nef and RT), after va and Ab) had weaker responses.	B10.A(5R) (H-2i5) showed part	icularly good CD4+ T cell
Gag	HIV-1 infected individ	luals at levels comparab	in vitro stimulation ng HIV-1 sequences, upon infection of m le to the response seen to HIV carried in ng HIV-1 sequences can also stimulate H	vaccinia vectors	
Gag	<ul><li>6 months after initiation</li><li>For one individual, pat terms of HLA restriction</li></ul>	on of HAART. There wa tient F45 CDC stage A2 on and Vbeta usage. Tw	HIV-1 infection  low p55-Gag-specific CD4+ T cell responses as no difference in level of response in the compact of the compac	ose with or without a detectable erated. Her response was considused TCR Vbeta 17+19 or 5.1.	e p55 response. stently strong and heterogeneous in Three clones were DRB1*03
Gag	p24 Vaccine Vector/Type:  • Mice were injected wi		Vaccine  :: GAG  and 4 weeks and lymphocyte proliferation ated a stronger response than standard Ga		

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• IFN-gamma levels were increased compared to an undetectable IL-4 response

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
	• CTL levels were also i	increased in secreted Ga	ag expression vaccination studies		
Gag	<ul> <li>DNA vaccinated BALL immunization</li> <li>Strong but non-lasting + protein boost</li> <li>Immunization with eit cultures stimulated by</li> </ul>	B/c mice primed and both HIV-specific CTL responder the multiepitopic D Tat and Gag, while Th2	Vaccine DNA with recombinant protein boost posted with a multiepitopic vaccine with sonses were detected by a Cr-release ass NA or with the mixed DNA vaccine responses but decreased anti-HIV antiboost	h IL18 showed lymphoproliferativ say and DNA prime + DNA boost sulted in Th1 cytokines production was not detectable	was more effective than DNA prime
Gag	<ul> <li>An avirulent rec coxsa and T help responses c</li> <li>This paper describes the</li> </ul>	ckievirus (CB4-P) cons can be elicited from pep the vaccine strategy and	Vaccine omponent: partial p24, polyepitope truct was generated that can express p2 tides embedded in a surface loop of the generation of constructs, and employs ria MHC class I presentation in BALB/	e VP1 capsid amino-terminal fusion of Gag sequ	
Gag	<ul> <li>BALB/c mice were given gp120 and Pr55gag</li> </ul>	ven intraperitoneal imm at humoral responses we	Vaccine  ain: gp120 A clade UG5.94UG018, HI unization in the absence of adjuvants were elicited against both gp120 and p24	vith virus-like particles (VLPs) exp	pressing recombinant subtype A
Gag	<ul> <li>BALB/c and C57BL/6 vaccinia expressing Ga</li> <li>L. monocytogenes is a are processed and pressing CD4+ Th1 T-cells median</li> </ul>	o mice were immunized ag gram-positive bacteria tented by both class I ar diated the Gag specific	Vaccine s Strain: HXB2 HIV component: G with rec Listeria monocytogenes (Lm-that enters the macrophage on phagocytoglass II pathways mmunological protection in mice imme via IFNγ secretion, but are not essented.	Gag) expressing HIV-1 HXB2 Gag ytosis and lives in the cytoplasm – unized with Lm-Gag and challeng	secreted L. monocytogenes antigens
Gag	<ul> <li>BALB/c and C57BL/6 vaccinia expressing Ga</li> <li>L. monocytogenes is a</li> </ul>	mice were immunized ag	Vaccine So HIV component: Gag With rec Listeria monocytogenes (Lm- that enters the macrophage on phagocytod class II pathways		-

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References				
	• This article is a review of L. monocytogenes biology and its potential as a vaccine vector for HIV, comparing to other vector systems, and discussing CD4+								
	Th1 T-cells mediated G	ag specific immunolo	gical protection in mice and the Gag CT	L response					

## III-B-5 RT Helper T-Cell Epitopes

<b>HXB2</b> Location	<b>Author's Location</b>	Sequence	Immunogen	Species (HLA)	References
RT (36–52)	RT (36–52 BRU) • 9 out of 17 humans can	EICTEMEKEGKISKIGP make strong IL2 responses to this	HIV-1 infection s epitope	human	De Groot1991
RT (38–52)		CTEMEKEGKISKIGP ecombinant protein Strain: BRU ized mice have enhanced prolifera		murine (H-2 <sup>k</sup> )	De Groot1991
RT (39–53)	RT (194–208) • Protein priming induced	TEMEKEGKISKIGPE d T-cells that recognize peptide, 4	in vitro stimulation clones from a single donor recognize	human ed this peptide	Manca1995a
RT (48–62)		SKIGPENPYNTPVFA combinant protein Strain: BRU ized mice have enhanced prolifera		murine (H-2 <sup>k</sup> )	De Groot1991
RT (62–77)		AIKKKDSTKWRKLVDF ecombinant protein Strain: BRU ized mice have enhanced prolifera		murine (H-2 <sup>k</sup> )	De Groot1991
RT (88–102)		WEVQLGIPHPAGLKK ecombinant protein Strain: BRU ized mice have enhanced proliferations.		murine (H-2 <sup>t4</sup> )	De Groot1991
RT (124–138)	responses from multiple This epitope binds seve IC <sub>50</sub> threshold below 1, This epitope sequence i 8/22 HIV infected indiv	e HIV-infected donors n HLA-DR alleles: DRB1*0901, 000 nM s conserved in 68% of clade B iso	13/22 responded to some of the DR s	405, DRB1*0401, DRB1*	and all elicited proliferative 1501 and DRB1*0101, with an
RT (124–138)	<ul> <li>Epitope name: Pol 303</li> <li>Four Th HIV epitopes proaccine strategies of in</li> <li>Responses to pooled perpromotor were compared</li> </ul>	oresented by HLA-DR molecules H-2b mice. ptides, polyepitope peptides in a led. A linear arrangement in polyeprepitope construct with the GPGP	Vaccine  e HIV component: polyepitope Adverse identified that also could be prelinear construct or in a branched MA pitope construct created a junctional G spacer worked well in terms of elicentees.	esented my murine class II is P construct, and a DNA polepitope that could be disruj	lyepitope construct with a CMV pted with the addition of GPGPG

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
RT (133–147)		PSINNETPGIRYQYN combinant protein Strain: BRU zed mice have enhanced prolifera		murine (H- $2^{k,i5}$ )	De Groot1991
RT (144–158)	**	YQYNVLPQGWKGSPA combinant protein Strain: BRU zed mice have enhanced prolifera	•	murine (H-2 <sup>t4</sup> )	De Groot1991
RT (156–170)	responses from multiple This epitope binds nine land DRB3*0101, with a This epitope sequence is 7/22 HIV infected indivi	HIV-infected donors HLA-DR alleles: DRB1*0101, D n IC <sub>50</sub> threshold below 1,000 nM conserved in 79% of clade B iso	olates 13/22 responded to some of the DR s	01, DRB1*1302, DRB1*0	701, DRB1*0901, DRB5*0101
RT (156–170)	<ul> <li>Epitope name: Pol 335</li> <li>Four Th HIV epitopes provaccine strategies of in F</li> <li>Responses to pooled perpromotor were compared</li> </ul>	resented by HLA-DR molecules of H-2b mice.  otides, polyepitope peptides in a l.d. A linear arrangement in polyepepitope construct with the GPGPO	Vaccine  HIV component: polyepitope Adverse identified that also could be presinear construct or in a branched MA pitope construct created a junctional G spacer worked well in terms of elimeters.	esented my murine class II is P construct, and a DNA polepitope that could be disruj	lyepitope construct with a CMV oted with the addition of GPGPG
RT (171–190)	naturally processed for n • Epitope binds to HLA-D	nultiple HLA-DR molecules PR1, -DR2, -DR3, -DR4, and DR	HIV-1 infection  re stimulated when presented with tar  7, and can elicit Th1 cells that recog more than half of the general popula	nize peptide, protein, and H	
RT (171–190)	<ul><li>could bind to more than donors.</li><li>This highly conserved ep PBMC individuals with</li></ul>	one HLA class II protein, and bu pitope binds with high affinity to the appropriate HLA alleles.	HIV-1 infection, in vitro stimulation uld be cross-presented by multiple clut only 2/5 could stimulate strong pro HLA-DR1, -DR2, -DR3, -DR4, and a pulsed stimulator cells, and respond	liferation responses in PBM -DR7 but not HLA-DR5, a	MC derived from multiple healthy and stimulated proliferation in 3/3

<b>HXB2</b> Location	<b>Author's Location</b>	Sequence	Immunogen	Species (HLA)	References
	• This epitope is highly of	conserved and spans the highly cor	served YMDD motif, and sho	owing only minor variability in c	clades A, B, and D.
RT (195–209)	RT (IIIB) • Protein priming induce	IGQHRTKIEELRQHL d T-cells that recognize peptide	in vitro stimulation	human	Manca1995b
RT (196–215)	RT (351–370) • Protein priming induce	GQHRTKIEELRQHLLRWGLT d T-cells that recognize peptide, 4		human cognized this peptide	Manca1995a
RT (249–263)		KDSWTWNDIQKLVGK PBMC from non-infected individu t induce T-cells that recognize who		human	Manca1995b
RT (249–263)	<ul> <li>A subset of T-cell lines major coat protein gVI</li> <li>This peptide was select</li> </ul>	KDSWTVNDIQKLVGK D (HLA DR 11; DRB52) and LD ( generated from these donors were IIp ed to study phage presentation of point a naive repertoire [Manca1995a	capable of recognizing pep23	3 expressed on the surface of fila	
RT (249–263)	<ul> <li>Epitope name: RT2</li> <li>Phage display of the C</li> <li>HIV negative individua</li> <li>Bacteriophage presenta suggests new possibilit</li> </ul>	als and in vivo in immunization of ation of peptides is generally used to	I with T helper epitope KDSW HLA-A2 transgenic mice for stimulation of antibodies, a	HIV component: RT peptides /TVNDIQKLVGK, elicited spectand this novel discovery of CTL	De Berardinis2000  cific CTL responses in PBMC from epitope processing and presentatio
RT (249–263)	The glutathione S-trans	KDSSTVNDIQKLVGK  bited antagonistic activity against p  sferase (GST)-peptide system can l  nism resulted when this peptide was	be used to display peptides; an	ntigenicity was maintained when	
RT (251–261)	<ul><li>One Th line was stimul</li><li>Constructs linking GST</li></ul>	SSTVNDIQKLV inimal stimulatory sequence ated by p66, one by a Glutathione to the KDSSTVNDIQKLVGK pe GST are not intrinsically permiss	eptide at the N-term end of GS	ST stimulated Th cells, but not c	Manca1996 onstructs linking at the C-term end ILKCNNK for contrast)
RT (258–272)	•	QKLWGKLNWASQIYP PBMC from non-infected individu t induce T-cells that recognize who		human	Manca1995b
RT (271–290)		YPGIKVRQLCKLLRGTKALT east 5 different HLA-DR molecule on to be processed properly from v	es, and peptide on target cells	human can elicit Th responses from PB	vanderBurg1999 MC cultures from healthy donors,

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References		
RT (271–290)	RT (271–290 HXB2)	YPGIKVRQLCKLLRGTKALT	HIV-1 infection, in vitro stimulation	human (DR1, DR2, DR3, DR5, DR7)	vanderBurg1999		
	<ul> <li>The goal of this study was to identify Th epitopes that could be cross-presented by multiple class II HLA molecules. 5 RT peptides were identified that could bind to more than one HLA class II protein, but only 2/5 could stimulate strong proliferation responses in PBMC derived from multiple healthy donors.</li> <li>This epitope binds with high affinity to HLA-DR1, -DR2, -DR3, -DR5, and -DR7 but not HLA-DR4, and stimulated proliferation in 3/4 individuals with the appropriate HLA alleles.</li> </ul>						
		le to be naturally processed in pro	otein-pulsed stimulator cells.				
RT (276–290)	RT (IIIB) • Protein priming induced	WRQLCKLLRGTKALT  I T-cells that recognize peptide	in vitro stimulation	human	Manca1995b		
RT (285–299)	RT (IIIB) • Protein priming induced	GTKALTEVIPLTEEA  I T-cells that recognize peptide	in vitro stimulation	human	Manca1995b		
RT (294–308)	RT (IIIB) • Protein priming induced	PLTEEAELELAENRE  I T-cells that recognize peptide	in vitro stimulation	human	Manca1995b		
RT (303–317)	RT (IIIB) • Protein priming induced	LAENREILKEPVHGV  I T-cells that recognize peptide	in vitro stimulation	human	Manca1995b		
RT (384–398)	RT (IIIB) • Protein priming induced	GKTPKFKLPIQKETW  I T-cells that recognize peptide	in vitro stimulation	human	Manca1995b		
RT (414–428)	Pol (596–610) • Epitope name: Pol 596	WEFVNTPPLVKLWYQ	HIV-1 infection	human (DR supermotif)	Wilson2001		
	• Eleven peptides were identified that had the HLA-DR supermotif, all were found to bind to MHC class II DR molecules and all elicited proliferative						
	responses from multiple HIV-infected donors  • This epitope binds eleven HLA-DR alleles: DRB1*0101, DRB1*1501, DRB1*0401, DRB1*0405, DRB1*1101, DRB1*1302, DRB1*0701, DRB1*0802, DRB1*0901, DRB5*0101 and DRB4*0101, with an IC <sub>50</sub> threshold below 1,000 nM						
	<ul> <li>This epitope sequence is conserved in 84% of clade B isolates</li> <li>6/22 HIV infected individuals responded to this epitope (13/22 responded to some of the DR supermotif epitopes, the 9 non-responder peptides tended to also not have recall responses to rec HIV-1 whole proteins)</li> </ul>						
RT (429–443)	RT (IIIB) • Protein priming induced	LEKEPIVGAETFYVD I T-cells that recognize peptide	in vitro stimulation	human	Manca1995b		
RT (432–450)	RT (431–450 HXB2)	EPIVGAETFYVDGAANRET	HIV-1 infection, in vitro stimulation	human (DR1, DR2, DR3, DR4)	vanderBurg1999		
	• The goal of this study was to identify Th epitopes that could be cross-presented by multiple class II HLA molecules. 5 RT peptides were identified that could bind to more than one HLA class II protein, and but only 2/5 could stimulate strong proliferation responses in PBMC derived from multiple healthy donors.						
	This epitope binds with was not considered broa		, -DR3, and -DR4, but stimulated a s	strong proliferation respons	e in only 1/4 individuals tested so		

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References	
RT (526–540)	<ul> <li>Epitope name: W9</li> <li>Of 5 mouse inbred lines proliferative responses t</li> <li>B10.BR (H-2k, Ak, Ek)</li> </ul>	tested: DBA/2 (H-2d, A o HIV proteins (gp160, g and C57BL/6 (H-2b and	recombinant protein Strain: BRU d, Ed), B10.A(4R) (H-2h4, Ak) an	murine (Ad or Dd)  J HIV component: whole virus, RT  ad B10.A(5R) (H-2i5) showed particular vaccination with inactivated virus.	-	
RT (528–541)	<ul> <li>Epitope name: A3</li> <li>Of 5 mouse inbred lines proliferative responses t</li> <li>B10.BR (H-2k, Ak, Ek)</li> <li>The peptide KEKVYLA</li> </ul>	tested: DBA/2 (H-2d, A to HIV proteins (gp160, g and C57BL/6 (H-2b and WVPAHKG was one of	d, Ed), B10.A(4R) (H-2h4, Ak) an p120, p17, p24, Nef and RT), after Ab) had weaker responses.	murine (Ad and Dd)  J HIV component: whole virus, RT  ad B10.A(5R) (H-2i5) showed particular vaccination with inactivated virus.  ognition. It could by itself prime differ-2 and SIV strains.	larly good CD4+ T cell	
RT (528–543)	RT (528–543 BRU)  Vaccine Vector/Type: po  T-cells from peptide-pri			murine $(H-2^{f,k,d})$	Haas1991	
RT (529–543)	Pol (711–725) EKVYLAWVPAHKGIG HIV-1 infection human (DR supermotif) Wilson2001  • Epitope name: Pol 711  • Eleven peptides were identified that had the HLA-DR supermotif, all were found to bind to MHC class II DR molecules and all elicited proliferative responses from multiple HIV-infected donors  • This epitope binds ten HLA-DR alleles: DRB1*0101, DRB1*1501, DRB1*0401, DRB1*0405, DRB1*1101, DRB1*0701, DRB1*0802, DRB1*0901, DRB5*0101 and DRB4*0101, with an IC <sub>50</sub> threshold below 1,000 nM  • This epitope sequence is conserved in 94% of clade B isolates  • 6/22 HIV infected individuals responded to this epitope (13/22 responded to some of the DR supermotif epitopes, the 9 non-responder peptides tended to also not have recall responses to rec HIV-1 whole proteins)					
RT (529–543)	Pol (711–725) EKVYLAWVPAHKGIG Vaccine murine (I-Ab and Livingston2002 HLA-DR)  Vaccine Vector/Type: DNA with CMV promotor, peptide HIV component: polyepitope Adjuvant: CFA  Epitope name: Pol 711  Four Th HIV epitopes presented by HLA-DR molecules were identified that also could be presented my murine class II molecule I-Ab, enabling testing of vaccine strategies of in H-2b mice.  Responses to pooled peptides, polyepitope peptides in a linear construct or in a branched MAP construct, and a DNA polyepitope construct with a CMV promotor were compared. A linear arrangement in polyepitope construct created a junctional epitope that could be disrupted with the addition of GPGPG spacers. The linear polyepitope construct with the GPGPG spacer worked well in terms of eliciting responses to all four peptides, using either DNA or protein for the vaccination.  Although responses to this peptide indicated it was immunodominant, responses to all four peptides were made upon vaccination with linear constructs when GPGPG spacers were used.					

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References		
RT (530–544)	Pol (712–726) • Epitope name: Pol 712	KVYLAWVPAHKGIGG	HIV-1 infection	human (DR supermotif)	Wilson2001		
	<ul> <li>Eleven peptides were identified that had the HLA-DR supermotif, all were found to bind to MHC class II DR molecules and all elicited proliferative responses from multiple HIV-infected donors</li> <li>This epitope binds ten HLA-DR alleles: DRB1*0101, DRB1*1501, DRB1*0401, DRB1*0405, DRB1*1101, DRB1*0701, DRB1*0802, DRB1*0901,</li> </ul>						
	DRB5*0101 and DRB4*0101, with an IC <sub>50</sub> threshold below 1,000 nM  • This epitope sequence is conserved in 89% of clade B isolates						
	• 6/22 HIV infected individuals responded to this epitope (13/22 responded to some of the DR supermotif epitopes, the 9 non-responder peptides tended to also not have recall responses to rec HIV-1 whole proteins)						

# III-B-6 RT-Integrase Helper T-Cell Epitopes

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
RT-Integrase (553–3)	RT (720-730 LAI)	SAGIRKVLFLD	HIV-1 infection	human	Schrier1989
• Stimulates T-cell proliferation in HIV-infected donors					

## III-B-7 Integrase Helper T-Cell Epitopes

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References		
Integrase (16–30)	Pol (758–772) • Epitope name: Pol 758	HSNWRAMASDFNLPP	HIV-1 infection	human (DR supermotif)	Wilson2001		
	• Eleven peptides were identified that had the HLA-DR supermotif, all were found to bind to MHC class II DR molecules and all elicited proliferative responses from multiple HIV-infected donors						
	• This epitope binds eight DRB1*0101, with an IC	HLA-DR alleles: DRB4*0101, 50 threshold below 1,000 nM		, DRB1*0701, DRB1*1101, DRB1*(	0405, DRB1*0401 and		
	• 8/22 HIV infected indivi	conserved in 68% of clade B is duals responded to this epitope onses to rec HIV-1 whole protein	(13/22 responded to some	of the DR supermotif epitopes, the 9 r	non-responder peptides tended to		
Integrase (172–186)		LKTAVQMAVFIHNFK ration in HIV-infected donors	HIV-1 infection	human	Schrier1989		
Integrase (173–187)	• Epitope name: Pol 915	KTAVQMAVFFIHNFKR	HIV-1 infection	human (DR supermotif)	Wilson2001		
	<ul> <li>Eleven peptides were identified that had the HLA-DR supermotif, all were found to bind to MHC class II DR molecules and all elicited proliferative responses from multiple HIV-infected donors</li> <li>This epitope binds seven HLA-DR alleles: DRB5*0101, DRB1*1302, DRB1*1101, DRB1*0405, DRB1*0401, DRB1*1501 and DRB1*0101, with an IC<sub>50</sub> threshold below 1,000 nM</li> </ul>						
	<ul><li>This epitope sequence is</li><li>6/22 HIV infected indivi</li></ul>	conserved in 94% of clade B is	(13/22 responded to some	of the DR supermotif epitopes, the 9 r	non-responder peptides tended to		
Integrase (196–210)		AGERIVDIIATDIQT ration in HIV-infected donors	HIV-1 infection	human	Schrier1989		
Integrase (214–228)	Pol (956–970) • Epitope name: Pol 956	QKQITKIQNFRVYYR	HIV-1 infection	human (DR supermotif)	Wilson2001		
	• Eleven peptides were identified that had the HLA-DR supermotif, all were found to bind to MHC class II DR molecules and all elicited proliferative responses from multiple HIV-infected donors						
	• This epitope binds twelve HLA-DR alleles: DRB4*0101, DRB5*0101, DRB1*0901, DRB1*0802, DRB1*0701, DRB1*1302, DRB1*1201, DRB1*1101, DRB1*0405, DRB1*0401, DRB1*1501 and DRB1*0101, with an IC <sub>50</sub> threshold below 1,000 nM						
	<ul> <li>This epitope sequence is conserved in 95% of clade B isolates</li> <li>8/22 HIV infected individuals responded to this epitope (13/22 responded to some of the DR supermotif epitopes, the 9 non-responder peptides tended to also not have recall responses to rec HIV-1 whole proteins)</li> </ul>						
Integrase (215–227)		KQITKIQNFRVYY ration in HIV-infected donors	HIV-1 infection	human	Schrier1989		

# **III-B-8** Pol Helper T-Cell Epitopes

<b>HXB2</b> Location	<b>Author's Location</b>	Sequence	Immunogen	Species (HLA)	References
Pol	<ul> <li>A gag/pol DNA vaccin</li> </ul>		Vaccine GAG, POL, VIF Adjuvant: B7 and on with the plasmid encoding the co-sce		Kim1997b -12 gives a dramatic increase in both
Pol			Vaccine gp160, GAG, POL Adjuvant: CD8 on with the plasmid encoding the co-s		Kim1997d s an increase in proliferative responses
Pol	<ul> <li>Co-stimulatory molec</li> </ul>	ules co-expressed with a	Vaccine  IV component: GAG, POL, ENV Aa n HIV-1 immunogen in a DNA vaccin v and Gag/Pol specific CTL and Th p	e used to enhance the immune re	Kim1998 sion vectors esponse – co-expression of CD86, but
Pol	and p66 T-helper CD4 treatment	proliferative responses,	HIV-1 infection w CD4+ counts who received HAART in contrast to 0/8 chronically HIV infe CD4 nadir patients being more likely t	ected patients with high CD4+ co	ounts at the initiation of antiretroviral
Pol	CD4 proliferative resp	onses and were able to r	HIV-1 infection ction (three with sustained therapy, tw naintain a CTL response even with un e responses and lost their CTL respon-	detectable viral load - three pati	ents that had delayed initiation of
Pol	<ul><li>(HAART failures and patient groups with ac</li><li>No differences in the f</li></ul>	HAART naive). Patients tive HIV-1 replication, s		ronger p24- and p66-specific pro vo specifically reduces proliferat	liferative responses compared to
Pol	<ul> <li>Of 5 mouse inbred line responses to HIV prote</li> </ul>	es tested DBA/2 (H-2d, a eins (gp160, gp120, p17	Vaccine n: BRU HIV component: whole viru Ad, Ed), B10.A(4R) (H-2h4, Ak) and p24, Nef and RT), after vaccination v nd Ab) had weaker responses.	B10.A(5R) (H-2i5) showed part	Haas1991 vant (CFA) icularly good CD4+ T cell proliferative
Pol	RT (248–256 HXB2) • CD4+ T-cell lines from	m uninfected individuals	in vitro stimulation by stimulation with p66-pulsed APC	human (DR5)	Manca1995b

HXB2 Location	<b>Author's Location</b>	Sequence	Immunogen	Species (HLA)	References
		sponses to peptides thro	n p66-specific T-cell clones oughout p66, but because of uncertai vith DR5	n locations, they have not been map	ped
Pol	Co-stimulatory molecut	les co-expressed with a	Vaccine • GAG, POL, ENV Adjuvant: IL-2 n HIV-1 immunogen in a DNA vacconses and enhanced CTL responses		Kim2000  ponse – co-expression of Th1
Pol	A live attenuated bacte	Salmonella HIV comp rial vaccine, Salmonella response in BALB/c n	a SL3261-pHART, with an inserted I	murine $(H-2^d)$ HIV RT gene in the Lpp-OmpA-HIV	Burnett2000  7 fusion protein, induced a

# III-B-9 Vif Helper T-Cell Epitopes

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References			
Vif (65–76)	Vif (65–80) • T-cell response to this	VITTYWGLHTGE epitope persisted after serorevers	HIV-1 infection sion	human	Ranki1997			
Vif (81–96)	Vif (81–96) • T-cell response to this	LGQGVSIEWRKQRYST epitope persisted after serorevers	HIV-1 infection	human	Ranki1997			
Vif	<ul> <li>T-cell response to this epitope persisted after seroreversion</li> <li>Vif Vaccine murine (H-2<sup>d</sup>) Ayyavoo2000</li> <li>Vaccine Vector/Type: DNA HIV component: Vif, Vpu, Nef</li> <li>Splenocytes from BALB/c mice immunized with pVVN-P DNA were incubated with Vif, Vpu or Nef antigens for 3 days and assayed for IL-4 and IFN-gamma levels</li> <li>Antigen stimulation increased IFN-gamma production in pVVN-P immunized mice, indicating a Th1 response</li> <li>IL-4 production was not significantly changed after antigen stimulation compared to control levels</li> </ul>							

# III-B-10 Vpr Helper T-Cell Epitopes

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References			
Vpr (66–80)	Vpr (66–80 IIIB) QLLFIHFRIGCRHSR HIV-1 infection human Sarobe1994  ◆ This peptide was found to stimulate proliferative responses in 37.5% of HIV-1 positive individuals							
Vpr (66–80)	Vpr (66–80 IIIB)  Vaccine Vector/Type: pe		Vaccine	murine (H-2 <sup>d</sup> )	Sarobe1994			
	<ul> <li>Included as a Th stimulatory component of peptide vaccines that also incorporated B-cell epitopes</li> </ul>							

### **III-B-11** Tat Helper T-Cell Epitopes

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
Tat (1–20)	Stronger, broader resp.	MEPVDPRLEPWKHPGSQPFDNA Strain: LAI HIV componses were observed in animals ponse to vaccination was observed.	onent: NEF, TAT, REV vaccinated with DNA epiders	murine $(H-2^d)$ mally rather than with intramuscula f and Tat, less for Rev	Hinkula1997 r protein
Tat (16–35)	Stronger, broader resp.	SQPKTACTTCYCKKCCFHC DNA Strain: LAI HIV comp onses were observed in animals ponse to vaccination was observed.	conent: NEF, TAT, REV vaccinated with DNA epidern	murine $(H-2^d)$ mally rather than with intramuscula f and Tat, less for Rev	Hinkula1997 r protein
Tat (17–32)	Tat (17–32) • T-cell response to this	QPKTACTNCYCKRCCF epitope persisted after serorever	HIV-1 infection sion	human	Ranki1997
Tat (17–32)			•	1 0	Blazevic1993 t one Tat-derived synthetic peptides
	<ul> <li>3/12 peptides were rec</li> <li>This immunodominan secondary structure was</li> </ul>	t, highly conserved and most free as predicted at aa residues 21-28. I epitopes restricted by several H	quently recognized peptide w but no amphipathic helix str	vas recognized by 57% of the HIV-1	ole for T-cell epitopes, was indicated
Tat (31–50)	Stronger, broader resp.	CFHCQVCFTTKALGISYGF DNA Strain: LAI HIV comp onses were observed in animals ponse to vaccination was observe	onent: NEF, TAT, REV vaccinated with DNA epiders	murine $(H-2^d)$ mally rather than with intramuscula f and Tat, less for Rev	Hinkula1997 r protein
	-				
Tat (33–48)	Tat (33–48) • T-cell response to this	HCQVCFMTKGLGISYG epitope persisted after serorever	HIV-1 infection sion	human	Ranki1997

- 9/14 (64%) of HIV-1 positive patients had proliferative T-cell responses associated with IL-2 production against at least one Tat-derived synthetic peptides of twelve overlapping 15-16 mer peptides spanning Tat. T cell proliferation was associated with IL-2 production.
- 3/12 peptides were recognized.
- 4/14 HIV+ people recognized this peptide.
- An alpha-helix structure was predicted at residues 39-44, but charge patterns did not indicate it was an amphipathic helix, suggested to be most favorable for T-cell epitopes.

HXB2 Location	<b>Author's Location</b>	Sequence	Immunogen	Species (HLA)	References	
	<ul> <li>This peptide contained recognized the peptide.</li> </ul>		ILA DR alleles, although the	e frequency of DR5 was enriched (2	2/4) among the patients that	
Tat (46–65)		SYGRKKRRQRRRPPQGSQʻ DNA <i>Strain:</i> LAI <i>HIV com</i> p	oonent: NEF, TAT, REV	murine $(H-2^d)$	Hinkula1997	
		onses were observed in animals onse to vaccination was observ		mally rather than with intramusculer and Tat, less for Rev	lar protein	
Tat (61–80)	Stronger, broader respo	GSQTHQVSLSKQPTSQPRO DNA Strain: LAI HIV composes were observed in animals conse to vaccination was observed	conent: NEF, TAT, REV vaccinated with DNA epider	murine $(H-2^d)$ rmally; rather than with intramuscuef and Tat, less for Rev	Hinkula1997 ılar protein	
Tat (65–80)	Tat (65–80 HXB2)	HQASLSKQPTSQPRGD	HIV-1 infection	human (DR2? plus others)	Blazevic1993	
	of twelve overlapping 1  3/12 Tat peptides were  3/14 HIV+ people reco  An alpha-helix structur for T-cell epitopes	15-16 mer peptides spanning Tarecognized. gnized this peptide. e was predicted at residues 65- epitopes restricted by several F	at. T cell proliferation was as	sociated with IL-2 production.	elix, suggested to be most favorable 2/3) among the patients that	
Tat (67–86)		VSLSKQPTSQPRGDPTGPI DNA <i>Strain:</i> LAI <i>HIV comp</i> onses were observed in animals	oonent: NEF, TAT, REV	murine (H-2 <sup>d</sup> )	Hinkula1997 lar protein	
	Some proliferative resp	onse to vaccination was observ	ed to peptides throughout No	ef and Tat, less for Rev		
Tat	Tat Vaccine human Calarota1999  Vaccine Vector/Type: DNA HIV component: NEF, REV, TAT  9/9 HIV-1+ subjects were given one of three DNA vaccinations for nef, rev or tat, and novel proliferative and CTL responses were generated  The nef DNA immunization induced the highest and most consistent CTLp activity, IFN-gamma production, and IL-6 and IgG responses  Highly active antiretroviral treatment (HAART) did not induce new HIV-specific CTL responses but reduced viral load, while DNA vaccination induced					
		but did not reduce viral load –		nplementary and promising combin		
Tat	<ul> <li>This review discusses the</li> </ul>	DNA HIV component: Nef, R he cellular immune response, a L and Th proliferative response	nd comments on CpG induct	tifs ion of Th1 cytokines and enhanced	Calarota2001 d immune responses, and HIV-1 DNA	
Tat	Tat • In vitro delivery of reco		in vitro stimulation	human via avidin-biotin bridges (RBC-Tat)	Corinti2002 to human dendritic cells was	

HXB2 Location	<b>Author's Location</b>	Sequence	Immunogen	Species (HLA)	References	
	DCs stimulated with  • Dendritic cells which	soluble Tat. were maturated in the pre	ecific and significantly stronger CD4+ esence of IFNgamma induced elevated lect Th1 and Th2 cells, respectively.	•	nd required 1250-fold less antigen than on. IFNgamma upregulated IP-10 and	
Tat	<ul> <li>Tat (IIIB, BH10) in vitro stimulation human Fanales-Belasio2002</li> <li>Biologically active HIV-1 Tat is readily taken up by monocyte-derived dendritic cells (MDDC) (and activated endothelial cells), but not other APCs. Tat must be in a native, non-oxidized conformation for efficient uptake. Tat upregulates MHC molecules, IL-12, TNFα, RANTES and MIP-1-α and MIP-1-β production which drives Th1 immune responses and enhances antigen presentation.</li> <li>Native Tat enhanced the antigen presentation of MDDC and boosted proliferative recall and allogeneic antigen responses, and the authors propose it could be used as an adjuvant to drive the immune response as well as an antigen.</li> </ul>					
Tat	<ul> <li>DNA vaccinated BAI</li> <li>Strong but non-lasting + protein boost</li> <li>Immunization with eigenful cultures stimulated by</li> </ul>	LB/c mice primed and boo g HIV-specific CTL respon- ther the multiepitopic DN y Tat and Gag, while Th2 of		IL18 gave lymphoproliferative y and DNA prime + DNA boolted in Th1 cytokines product as not detectable	re responses 7 weeks post immunization ost was more effective than DNA prime	

# III-B-12 Rev Helper T-Cell Epitopes

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
Rev (9–23)	Rev (9–23 HXB2) • One of four peptides th were stimulated	DEELIRTVRLIKLLY at stimulates in PBLs from HIV-1	HIV-1 infection + donors both CD4+ Th cell prolifer	human ation and CTL to autologo	Blazevic1995 us targets incubated with peptide
Rev (16–35)	<ul> <li>Stronger, broader respo</li> </ul>				Hinkula1997 protein
Rev (25–39)	Rev (25–39 HXB2)  • One of four peptides th were stimulated	SNPPPNPEGTRQARR at stimulates in PBLs from HIV-1	HIV-1 infection + donors both CD4+ Th cell prolifer	human ation and CTL to autologo	Blazevic1995 us targets incubated with peptide
Rev (31–50)	Stronger, broader respo				Hinkula1997 protein
Rev (33–48)	Rev (33–48 HXB2)  • One of four peptides th were stimulated	GTRQARRNRRRRWRER at stimulates in PBLs from HIV-1	HIV-1 infection + donors both CD4+ Th cell prolifer	human ation and CTL to autologo	Blazevic1995 us targets incubated with peptide
Rev (41–56)	Rev (41–56 HXB2)  • One of four peptides th were stimulated	RRRRWRERQRQIHSIS at stimulates in PBLs from HIV-1	HIV-1 infection + donors both CD4+ Th cell prolifer	human ation and CTL to autologo	Blazevic1995 us targets incubated with peptide
Rev (76–95)	Stronger, broader respo				Hinkula1997 protein
Rev (96–116)	<ul> <li>Stronger, broader respo</li> </ul>				Hinkula1997 protein
Rev	• Rev M10 is a construct	_	Vaccine  ough a genetic vaccination  ected cells as a method for gene there	murine apy – in the course of this s	Chan1998 tudy, Rev-specific IL-2 producing

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References			
Rev	Rev	DNA HW some or out	Vaccine  Nof Pay Tet	human	Calarota1999			
	<ul><li>9/9 HIV-1+ subjects v</li><li>The nef DNA immuni</li><li>Highly active antiretro</li></ul>	zation induced the higher coviral treatment (HAAR)	Net, Rev 1at DNA vaccinations for nef, rev or tat, and no est and most consistent CTLp activity, IFN Γ) did not induce new HIV-specific CTL re al load – thus this is a potentially complem	-gamma production, and IL esponses but reduced viral lo	-6 and IgG responses oad, while DNA vaccination induced			
Rev	Rev HIV-1 infection, Vaccine human Calarota2001  Vaccine Vector/Type: DNA HIV component: Nef, Rev, Tat Adjuvant: CpG motifs  This review discusses the cellular immune response, and comments on CpG induction of Th1 cytokines and enhanced immune responses, and HIV-1 DNA vaccine boosting of CTL and Th proliferative responses in asymptomatic HIV+ individuals							
Rev	vaccine boosting of CTL and Th proliferative responses in asymptomatic HIV+ individuals  Rev  Vaccine  No MacGregor2002  Vaccine Vector/Type: DNA with CMV promotor Strain: MN HIV component: Env, Rev Adjuvant: bupivacaine  A phase I clinical trial of a HIV-1 Env and Rev DNA vaccine with a CMV promoter was conducted and Th proliferative, CTL and Elispot responses monitored. The construct was modified for safety and included no LTRs or packaging signals. The vaccine strategy was safe, and elicited strong CD responses, but not CD8 T-cell responses. Rev elicited strong Th responses, and is a early produced protein so may confer advantages.  With a 300 ug dose, 4/6 individuals had a lymphocyte proliferation (LP) responses to gp120, 3/6 to Rev.  With a 1000 ug dose, 4/6 individuals had a LP and 2/6 had IFNgamma Elispot responses to gp160; 3/6 had LP, and 4/6 had IFNgamma Elispot responses to three specific CTL epitopes were observed by Elispot in individuals with appropriate HLA. Some cytoxic activity against whole provided that was CD4+ T-cell mediated.							

# III-B-13 Vpu Helper T-Cell Epitopes

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References			
Vpu (19–34)	Vpu (19–34)	AIVVWSIVLIEYRKIL	HIV-1 infection	human	Ranki1997			
	<ul> <li>T-cell response to this ep</li> </ul>	pitope persisted after seroreversi	on					
Vpu	Vpu		Vaccine	murine (H-2 <sup>d</sup> )	Ayyavoo2000			
	Vaccine Vector/Type: D	NA HIV component: Vif, Vpu	, Nef					
	<ul> <li>Splenocytes from BALE</li> </ul>	3/c mice immunized with pVVN	-P DNA were incubated with Vif	, Vpu or Nef antigens for 3 da	ys and assayed for IL-4 and			
	IFN-gamma levels							
	<ul> <li>Antigen stimulation increased IFN-gamma production in pVVN-P immunized mice, indicating a Th1 response</li> </ul>							
	• IL-4 production was not significantly changed after antigen stimulation compared to control levels							
	• Cross-clade CTL activity was also observed: A, B clade, CRF01(AE) clade antigens could serve as targets for the B clade immunization stimulated CTL –							
	an HIV-1 AC recombinant, however, did not stimulate a CTL response, but was expressed at lower levels on the target cell							

# III-B-14 gp160 Helper T-Cell Epitopes

HXB2 Location	<b>Author's Location</b>	Sequence	Immunogen	Species (HLA)	References			
gp160 (30–51)	gp120 (30–51 IIIB)	ATEKLWVTVYYGVPVWKEA- TTT?	HIV-1 infection	human	Geretti1994			
	<ul> <li>Epitope name: A1</li> </ul>							
	• Th proliferative respon	ses were studied in 36 asymptoma	tic HIV-1+ patients. PBMC	from 15/36 patients responded to	stimulation with gp120 syntheti			
		ols. 10 of the responding patients						
	<ul> <li>After 12 months, most months, as did 5/15 nor</li> </ul>		, and specific responses fluc	etuated. 4/10 of the responders at b	aseline had new responses at 12			
		more sensitive and well-preserved	measure of Th function that	n proliferation.				
	<ul> <li>2/15 responders recogn</li> </ul>	fized this peptide, mean $SI = 4.6$ .						
gp160 (32–44)	gp120 (39–51)	EQLWVTVYYGVPV	Vaccine	murine (H-2 <sup>bxk</sup> )	Sastry1991			
,1	Vaccine Vector/Type: p	peptide		. ,	,			
	Peptides induced T-cell	proliferative response to immunization	zing peptide and to gp160					
gp160 (38–48)	Env (45–55)	VYYGVPVWKEA	Vaccine	Rhesus macaque	Nehete1993			
,	Vaccine Vector/Type: peptide							
	Synthetic peptide deriv	ed from conserved region of the H	IIV-1 envelope that stimulate	es a proliferative response in mice				
		o this peptide was observed in 3/3						
p160 (38–48)	Env (45–55)	VYYGVPVWKEA	HIV-1 infection	human, chimpanzee	Nehete1998b			
Si ()	• Seven out of nine HIV-infected chimpanzees and eight out of seventeen HIV-positive humans exhibited positive proliferative responses to this conserved							
	peptide (peptide 104) – no HIV negative individuals showed a response							
				duce proliferative responses to HI	V and may be useful for vaccine			
	Peptide 104 elicited pro	oliferative responses in inbred mou	use strains and outbred rhest	us monkeys in previous study by s	ame group			
gp160 (38–48)	gp120 (45–55)	VYYGVPVWKEA	Vaccine	murine (H-2 <sup>bxk,sxd</sup> )	Sastry1991			
SF ()	Vaccine Vector/Type: p			,	2.00.03			
	<ul> <li>Peptides induced T-cell proliferative response to immunizing peptide and to gp160</li> </ul>							
gp160 (41–54)	Env (48–60)	GVPVWKEATTLFC	Vaccine	Rhesus macaque	Nehete1993			
gp100 (41–34)	Vaccine Vector/Type: peptide							
	Vaccine Vector/Type: r	peptide						
			IIV-1 envelope that stimulate	es a proliferative response in mice				
	Synthetic peptide deriv			es a proliferative response in mice in 3 rhesus monkeys				
on160 (41–54)	<ul><li>Synthetic peptide deriv</li><li>Despite the proliferativ</li></ul>	ed from conserved region of the He response to this peptide in mice,	no response was observed i	in 3 rhesus monkeys				
gp160 (41–54)	<ul> <li>Synthetic peptide deriv</li> <li>Despite the proliferativ</li> <li>gp120 (48–61)</li> </ul>	ed from conserved region of the He response to this peptide in mice,			Sastry1991			
gp160 (41–54)	<ul> <li>Synthetic peptide deriv</li> <li>Despite the proliferativ</li> <li>gp120 (48–61)</li> <li>Vaccine Vector/Type: p</li> </ul>	ed from conserved region of the He response to this peptide in mice,	no response was observed i Vaccine	in 3 rhesus monkeys				
gp160 (41–54)	<ul> <li>Synthetic peptide deriv</li> <li>Despite the proliferativ</li> <li>gp120 (48–61)</li> <li>Vaccine Vector/Type: p</li> <li>Peptides induced T-cell</li> </ul>	ed from conserved region of the He response to this peptide in mice,  GVPVWKEATTLFC reptide  proliferative response to immunic	no response was observed i Vaccine zing peptide and to gp160	murine (H-2 <sup>sxd</sup> )	Sastry1991			
	<ul> <li>Synthetic peptide deriv</li> <li>Despite the proliferativ</li> <li>gp120 (48–61)</li> <li>Vaccine Vector/Type: p</li> <li>Peptides induced T-cell</li> <li>gp120 (40–59 89.6)</li> </ul>	ed from conserved region of the He response to this peptide in mice,  GVPVWKEATTLFC reptide  proliferative response to immunized the province of the province	vaccine vaccine vaccine vaccine vaccine vaccine	murine (H-2 <sup>sxd</sup> )  murine	Sastry1991 Dai2001			
gp160 (41–54) gp160 (41–60)	<ul> <li>Synthetic peptide deriv</li> <li>Despite the proliferativ</li> <li>gp120 (48–61)</li> <li>Vaccine Vector/Type: p</li> <li>Peptides induced T-cell</li> <li>gp120 (40–59 89.6)</li> </ul>	ed from conserved region of the He response to this peptide in mice,  GVPVWKEATTLFC reptide  proliferative response to immunized the province of the province	vaccine vaccine vaccine vaccine vaccine vaccine	murine (H-2 <sup>sxd</sup> )	Sastry1991 Dai2001			

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
	gp120. Promiscuously with regions of local st frequency of immunog	immunodominant per tructural disorder in pr genic sequences.	O vaccines in 2 mouse strains, CBA/3 ptides were identified in both mice stroximal N-terminal segments, sugges ALB/c mice tested, but only in 5/10 C	rains that were located in the outer of ting 3-D protein structure influence	domain of gp120 and were associated
gp160 (41–60)	<ul> <li>Promiscuous immunod in the outer domain, pr</li> <li>This peptide was recog recognized well not by</li> </ul>	recombinant protein dominant epitopes in g roximal to regions of s gnized by 10/10 BALF v CBA/J mice, so is co	Strain: 89.6 HIV component: gp12 gp120 were mapped by overlapping p structural disorder indicated by the cr 3/c with an average SI of 6.4, the stronsidered to be uniquely immunodom d to be in the inner domain of the pro-	eptides in CBA/J H- $2^k$ and BALB/c ystal structure or by sequence divergoes reaction among BALB/c mice inant for H- $2^d$	$^{c}$ H-2 $^{d}$ mice, and all were found to be gence.
gp160 (42–61)	<ul> <li>overlapping peptide po</li> <li>After 12 months, most months, as did 5/15 no</li> </ul>	Y?  nses were studied in 36 pols. 10 of the responder responses were lost on-responders.  more sensitive and we	CASDAKA – HIV-1 infection  6 asymptomatic HIV-1+ patients. PBl ling patients recognized three or more r diminished, and specific responses	e peptide pools. fluctuated. 4/10 of the responders a	
gp160 (52–71)	gp120 (52–71 IIIB)  • Epitope name: A3  • Th proliferative responding peptide powerlapping pe	LFCASDAKAYDT T?  asses were studied in 36 pols. 10 of the responder responses were lost of polymers ponders.  more sensitive and we	EVHNVWA— HIV-1 infection  6 asymptomatic HIV-1+ patients. PBI ling patients recognized three or more r diminished, and specific responses bell-preserved measure of Th function	e peptide pools. fluctuated. 4/10 of the responders a	
gp160 (61–80)	coli (mLT)  • Epitope name: Peptide  • Helper T-cell prolifera gp120. Promiscuously with regions of local strequency of immunog	e 4 tive responses to gp12 immunodominant per tructural disorder in pr genic sequences.	ACVPTDPN Vaccine  Strain: 89.6 HIV component: gp12  O vaccines in 2 mouse strains, CBA/2 ptides were identified in both mice stroximal N-terminal segments, sugges  LB/c mice tested, but only in 1/10 CE	and BALB/c, were mapped using a rains that were located in the outer of ting 3-D protein structure influence	47 overlapping peptides that span domain of gp120 and were associated

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
gp160 (62–80)	<ul> <li>After 12 months, most months, as did 5/15 nor</li> </ul>	ols. 10 of the responding patients responses were lost or diminished	tic HIV-1+ patients. PBMC recognized three or more p, and specific responses flu	ctuated. 4/10 of the responders at b	
		ized this peptide, $SI = 3.5$ .		•	
gp160 (65–75)	gp120 (72–82)  Vaccine Vector/Type: p  • Peptides induced T-cell	AHKVWATHACV eptide proliferative response to immuniz	Vaccine zing peptide and to gp160	murine (H-2 <sup>bxk,sxd</sup> )	Sastry1991
gp160 (74–85)	gp120 (74–85 LAI) • Stimulates T-cell prolife	CVPTDPNPQEVV eration in HIV-infected donors	HIV-1 infection	human	Schrier1989
gp160 (74–85)	gp120 (81–92)  Vaccine Vector/Type: p  • Peptides induced T-cell	CVPTNPVPQEVV eptide proliferative response to immuniz	Vaccine zing peptide and to gp160	murine (H-2 <sup>bxk,sxd</sup> )	Sastry1991
gp160 (80–99)	13 usage	NPQEVVLVNTENFNMWKND as broad for a recall response to to cognized this epitope had HLA-D		human digoclonal to primary HIV antigen	Li Pira1998 s, dominated in this case by TCR V $oldsymbol{eta}$
gp160 (81–100)	coli (mLT)  • Epitope name: Peptide  • Helper T-cell proliferati gp120. Promiscuously with regions of local str frequency of immunoge	6 ive responses to gp120 vaccines in immunodominant peptides were in cuctural disorder in proximal N-ter	HIV component: gp120  1 2 mouse strains, CBA/J ardentified in both mice strains rminal segments, suggesting	g 3-D protein structure influences	overlapping peptides that span main of gp120 and were associated
gp160 (81–100)	<ul><li>Promiscuous immunod in the outer domain, pro</li><li>This peptide was recogn</li></ul>	ominant epitopes in gp120 were noximal to regions of structural disc	HIV component: gp120 napped by overlapping peptorder indicated by the cryst rage SI of 8.2, and not by B	tides in CBA/J H-2 <sup>k</sup> and BALB/c I tal structure or by sequence diverge BALB/c mice, so is considered to be	Dai2001 bile toxin from E. coli as adjuvant H-2 <sup>d</sup> mice, and all were found to be ence. e uniquely immunodominant for H-2 <sup>k</sup>
gp160 (81–101)	gp120 (81–101 IIIB)  • Epitope name: B1	PQEVVLVNVTENFNMWKND- MV?	HIV-1 infection	human	Geretti 1994

HXB2 Location	<b>Author's Location</b>	Sequence	Immunogen	Species (HLA)	References
	<ul> <li>overlapping peptide pool</li> <li>After 12 months, most a months, as did 5/15 nor</li> </ul>	ols. 10 of the respondi responses were lost or n-responders. more sensitive and wel	ng patients recognized three or r diminished, and specific respon- l-preserved measure of Th funct	ses fluctuated. 4/10 of the responders at l	
gp160 (92–101)	<ul><li>An HIV seronegative vo</li><li>One T-cell clone reacts</li><li>The first 20-mer peptide</li></ul>	ecombinant protein a colunteer was vaccinate with two overlapping that this clone reacts	ed with rgp120 and a QS21/MPL peptides, and the region of overl	MWKNNMV, and the IIIB version of this	were isolated
gp160 (92–111)	<ul><li>An HIV seronegative vo</li><li>The IIIB version of this</li></ul>	ecombinant protein of a combinant protein of	Strain: W61D HIV component by with rgp120 and a QS21/MPL ce proliferation in the T-cell line	human : gp120 Adjuvant: QS21/MPL adjuvar adjuvant and HIV-1 specific T-cell lines that responds to the W61D version of the	were isolated e peptide NfDmwknDmvEqmhediisl.
gp160 (101–126)	gp120 (101–126)  Vaccine Vector/Type: re  Study showing that T-ce	VKLTPLC ecombinant protein	1 61	murine $(H-2^k)$ on the glycosylation of the protein	Sjolander1996
gp160 (102–114)	gp120 (109–121)  Vaccine Vector/Type: p  • Peptides induced T-cell	-	Vaccine to immunizing peptide and to g	murine (H-2 <sup>bxk</sup> )	Sastry1991
gp160 (102–116)	• B10.D2 (H-2A $^d$ , E $^d$ ) ar	nd B10.A(R5) (H- $2A^b$	Strain: IIIB HIV component: $g$ , $E^b$ ) mice immunized with rec $g$	murine $(H-2^d, H-2^b)$ sp160 <i>Adjuvant</i> : Freund's adjuvant sp160 showed a proliferative response to luding HEDIISLWDQSLK and is referred	
gp160 (102–116)			Vaccine  Strain: IIIB HIV component: gerecognized by mice of three or		Hale1989
gp160 (102–121)		K?	OSLKPCV- HIV-1 infection asymptomatic HIV-1+ patients.	human PBMC from 15/36 patients responded to	Geretti1994 stimulation with gp120 synthetic

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overlapping peptide pools. 10 of the responding patients recognized three or more peptide pools.

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
	months, as did 5/15 non-	responders. nore sensitive and well-preserved	and specific responses fluctuated measure of Th function than proli	•	seline had new responses at 12
gp160 (102–121)	gp160 (109–128 IIIB)	EQMHEDIISLWDQSLKPCVK	HIV-1 infection, Vaccine	human, murine (H- $2^k$ , H- $2^s$ )	Berzofsky1991b, Berzofsky1991a
	<ul> <li>EQMHEDIISLWDQSL</li> <li>Six multideterminant reginfected people</li> <li>This cluster peptide elicipeptides from within thi</li> </ul>	KPCVK encompasses several mugion cluster peptides were evaluated proliferative responses in cells are gion stimulated $H-2^k$ , $H-2^d$ are	ls from vaccinated B10.BR mice (	ant: Freund's adjuvant as a "multideterminant region of the C/HLA backgrounds after vac H-2A <sup>k</sup> , E <sup>k</sup> ) and B10.S(9R) r	on" or cluster peptide excination of mice with gp160, or in
gp160 (105–117)	gp120 (112–124 IIIB) • Epitope name: T2 • Used in a study of pento	HEDIISLWDQSLK	HIV-1 infection ific T-cells	human	Clerici1997
gp160 (105–117)	• Epitope name: T2	HEDIISLWDQSLK Accinia Strain: IIIB HIV comp		human	Berzofsky1988
gp160 (105–117)	gp120 (112–124 IIIB) • Epitope name: T2 • IL-2 production detection	HEDIISLWDQSLK	HIV-1 infection stomatic HIV-positive individuals	human	Clerici1989
gp160 (105–117)	gp120 (112–124 IIIB)  • Epitope name: T2  • Peptides stimulate Th ce	HEDIISLWDQSLK	HIV-1 infection milar patient populations	human	Clerici1991a
gp160 (105–117)	• Epitope name: T2	HEDIISLWDQSLK combinant protein Strain: IIIB individuals with rgp160 results in	Vaccine HIV component: gp160 stronger Th response than does no	human atural infection	Clerici1991b
gp160 (105–117)	gp120 (112–124 IIIB)  • Epitope name: T2  • Cell-mediated immune r	HEDIISLWDQSLK	√-1 exposed seronegative men	human	Clerici1992
gp160 (105–117)	• Epitope name: T2	HEDIISLWDQSLK eptide prime with protein boost ce T-cell help enhances antibody i	Vaccine Strain: IIIB HIV component: gpresponse to gp160 immunization	Rhesus macaque p160	Hosmalin1991

	Author's Location	Sequence	Immunogen	Species (HLA)	References			
gp160 (105–117)	gp120 (112–124 IIIB) • Epitope name: T2	HEDIISLWDQSLK		human	Pinto1995			
	CTL activity analyzed in parallel with Th reactivity in exposed but uninfected health care workers							
gp160 (105–117)	gp120 (112–124 IIIB) • Epitope name: T2	HEDIISLWDQSLK	HIV-1 infection	human	Kaul1999			
	cases) and mucosal geni	ital tract anti-HIV IgA (16/21	e found to frequently have HIV-env per l cases) previously described [Clerici1989], and					
gp160 (105–117)	gp120	HEDIISLWDQSLK	HIV-1 infection, HIV-1 exposed seronegative	l human	Kuhn2001			
	<ul> <li>(measured by a bioassay epitopes P18 MN, P18 I</li> <li>The mothers were predobased on B subtype reag</li> <li>3/33 infants with cord b with cord blood that was</li> <li>Measurable HIV specifications</li> </ul>	y measuring IL2 production in IIIB, T1, T2, and TH4 cominantly infected with subty gents. Solood T help responses to Envis unresponsive to Env peptide in T help responses elicited in	8/86) of cord blood samples from infann a murine cell line and confirmed with type C, but the T help response was determined with the confirmed with the confirmed with the confirmed with the infant transmission of HIV-1.	h a proliferation assay) ag ectable in a number of cor to follow up, and 28/33 v very, and 8/47 contracted	ainst a peptide cocktail containing Th d blood samples despite using peptide vere not infected. 6/53 of the infants HIV intrapartum or via breast-feeding			
gp160 (105–117)	gp120 (112–124 IIIB) Vaccine Strain: IIIB   H	HEDIISLWDQSLK HIV component: gp160	Vaccine	murine (H-2 <sup>k</sup> )	Hale1989			
	<ul><li> Epitope name: T2</li><li> Six multideterminant he</li></ul>	. 0.	nized by mice of three or four MHC ty	pes				
gp160 (105–117)		. 0.	nized by mice of three or four MHC ty  Vaccine	murine (H-2 <sup>k</sup> )	Berzofsky1991b, Berzofsky1991a			
gp160 (105–117)	• Six multideterminant he gp160 (112–124 IIIB)  Vaccine Vector/Type: re • B10.BR (H-2A <sup>k</sup> , E <sup>k</sup> ) mi HEDIISLWDQSLK, and	HEDIISLWDQSLK ecombinant protein Strain: ice immunized with rec gp16 ad DIISLWDQSLKPCVK, an		murine (H-2 <sup>k</sup> )  vant: Freund's adjuvant se to three overlapping per	Berzofsky1991a ptides, QMHEDIISLWDQSL,			
gp160 (105–117)	• Six multideterminant he gp160 (112–124 IIIB)  Vaccine Vector/Type: re • B10.BR (H-2A <sup>k</sup> , E <sup>k</sup> ) mi HEDIISLWDQSLK, and • EQMHEDIISLWDQSL or cluster peptide  gp120 (112–124 BH10) • Epitope name: T2	elper T-cell regions are recognicated the protein of the protein o	Vaccine  IIIB HIV component: gp160 Adjuv 0 showed a strong proliferative respond HEDIISLWDQSLK is common to b	murine (H-2 <sup>k</sup> )  vant: Freund's adjuvant use to three overlapping perfetween them  ISLWDQSLK and is refermurine (H-2 <sup>k</sup> ,s)	Berzofsky1991a ptides, QMHEDIISLWDQSL,			

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
gp160 (108–119)	gp120 (108–119 LAI) • Stimulates T-cell prolife	IISLWDQSLKPC ration in HIV-infected donors	HIV-1 infection	human	Schrier1989
gp160 (110–125)	<ul><li>activation antigens CD2.</li><li>The ability to express ac</li><li>This study investigated 0</li></ul>	5 and CD71 tivation markers in response to H	HIV-1 infection s show reduced ability to proliferate in HIV is retained, but the response to te BMC from patients at various stages ss, or p17 and p24	tanus toxoid recall antigen	is lost
gp160 (111–123)			Vaccine  IIV-1 envelope that stimulates a proli immunized rhesus monkeys	Rhesus macaque ferative response in mice	Nehete1993
gp160 (112–130)	overlapping peptide poo  • After 12 months, most remonths, as did 5/15 non  • IL-2 production was a m	ls. 10 of the responding patients esponses were lost or diminished responders.	tic HIV-1+ patients. PBMC from 15, recognized three or more peptide poor, and specific responses fluctuated. 4 measure of Th function than prolifer	ols. /10 of the responders at base	
gp160 (112–141)	<ul> <li>There was a great breadt</li> </ul>	CTDLGNATNTN combinant protein Strain: NL4	3 HIV component: gp120, gp160 peptides in 19 HIV-1 infected rgp16	human 50 and 17 HIV-1 infected rg	Sitz1999 gp120 vaccine recipients
gp160 (115–126)	gp120 (115–126 LAI) • Stimulates T-cell prolife	SLKPCVKLTPLC ration in HIV-infected donors	HIV-1 infection	human	Schrier1989
gp160 (115–129)		SLKPCVKLTPLCVSL  LA-DR*1101 and HLA-DR*040  e binding pockets of HLA-DR*1	Peptide-HLA interaction 11 with high affinity 101 and HLA-DR*0401, peptides the	human (HLA-DR) at bound both were consid	Gaudebout1997 ered candidates for promiscuous
gp160 (121–140)	gp120 (120–139 89.6)  Vaccine Vector/Type: re coli (mLT)  • Epitope name: Peptide 1	-	Vaccine HIV component: gp120 Adjuvan	murine at: R192G mutant heat-labi	Dai2001 le toxin from enterotoxigenic E.

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References		
	gp120. Promiscuously i with regions of local str frequency of immunoge	mmunodominant pep ructural disorder in pro enic sequences.	tides were identified in both mid	te strains that were located in the ouggesting 3-D protein structure influe	ing 47 overlapping peptides that span iter domain of gp120 and were associated ences Th antigen processing and the		
gp160 (121–141)	<ul><li>overlapping peptide poo</li><li>After 12 months, most r</li></ul>	TN? ses were studied in 36 ols. 10 of the responderesponses were lost or	ing patients recognized three or	more peptide pools.	Geretti1994  ded to stimulation with gp120 synthetic ers at baseline had new responses at 12		
	months, as did 5/15 non  IL-2 production was a n  3/15 responders recogni	nore sensitive and we	ll-preserved measure of Th func rage SI = 3.9.	tion than proliferation.			
gp160 (122–141)	<ul> <li>Epitope name: 1931</li> <li>Hartley guinea pigs wer (DTH) responses after v</li> <li>A total of 7 gp120 pepti gp120. The vaccine deli</li> </ul>	re intradermally inject vaccination, which are ides elicited a delayed ivery system, DNA ve	ted with either recombinant prote e related to Th1 T-cell responses It type hypersensivity (DTH) res ersus rec protein, resulted in the	CFA did not augment responses in conse after vaccination, out of a set	monitored for delayed type hypersensivity animals vaccinated with plasmid. of 60 overlapping peptides that spanned		
gp160 (122–141)	gp120 (122–141 IIIB)  • Epitope name: B5	LTPLCVSLKCTD	LKNDTNT- HIV-1 infection	human	Geretti1994		
	<ul> <li>Th proliferative responses were studied in 36 asymptomatic HIV-1+ patients. PBMC from 15/36 patients responded to stimulation with gp120 synthetic overlapping peptide pools. 10 of the responding patients recognized three or more peptide pools.</li> <li>After 12 months, most responses were lost or diminished, and specific responses fluctuated. 4/10 of the responders at baseline had new responses at 12 months, as did 5/15 non-responders.</li> <li>1/15 responders recognized this peptide, SI = 3.1.</li> </ul>						
gp160 (136–155)	<ul> <li>Epitope name: 1932</li> <li>Hartley guinea pigs wer (DTH) responses after v</li> <li>A total of 7 gp120 pepti gp120. The vaccine deli</li> </ul>	re intradermally inject vaccination, which are ides elicited a delayed ivery system, DNA ve	ted with either recombinant prote e related to Th1 T-cell responses I type hypersensivity (DTH) res ersus rec protein, resulted in the	. CFA did not augment responses in conse after vaccination, out of a set	monitored for delayed type hypersensivity animals vaccinated with plasmid. of 60 overlapping peptides that spanned		

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References		
gp160 (138–159)	gp120 (141–160 W6.ID) TTSNGWTGEIRKGEIKNCSF Vaccine human Jones1999  Vaccine Vector/Type: recombinant protein Strain: W61D HIV component: gp120 Adjuvant: QS21/MPL adjuvant  An HIV seronegative volunteer was vaccinated with rgp120 and a QS21/MPL adjuvant and HIV-1 specific T-cell lines were isolated  The IIIB version of this peptide does not induce proliferation in the T-cell line that responds to the W61D version of the peptide: IIIB: ttsnSSGRMIMEgeikncsf.						
gp160 (142–161)	<ul> <li>overlapping peptide pool</li> <li>After 12 months, most remonths, as did 5/15 non-</li> <li>IL-2 production was a m</li> <li>Five peptides were recogwere in or near V2, the o</li> </ul>	s. 10 of the responding patients esponses were lost or diminished responders.  ore sensitive and well-preserved	atic HIV-1+ patients. PBMC from recognized three or more peptide I, and specific responses fluctuated I measure of Th function than prol 42-161), C3 (aa 152-171), C5 (aa 73 and V4 loops.	pools. d. 4/10 of the responders at liferation.	Geretti1994  o stimulation with gp120 synthetic baseline had new responses at 12  and G4 (aa 380-393). The first three		
gp160 (147–168)	gp120 (152–173 NL43)  Vaccine Vector/Type: rec  There was a great breadtl	MMMEKGEIKNCSFNISTSI- RGK combinant protein <i>Strain:</i> NL4 h of proliferative response to en	Vaccine  43 HIV component: gp120, gp16 v peptides in 19 HIV-1 infected rg		Sitz1999 rgp120 vaccine recipients		
gp160 (152–171)	<ul> <li>Over 50% of vaccinees had a stimulation index of greater than 5 to this peptide</li> <li>gp120 (152–171 IIIB) GEIKNCSFNISTSIRGKVQ- HIV-1 infection human Geretti1994</li> <li>Epitope name: C3</li> <li>Th proliferative responses were studied in 36 asymptomatic HIV-1+ patients. PBMC from 15/36 patients responded to stimulation with gp120 synthetic overlapping peptide pools. 10 of the responding patients recognized three or more peptide pools.</li> <li>After 12 months, most responses were lost or diminished, and specific responses fluctuated. 4/10 of the responders at baseline had new responses at 12 months, as did 5/15 non-responders.</li> <li>IL-2 production was a more sensitive and well-preserved measure of Th function than proliferation.</li> <li>Five peptides were recognized most frequently: C2 (aa 142-161), C3 (aa 152-171), C5 (aa 172-191), E5 (aa 272-291) and G4 (aa 380-393). The first thre were in or near V2, the other two were proximal to the V3 and V4 loops.</li> <li>4/15 responders recognized this immunodominant peptide, average SI = 4.4.</li> </ul>						
gp160 (155–169)	<ul><li>adjuvant</li><li>This epitope is located in</li><li>C57BL/6 mice were imm</li></ul>	the V2 region of UG92005 (UG) nunized with a prime-boost strat	G, clade D) and the hybridoma tha	at recognized it used V $\beta$ 5 tigens: Mice were primed w	Surman2001  onent: gp140 Adjuvant: Freund's  vith DNA given i.m., 3-4 weeks later		

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References			
	• The vaccinia construct is a pSC11-based VV vector with the first 38 amino acids contributed by BH10 and the rest of gp120 and gp41 by the vaccine strain, the DNA construct is in the pJW4303 vector with a CMV promotor, and the purified protein is expressed from the pJW4303 vector transfected into CHO-K1 cells							
	<ul> <li>Ten days after the final and Vβ usage was dete</li> </ul>		ere made and tested for IL-2 production	using either B6 spleen cells or H	-2 IA <sup>b</sup> transfected L cells as targets			
	• Mice were immunized	with an Env from eith de D vaccine isolated	ner one of two clades: HIV-1 1007, a cla from Uganda in 1992 through the WHO m six mice		vidual from Memphis Tennesee, and			
	• H-2 IA <sup>b</sup> restricted T-he in V4C4, and 7 in gp41	lper epitopes were co.).	ncentrated in 5 distinct regions within the					
		on may be influenced	eavily glycosylated regions of the Env se by differential antigen processing and the ways.					
gp160 (155–169)			GKV LA-DR*0401 with high affinity FHLA-DR*1101 and HLA-DR*0401, po	human (HLA-DR) eptides that bound both were con	Gaudebout1997 sidered candidates for promiscuous			
gp160 (159–178)	coli (mLT)  • Epitope name: Peptide  • Helper T-cell proliferat gp120. Promiscuously with regions of local strangering frequency of immunogeness.	ecombinant protein  14  ive responses to gp12  immunodominant per  ructural disorder in pr  enic sequences.	KEYALFNR Vaccine Strain: 89.6 HIV component: gp120  0 vaccines in 2 mouse strains, CBA/J an otides were identified in both mice strain oximal N-terminal segments, suggesting LB/c mice tested, and in 4/10 CBA/J mice	d BALB/c, were mapped using 4 as that were located in the outer d g 3-D protein structure influences	7 overlapping peptides that span omain of gp120 and were associated			
gp160 (162–181)	gp120 (162–181 IIIB)  Vaccine Vector/Type: I  HIV-1 env DNA vaccin	ONA Strain: IIIB	AFFYKLDI Vaccine  HIV component: ENV  ponse to this epitope in a rhesus monkey	Rhesus macaque	Lekutis1997b			
gp160 (162–182)	gp120 (162–182 IIIB)  • Epitope name: C4	STSIRGKVQKEY II?	AFFYKLD- HIV-1 infection	human	Geretti1994			
	<ul> <li>Th proliferative responsions overlapping peptide potential.</li> <li>After 12 months, most months, as did 5/15 not</li> </ul>	ols. 10 of the respond responses were lost on-responders. more sensitive and we	asymptomatic HIV-1+ patients. PBMC ling patients recognized three or more per diminished, and specific responses fluctell-preserved measure of Th function that = 3.3.	eptide pools. ctuated. 4/10 of the responders at				

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References			
gp160 (169–189)	gp120 (141–160 W6.ID)	VQKEYALFYNLDVVPIDDD- NA	Vaccine	human	Jones1999			
	<ul> <li>An HIV seronegative vol</li> </ul>	unteer was vaccinated with rgp1 peptide does not induce proliferance.	20 and a QS21/MPL adjuvar	Adjuvant: QS21/MPL adjuvant and HIV-1 specific T-cell lines ponds to the W61D version of the W61D version	were isolated			
gp160 (172–191)		EYAFFYKLDIIPIDNDTTSY NA <i>Strain:</i> IIIB <i>HIV compon</i> induced Th cell response to this	ent: ENV	Rhesus macaque	Lekutis1997b			
gp160 (172–191)	gp120 (172–191 IIIB)	EYAFFYKLDIIPIDNDTTS- Y?	HIV-1 infection	human	Geretti1994			
	<ul> <li>overlapping peptide pool</li> <li>After 12 months, most remonths, as did 5/15 non-</li> <li>IL-2 production was a m</li> <li>Five peptides were recogwere in or near V2, the o</li> </ul>	s. 10 of the responding patients esponses were lost or diminished responders.  ore sensitive and well-preserved	recognized three or more per l, and specific responses fluct measure of Th function than 42-161), C3 (aa 152-171), C5 3 and V4 loops.	otide pools. uated. 4/10 of the responders at proliferation.	baseline had new responses at 12 and G4 (aa 380-393). The first three			
gp160 (175–189)	adjuvant	_			Surman2001  onent: gp140 Adjuvant: Freund's			
	<ul> <li>This epitope is located in the V2 region of UG92005 (UG, clade D) and the Vβ usage of the TCR was not determined</li> <li>C57BL/6 mice were immunized with a prime-boost strategy involving three HIV-1 Env antigens: Mice were primed with DNA given i.m., 3-4 weeks later boosted with VV, and 3-4 weeks later boosted again with purified protein in Freund's adjuvant</li> <li>The vaccinia construct is a pSC11-based VV vector with the first 38 amino acids contributed by BH10 and the rest of gp120 and gp41 by the vaccine strain, the DNA construct is in the pJW4303 vector with a CMV promotor, and the purified protein is expressed from the pJW4303 vector transfected into CHO-K1 cells</li> </ul>							
	and $V\beta$ usage was determage.  • Mice were immunized whiv-1 92UG005, a clade	nined	o clades: HIV-1 1007, a clade	-	$^{2}$ IA $^{b}$ transfected L cells as targets idual from Memphis Tennesee, and			
		per epitopes were concentrated in	n 5 distinct regions within the	Env sequence (2 clonotype resp	onses in V2, 26 in C2, 22 in V3, 23			

<b>HXB2</b> Location	<b>Author's Location</b>	Sequence	Immunogen	Species (HLA)	References
	non-uniform localization			sequence, in exposed, non-helical s the glycosylation site proximity ma	
gp160 (186–215)	gp120 (191–220 NL43)	NDTTSYTLTSCNTSVITQA- CPKVSFEPIPI	Vaccine	human	Sitz1999
	• There was a great breadt	combinant protein <i>Strain:</i> NL4 h of proliferative response to envada a stimulation index of greater	peptides in 19 HIV-1 infe	20, gp160 ected rgp160 and 17 HIV-1 infected	1 rgp120 vaccine recipients
gp160 (188–207)	coli (mLT)  • Epitope name: Peptide 1  • Helper T-cell proliferativ gp120. Promiscuously ir with regions of local strufrequency of immunoger	7 ye responses to gp120 vaccines in nmunodominant peptides were in cutural disorder in proximal N-tentic sequences.	HIV component: gp120 a 2 mouse strains, CBA/J a dentified in both mice stra rminal segments, suggesting	and BALB/c, were mapped using 4	omain of gp120 and were associated Th antigen processing and the
gp160 (188–207)	<ul> <li>Promiscuous immunodo in the outer domain, prov</li> <li>This peptide was recogniso is considered to be un</li> </ul>	minant epitopes in gp120 were n ximal to regions of structural disc	HIV component: gp120 napped by overlapping per order indicated by the crystage SI of 9.8, one of the twick	otides in CBA/J H-2 <sup>k</sup> and BALB/c stal structure or by sequence diverg we immunodominant peptides in C	Dai2001 abile toxin from E. coli as adjuvant $H-2^d$ mice, and all were found to be ence. BA/J mice, and not by BALB/c mice,
gp160 (192–211)	<ul> <li>gp120 (192–211 IIIB)</li> <li>Epitope name: D2</li> <li>Th proliferative response overlapping peptide pool</li> <li>After 12 months, most remonths, as did 5/15 non-</li> </ul>	KLTSCNTSVITQACPKVSF—E? es were studied in 36 asymptomals. 10 of the responding patients esponses were lost or diminished responders. ore sensitive and well-preserved	HIV-1 infection  tic HIV-1+ patients. PBM recognized three or more part and specific responses fluit	human C from 15/36 patients responded to peptide pools. actuated. 4/10 of the responders at	
gp160 (193–218)	gp120 (193–218)  Vaccine Vector/Type: rec	LTSCNSVITQACPKVSFEP- IPIHYC combinant protein HIV compor Il determinants from glycoprotein	nent: gp160	murine $(H-2^{d,b})$ e glycosylation of the protein	Sjolander1996

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References			
gp160 (198–212)	<ul><li>adjuvant</li><li>This epitope is located</li></ul>	l in the C2 region of 1007 (US	, clade B) and the V $\beta$ usage	murine (H-2 $IA^b$ ) B), UG92005 (clade D) HIV comp of the TCRs for two clonotypes was	$V\beta$ 3 and $V\beta$ 8.1-2			
	<ul><li>boosted with VV, and</li><li>The vaccinia construct</li></ul>	3-4 weeks later boosted again t is a pSC11-based VV vector	with purified protein in Freu with the first 38 amino acids	and's adjuvant contributed by BH10 and the rest of	with DNA given i.m., 3-4 weeks later gp120 and gp41 by the vaccine strain w4303 vector transfected into			
	the DNA construct is in the pJW4303 vector with a CMV promotor, and the purified protein is expressed from the pJW4303 vector transfected into CHO-K1 cells  • Ten days after the final boost, hybridomas were made and tested for IL-2 production using either B6 spleen cells or H-2 IA <sup>b</sup> transfected L cells as targets							
	and $V\beta$ usage was determined  • Mice were immunized with an Env from either one of two clades: HIV-1 1007, a clade B strain isolated from an individual from Memphis Tennesee, and HIV-1 92UG005, a clade D vaccine isolated from Uganda in 1992 through the WHO							
	<ul> <li>80 unique clonotypes were characterized from six mice</li> <li>H-2 IA<sup>b</sup> restricted T-helper epitopes were concentrated in 5 distinct regions within the Env sequence (2 clonotype responses in V2, 26 in C2, 22 in V3, 23 in V4C4, and 7 in gp41).</li> </ul>							
	non-uniform localizat			v sequence, in exposed, non-helical s d the glycosylation site proximity m				
gp160 (198–215)	Env (1007) <b>Vaccine</b> Vector/Type: adjuvant	TSVITQACPKVSFEPIP DNA, vaccinia, recombinant p		murine (H-2 IA <sup>b</sup> ) B), UG92005 (clade D) HIV comp	Surman2001 onent: gp140 Adjuvant: Freund's			
	• C57BL/6 mice were i	I in the C2 region of 1007 (US mmunized with a prime-boost 3-4 weeks later boosted again	strategy involving three HIV	-1 Env antigens: Mice were primed v	with DNA given i.m., 3-4 weeks later			
	• The vaccinia construc	t is a pSC11-based VV vector	with the first 38 amino acids		gp120 and gp41 by the vaccine strain W4303 vector transfected into			
	• Ten days after the final boost, hybridomas were made and tested for IL-2 production using either B6 spleen cells or H-2 IA <sup>b</sup> transfected L cells as targets and Vβ usage was determined							
	HIV-1 92UG005, a cl	I with an Env from either one of ade D vaccine isolated from U were characterized from six m	ganda in 1992 through the W	clade B strain isolated from an indiv /HO	idual from Memphis Tennesee, and			
	<ul> <li>H-2 IA<sup>b</sup> restricted T-l in V4C4, and 7 in gp<sup>2</sup></li> </ul>	<ul> <li>H-2 IA<sup>b</sup> restricted T-helper epitopes were concentrated in 5 distinct regions within the Env sequence (2 clonotype responses in V2, 26 in C2, 22 in V3, 23 in V4C4, and 7 in gp41).</li> </ul>						
	non-uniform localizat			v sequence, in exposed, non-helical s d the glycosylation site proximity m				
gp160 (199–211)	Env (204–216) <b>Vaccine</b> Vector/Type:	SVITQACSKVSFE	Vaccine	Rhesus macaque	Nehete1993			

others not determined

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
			HIV-1 envelope that stimulates a e was observed in 3/3 immunized		
gp160 (199–211)	Env (204–216)  • HIV-infected chimpanze Env	SVITQACSKVSFE ses and HIV-positive patients sho	HIV-1 infection ow positive proliferative response	human, chimpanzee es to multiple peptides from fiv	Nehete1998b ve conserved regions of the HIV-1
gp160 (199–211)	gp120 (204–216)  Vaccine Vector/Type: pe  • Peptides induced T-cell	SVITQACSKVSFE eptide proliferative response in mice re	Vaccine presenting four haplotypes	murine (H-2 <sup>bxk,sxd</sup> )	Sastry1991
gp160 (200–214)		VITQACPKVSFEPIP LA-DR*1101 and HLA-DR*040 re binding pockets of HLA-DR*		human (HLA-DR)  des that bound both were consi	Gaudebout1997  idered candidates for promiscuous
gp160 (201–212)	<ul> <li>adjuvant</li> <li>This epitope is located it</li> <li>The epitope described he (TSVITQACPKVSFEP)</li> <li>C57BL/6 mice were implementation boosted with VV, and 3-</li> <li>The vaccinia construct is the DNA construct is in CHO-K1 cells</li> <li>Ten days after the final beand Vβ usage was detered mice were immunized white HIV-1 92UG005, a clade 80 unique clonotypes were invested to the in V4C4, and 7 in gp41)</li> <li>Epitope hotspots tended non-uniform localization</li> </ul>	n the C2 region of 1007 (US, clasere is the region of overlap of twand ITQACPKVSFEPIPI) munized with a prime-boost stra 4 weeks later boosted again with s a pSC11-based VV vector with the pJW4303 vector with a CM boost, hybridomas were made ar mined with an Env from either one of twe D vaccine isolated from Ugand ere characterized from six mice per epitopes were concentrated in to be proximal to heavily glyco	ade B) and the $V\beta$ usage of the T $V_0$ 15 mers that were both able to tegy involving three HIV-1 Env at the purified protein in Freund's adjusted in the first 38 amino acids contributed v promotor, and the purified protein that tested for IL-2 production using two clades: HIV-1 1007, a clade Eda in 1992 through the WHO	FCR was $V\beta 3$ ostimulate IL-2 production from the prime with street of the production of the product	ith DNA given i.m., 3-4 weeks later p120 and gp41 by the vaccine strain, 4303 vector transfected into 2 IA <sup>b</sup> transfected L cells as targets dual from Memphis Tennesee, and onses in V2, 26 in C2, 22 in V3, 23 rands of the protein. The
gp160 (206–220)	adjuvant	_		-	Surman2001  nent: gp140 Adjuvant: Freund's  ge of V $\beta$ 4,6,7,8.1-2,8.3,11,12 and

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
	<ul> <li>boosted with VV, and 3</li> <li>The vaccinia construct the DNA construct is in CHO-K1 cells</li> <li>Ten days after the final and Vβ usage was dete</li> <li>Mice were immunized HIV-1 92UG005, a cla</li> <li>80 unique clonotypes v</li> <li>H-2 IA<sup>b</sup> restricted T-he in V4C4, and 7 in gp4</li> <li>Epitope hotspots tende</li> </ul>	3-4 weeks later boosted is a pSC11-based VV in the pJW4303 vector value boost, hybridomas we be ermined with an Env from either de D vaccine isolated from elper epitopes were contacted by the boost of the proximal to head on may be influenced by the pSC11-based on the pSC11-base	with a CMV promotor, and the purified re made and tested for IL-2 production or one of two clades: HIV-1 1007, a clayrom Uganda in 1992 through the WHO is six mice incentrated in 5 distinct regions within the willy glycosylated regions of the Env so by differential antigen processing and the six mice in the six mice	's adjuvant intributed by BH10 and the rest of d protein is expressed from the pJV in using either B6 spleen cells or H ade B strain isolated from an individual of the Env sequence (2 clonotype respectively) equence, in exposed, non-helical sequence.	gp120 and gp41 by the vaccine strain, W4303 vector transfected into  2-2 IA <sup>b</sup> transfected L cells as targets vidual from Memphis Tennesee, and ponses in V2, 26 in C2, 22 in V3, 23 strands of the protein. The
gp160 (206–225)	gp120 (211–230 MN)  Vaccine Vector/Type: p  Epitope name: 1957  Hartley guinea pigs we (DTH) responses after  A total of 7 gp120 pep gp120. The vaccine de	PKISFEPIPIHYO protein, DNA Strain: ere intradermally injector vaccination, which are tides elicited a delayed livery system, DNA ve	CAPAGFAI Vaccine MN HIV component: gp120 Adju	plasmid expressed gp120 and mon did not augment responses in anin after vaccination, out of a set of 60 hition of distinct peptides.	nitored for delayed type hypersensivity nals vaccinated with plasmid.  O overlapping peptides that spanned
gp160 (206–230)	gp120 (206–230)  Vaccine Vector/Type: 1  • Study showing that T-c	ILKCNN recombinant protein	CAPAGFA— Vaccine  HIV component: gp160 glycoproteins can be dependent on the	murine $(H-2^{d,b})$ glycosylation of the protein	Sjolander1996
gp160 (208–218)	adjuvant  This epitope is located  The epitope described (PKITFEPIPIHYCAP)  C57BL/6 mice were in boosted with VV, and 3  The vaccinia construct the DNA construct is in CHO-K1 cells	in the C2 region of UC here is the region of over and ITFEPIPIHYCAP munized with a prime 3-4 weeks later boosted is a pSC11-based VV in the pJW4303 vector whose, hybridomas we	-boost strategy involving three HIV-1 again with purified protein in Freund	ognized by two hybridomas with Vole to stimulate IL-2 production fr Env antigens: Mice were primed v's adjuvant intributed by BH10 and the rest of d protein is expressed from the pJV	$^{7}\beta$ usage V $\beta$ 12 and not determined om the hybridoma with DNA given i.m., 3-4 weeks later gp120 and gp41 by the vaccine strain, W4303 vector transfected into

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
	<ul> <li>HIV-1 92UG005, a cla</li> <li>80 unique clonotypes v</li> <li>H-2 IA<sup>b</sup> restricted T-he in V4C4, and 7 in gp4</li> <li>Epitope hotspots tende non-uniform localization</li> </ul>	de D vaccine isolated from swere characterized from selper epitopes were concell).  d to be proximal to heavi	m Uganda in 1992 through the WH six mice entrated in 5 distinct regions within the glycosylated regions of the Enveloifferential antigen processing and	the Env sequence (2 clonotype ressequence, in exposed, non-helical sequence)	
gp160 (208–222)	<ul> <li>adjuvant</li> <li>This epitope is located determined</li> <li>C57BL/6 mice were in boosted with VV, and β</li> <li>The vaccinia construct the DNA construct is in CHO-K1 cells</li> <li>Ten days after the final and Vβ usage was dete</li> <li>Mice were immunized HIV-1 92UG005, a cla</li> <li>80 unique clonotypes v</li> <li>H-2 IA<sup>b</sup> restricted T-he in V4C4, and 7 in gp4</li> <li>Epitope hotspots tende non-uniform localization</li> </ul>	in the C2 region of UG9 munized with a prime-b 3-4 weeks later boosted a is a pSC11-based VV ve n the pJW4303 vector wi boost, hybridomas were ermined with an Env from either de D vaccine isolated fro were characterized from selper epitopes were conce 1). d to be proximal to heavi	ant protein Strain: 1007 (clade B 2005 (UG, clade D) and it was reconsisted that the purified protein in Freunch and the purified protein in Freunch and the purified that CMV promotor, and the purified made and tested for IL-2 production one of two clades: HIV-1 1007, a communication of the CMV promotor and the wholes in the purified made and tested for IL-2 production one of two clades: HIV-1 1007, a communication of the CMV promotor in the Six mice contracted in 5 distinct regions within the purification of the Environmental antigen processing and	egnized by five hybridomas with V Env antigens: Mice were primed of the distributed by BH10 and the rest of the protein is expressed from the properties of the protein is expressed from the properties of the sequence of the Env sequence (2 clonotype resequence, in exposed, non-helical)	with DNA given i.m., 3-4 weeks later gp120 and gp41 by the vaccine strain, W4303 vector transfected into I-2 IA <sup>b</sup> transfected L cells as targets vidual from Memphis Tennesee, and ponses in V2, 26 in C2, 22 in V3, 23 strands of the protein. The
gp160 (208–227)	coli (mLT)  • Epitope name: Peptide  • Helper T-cell proliferal gp120. Promiscuously with regions of local st frequency of immunog	recombinant protein Str 19 tive responses to gp120 v immunodominant peptid tructural disorder in prox- genic sequences.	rain: 89.6 HIV component: gp120 raccines in 2 mouse strains, CBA/J a	and BALB/c, were mapped using 4 ins that were located in the outer d	omain of gp120 and were associated
gp160 (210–223)	gp120 (215–228) <b>Vaccine</b> <i>Vector/Type</i> : 1	FEPIPIHYCAFPGF peptide	Vaccine	murine (H-2 <sup>bxk</sup> )	Sastry1991

HXB2 Location	<b>Author's Location</b>	Sequence	Immunogen	Species (HLA)	References
	• Peptides induced T-cell	proliferative response to immun	izing peptide and to gp160		
gp160 (212–231)	Vaccine Vector/Type: re	lunteer was vaccinated with rgp	Vaccine 1D HIV component: gp120 1 120 and a QS21/MPL adjuvant a		
gp160 (212–231)	overlapping peptide poo  • After 12 months, most remonths, as did 5/15 non  • IL-2 production was a m	ls. 10 of the responding patients esponses were lost or diminished responders.	atic HIV-1+ patients. PBMC fro recognized three or more peptic d, and specific responses fluctua I measure of Th function than pro-	de pools.  sted. 4/10 of the responders at base.	Geretti1994 stimulation with gp120 synthetic aseline had new responses at 12
gp160 (214–220)	<ul> <li>adjuvant</li> <li>This epitope is located in</li> <li>The epitope described he (PKVSFEPIPIHYCAP at PKVSFEPIPIHYCAP at</li></ul>	n the C2 region of 1007 (US, clasere is the region of overlap of two and PIHYCAPAGFAILKC) nunized with a prime-boost strated weeks later boosted again with a prime-boost strate and properties of a pSC11-based VV vector with the pJW4303 vector with a CM properties of the pJW4303 vector with a CM properties of the pJW4304 vector with an Env from either one of two properties of the pJ vaccine isolated from Ugandere characterized from six mice per epitopes were concentrated in the proximal to heavily glyco	ade B) and the $V\beta$ usage of the To 15 mers that were both able to tegy involving three HIV-1 Env in purified protein in Freund's admitted first 38 amino acids contributed promotor, and the purified protein detected for IL-2 production using the volume of the tested for IL-1 1007, a clade Fela in 1992 through the WHO	TCR was not determined o stimulate IL-2 production from antigens: Mice were primed with butted by BH10 and the rest of grotein is expressed from the pJW-ing either B6 spleen cells or H-2 B strain isolated from an individence of the sequence (2 clonotype response, in exposed, non-helical strain isolated from an individence, in exposed, non-helical strain isolated from an individence of the sequence in exposed, non-helical strain isolated from an individence of the sequence in exposed, non-helical strain isolated from an individence of the sequence of th	th DNA given i.m., 3-4 weeks later p120 and gp41 by the vaccine strain, 4303 vector transfected into e1Ab transfected L cells as targets dual from Memphis Tennesee, and onses in V2, 26 in C2, 22 in V3, 23 ands of the protein. The
gp160 (215–225)	adjuvant	_	Vaccine in Strain: 1007 (clade B), UG ade B) and the $V\beta$ usage of the T	· · · · · · · · · · · · · · · · · · ·	Surman2001  nent: gp140 Adjuvant: Freund's

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References				
		here is the region of ove and IHYCAPAGFAILK	rlap of two 15 mers that were both ab (CN)	ble to stimulate IL-2 production fr	om the hybridoma				
	• C57BL/6 mice were immunized with a prime-boost strategy involving three HIV-1 Env antigens: Mice were primed with DNA given i.m., 3-4 weeks later boosted with VV, and 3-4 weeks later boosted again with purified protein in Freund's adjuvant								
		<ul> <li>The vaccinia construct is a pSC11-based VV vector with the first 38 amino acids contributed by BH10 and the rest of gp120 and gp41 by the vaccine strain, the DNA construct is in the pJW4303 vector with a CMV promotor, and the purified protein is expressed from the pJW4303 vector transfected into CHO-K1 cells</li> </ul>							
	<ul> <li>Ten days after the final boost, hybridomas were made and tested for IL-2 production using either B6 spleen cells or H-2 IA<sup>b</sup> transfected L cells and Vβ usage was determined</li> <li>Mice were immunized with an Env from either one of two clades: HIV-1 1007, a clade B strain isolated from an individual from Memphis Tent HIV-1 92UG005, a clade D vaccine isolated from Uganda in 1992 through the WHO</li> <li>80 unique clonotypes were characterized from six mice</li> <li>H-2 IA<sup>b</sup> restricted T-helper epitopes were concentrated in 5 distinct regions within the Env sequence (2 clonotype responses in V2, 26 in C2, 25 in V4C4, and 7 in gp41).</li> </ul>								
	non-uniform localization		rily glycosylated regions of the Env so differential antigen processing and the ys.						
gp160 (216–225)	Env (UG92005)  Vaccine Vector/Type: 1 adjuvant	HYCAPAGFAI DNA, vaccinia, recombi	Vaccine nant protein Strain: 1007 (clade B).	murine (H-2 IA <sup>b</sup> ) , UG92005 (clade D) HIV comp	Surman2001 conent: gp140 Adjuvant: Freund's				
	<ul> <li>This epitope is located in the C2 region of UG92005 (UG, clade D) and Vβ usage of its TCR was not determined</li> <li>The epitope described here is the region of overlap of two 15 mers that were both able to stimulate IL-2 production from the hybridoma</li> </ul>								
	(EPIPIHYCAPAGFAI and HYCAPAGFAILKCND)								
			poost strategy involving three HIV-1 lagain with purified protein in Freund		with DNA given i.m., 3-4 weeks later				
			ector with the first 38 amino acids coith a CMV promotor, and the purified		gp120 and gp41 by the vaccine strain, W4303 vector transfected into				
			e made and tested for IL-2 production	using either B6 spleen cells or H	I-2 IA <sup>b</sup> transfected L cells as targets				
			one of two clades: HIV-1 1007, a cla om Uganda in 1992 through the WHO		vidual from Memphis Tennesee, and				
		elper epitopes were conc	six mice entrated in 5 distinct regions within t	he Env sequence (2 clonotype res	ponses in V2, 26 in C2, 22 in V3, 23				
	<ul> <li>in V4C4, and 7 in gp41).</li> <li>Epitope hotspots tended to be proximal to heavily glycosylated regions of the Env sequence, in exposed, non-helical strands of the protein. The non-uniform localization may be influenced by differential antigen processing and the glycosylation site proximity may allow binding to lectins and promote trafficking through processing pathways.</li> </ul>								
gp160 (220–234)	gp120 (225–240 SF2) • T-cell line derived from	PAGFAILKCNNKTI n unprimed, uninfected i			Manca1993				

HXB2 Location	<b>Author's Location</b>	Sequence	Immunogen	Species (HLA)	References
		d with either synthetic peptiond 450-D enhance APC gp12			
gp160 (220–234)	<ul> <li>Epitope name: pep24</li> <li>This previously describ the bacterium Streptocc</li> <li>Recombinant bacteria s</li> </ul>	occus gordonii. howed efficient MHC class l	epitope was fused to the streptoo	-	Pozzi1994 6.1), for expression on the surface of oliferative response in a human T cell
gp160 (220–235)	Peptide priming does no	PAGFAILKCNNKTFNY PBMC from non-infected incompared that always induce T-cells that T-cells that recognize this possible.	recognize whole protein	human (DR2)	Manca1995b
gp160 (220–235)	Listeria monocytogenes	) PAGFAILKCNNKTFNY s, an intracellular pathogen writer to deliver this gp120 epi		human (DR2) s and can escape from the phagos	Guzman1998 ome to replicate in the cytoplasm, was
gp160 (220–235)	<ul><li>gp120 pep24 epitope ex</li><li>The glutathione S-trans</li></ul>	ferase (GST)-peptide system			Fenoglio1999 nrelated amino acid sequence en this peptide was expressed at the
gp160 (222–241)	<ul> <li>overlapping peptide poo</li> <li>After 12 months, most months, as did 5/15 nor</li> <li>IL-2 production was a r</li> </ul>	ols. 10 of the responding pattersponses were lost or diminaresponders.	stomatic HIV-1+ patients. PBMC ients recognized three or more peished, and specific responses fluctured measure of Th function that	eptide pools. etuated. 4/10 of the responders at	Geretti1994 o stimulation with gp120 synthetic baseline had new responses at 12
gp160 (223–231)	<ul><li>22 usage</li><li>Donor of PBMC that re</li></ul>	as broad for a recall response cognized this epitope had H			Li Pira1998 ns, dominated in this case by TCR V $\beta$
gp160 (223–231)	One Th line was stimul	al stimulatory sequence defirated by gp120, one by a Glu	in vitro stimulation ned for two Th lines stimulated in athione-S-transferase (GST)-pep abrogated activity for the GST-pe		Manca1996 a gp120 stimulated line

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
	Constructs combining C	SST and the PAGFAILKCNNK	ΓFNY gp120 peptide at the C-term en	nd of GST stimulated Th cel	Is but not at the N-term end
gp160 (223–231)	<ul><li> One Th line was stimula</li><li> Alanine substitutions at</li><li> Constructs linking GST did not</li></ul>	al stimulatory sequence defined atted by p66, one by a Glutathion position 914, 196, and 202 abro to the PAGFAILKCNNKTFNY	in vitro stimulation for two Th lines stimulated in vitro ne-S-transferase (GST)-peptide fusion ogated activity for the GST-peptide sti gp120 peptide at the C-term end of G ssive or non-permissive, presentation	imulated line, but not for a g GST stimulated Th cells, co	nstructs linking at the N-term end
gp160 (223–231)	<ul><li>Substitutions in position</li><li>Most natural analogs the</li><li>Position 237 and 244 w.</li></ul>		all cause reduced recognition Eluding peptides based on clade A, B, an antagonistic response and the natur		Fenoglio2000 to loose antigenicity
gp160 (230–245)		NKTFNGKGPCTNVSTY BMC from non-infected individual indiv		human	Manca1995b
gp160 (232–251)	<ul> <li>overlapping peptide poc</li> <li>After 12 months, most r months, as did 5/15 non</li> <li>IL-2 production was a n</li> </ul>	ols. 10 of the responding patient esponses were lost or diminished responders.	natic HIV-1+ patients. PBMC from 15 s recognized three or more peptide poed, and specific responses fluctuated. 4 d measure of Th function than prolife	ools. 4/10 of the responders at base	
gp160 (235–247)		ed from conserved region of the	Vaccine  HIV-1 envelope that stimulates a prol /3 immunized rhesus monkeys, with a		Nehete1993 the other two
gp160 (238–257)	<ul><li>coli (mLT)</li><li>Epitope name: Peptide 2</li><li>Helper T-cell proliferati gp120. Promiscuously i</li></ul>	22 ve responses to gp120 vaccines mmunodominant peptides were uctural disorder in proximal N-t	T Vaccine .6 HIV component: gp120 Adjuvation in 2 mouse strains, CBA/J and BALB identified in both mice strains that we terminal segments, suggesting 3-D pro-	3/c, were mapped using 47 cere located in the outer dom	verlapping peptides that span ain of gp120 and were associated

HXB2 Location	<b>Author's Location</b>	Sequence	Immunogen	Species (HLA)	References
	• This peptide was highly	reactive in 6/10 BALB/c mice te	sted, but not in any (0/10) CBA	A/J mice.	
gp160 (240–255)	gp120 (IIIB) • Peptide stimulation of Pl	TNVSTVQCTHGRPIY BMC from non-infected individu	in vitro stimulation aals in vitro	human	Manca1995b
gp160 (242–261)	gp120 (242–261 IIIB)	VSTVQCTHGIRPVVSTQLL- L?	HIV-1 infection	human	Geretti 1994
	<ul> <li>After 12 months, most remonths, as did 5/15 non-</li> </ul>	ls. 10 of the responding patients esponses were lost or diminished responders. ore sensitive and well-preserved	recognized three or more pepti , and specific responses fluctua	ide pools. ated. 4/10 of the responders at	o stimulation with gp120 synthetic baseline had new responses at 12
gp160 (242–261)	gp120 (242–261 IIIB)	VSTVQCTHGIRPVVSTQLLL sitope was described in SHIV-89.		Rhesus macaque (DRB1*0406)	Lekutis1997a
gp160 (250–265)	gp120 (IIIB)  • Peptide stimulation of Pl	GIRPIVSTQLLLNGSC  BMC from non-infected individut t always induce T-cells that recog	in vitro stimulation nals in vitro	human	Manca1995b
gp160 (252–271)	gp120 (252–271 IIIB)	RPVVSTQLLLNGSLAEEEV- V?	HIV-1 infection	human	Geretti1994
	overlapping peptide pool     After 12 months, most remonths, as did 5/15 non-     IL-2 production was a m	ls. 10 of the responding patients esponses were lost or diminished	recognized three or more pepti , and specific responses fluctua measure of Th function than p	ide pools. ated. 4/10 of the responders at	o stimulation with gp120 synthetic baseline had new responses at 12
gp160 (262–281)	gp120 (262–281 IIIB)	NGSLAEEEVVIRSVNFTDN-A?	HIV-1 infection	human	Geretti1994
	<ul> <li>overlapping peptide pool</li> <li>After 12 months, most remonths, as did 5/15 non-</li> <li>IL-2 production was a m</li> </ul>	ls. 10 of the responding patients esponses were lost or diminished	recognized three or more pepti , and specific responses fluctua measure of Th function than p	ide pools. ated. 4/10 of the responders at	o stimulation with gp120 synthetic baseline had new responses at 12

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
gp160 (264–287)	gp120 (269–292 NL43)	SLAEEEVVIRSANFTDNAK- TIIVQ	Vaccine	human	Sitz1999
	There was a great breadt		3 HIV component: gp120, gp160 peptides in 19 HIV-1 infected rgp1 5 to this peptide	60 and 17 HIV-1 infected r	gp120 vaccine recipients
gp160 (269–283)	gp120 (269–283 IIIB, B10) • 12 gag and 18 env peptio	EVVIRSANFTDNAKT	HIV-1 infection  nmonly evoke T-cell responses.	human	Wahren1989b, Wahren1989a
gp160 (270–285)	gp120 (IIIB) • Peptide stimulation of Pl	VVIRSDNFTNNAKTIC BMC from non-infected individu t always induce T-cells that recog	in vitro stimulation als in vitro	human	Manca1995b
gp160 (272–291)	gp120 (272–291 IIIB)	IRSVNFTDNAKTIIVQLNT- S?	HIV-1 infection	human	Geretti 1994
	<ul> <li>overlapping peptide pool</li> <li>After 12 months, most remonths, as did 5/15 non-</li> <li>IL-2 production was a m</li> <li>Five peptides were recogwere in or near V2, the or</li> </ul>	ls. 10 of the responding patients a esponses were lost or diminished responders. ore sensitive and well-preserved		ols. 4/10 of the responders at ba eration.	seline had new responses at 12
gp160 (274–288)	gp120 (274–288 IIIB, B10) • 12 gag and 18 env peption	SANFTDNAKTIIVQL  les were identified that could con	HIV-1 infection  nmonly evoke T-cell responses.	human	Wahren1989b, Wahren1989a
gp160 (280–296)		NAKTIIVQLNESVAIC BMC from non-infected individu t always induce T-cells that recog		human	Manca1995b
gp160 (288–307)	coli (mLT)  • Epitope name: Peptide 2  • Helper T-cell proliferativ gp120. Promiscuously ir with regions of local strufrequency of immunoger	7 ye responses to gp120 vaccines in nmunodominant peptides were in actural disorder in proximal N-tentic sequences.	Vaccine HIV component: gp120 Adjuva.  a 2 mouse strains, CBA/J and BALB dentified in both mice strains that we rminal segments, suggesting 3-D proceed, but reacted in 8/10 CBA/J mice.	t/c, were mapped using 47 or ere located in the outer dom	overlapping peptides that span ain of gp120 and were associated

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
gp160 (289–297)		NESVAINCT combinant protein Strain: SF2 a of SF2 gp120, env 2-3, was used	Vaccine <i>HIV component:</i> gp120 d as an immunogen – 20% of T-cell	human clones do not recognize the	Botarelli1991 glycosylated form
gp160 (290–306)	gp120 (296–312 LAI) • Stimulates T-cell prolifer	SVVEINCTRPNNNTRKS ration in HIV-infected donors	HIV-1 infection	human	Schrier1989
gp160 (292–310)	<ul> <li>overlapping peptide pool</li> <li>After 12 months, most remonths, as did 5/15 non-</li> <li>IL-2 production was a month of the second of the second</li></ul>	s. 10 of the responding patients responses were lost or diminished, responders.	tic HIV-1+ patients. PBMC from 15 recognized three or more peptide po and specific responses fluctuated. 4 measure of Th function than prolife	ols. 4/10 of the responders at ba	
gp160 (296–307)	immunogenicity of its' T (RKSITKGPGRVIYATC) • This epitope embedded it	helper (KQIINMWQEVGKAM 6). n the T1-SP10RF peptide does no	HIV-1 infection solution conformation of a hybrid per a helical amphipathic conform a helical amphipathic conformation and be favored within ep	KGPGRVIYATG) and B-corrmation. It lacks random-co	ell epitopes
gp160 (296–314)	gp120 (303–321 IIIB)  Vaccine Vector/Type: pe Goats were immunized v		Vaccine -specific neutralizing determinants of	goat	Palker1989
gp160 (297–321)	<ul><li> Epitope presented as a ta</li><li> This study indicates that</li></ul>		onent: V3 s stronger B-cell and T-cell response due to neodeterminants created at the		
gp160 (297–330)	<ul> <li>administered in a phase I</li> <li>A CD4+ T cell proliferat</li> <li>9/12 tested mounted a C</li> </ul>	ccine consisting of six long pepti trial ive response to at least one of the	des derived from Nef, Gag and Env e six peptides was observed in 9/10 e six peptides, each of the six peptides	vaccinees – 6/10 reacted to	this peptide

HXB2 Location	<b>Author's Location</b>	Sequence	Immunogen	Species (HLA)	References
		ad an IgG response to g neutralizing antibodies v		be differentiated from HIV-1 seropo	ositive individuals with a commercial
gp160 (298–307)	<ul> <li>adjuvant</li> <li>This epitope is located</li> <li>The epitope described I (TINCTRPYNNTRKG)</li> <li>C57BL/6 mice were im boosted with VV, and 3</li> <li>The vaccinia construct the DNA construct is in CHO-K1 cells</li> <li>Ten days after the final and Vβ usage was dete</li> <li>Mice were immunized HIV-1 92UG005, a clade 80 unique clonotypes well H-2 IA<sup>b</sup> restricted T-he in V4C4, and 7 in gp41</li> <li>Epitope hotspots tended non-uniform localization</li> </ul>	in the V3 region of UG9 here is the region of over I and RPYNNTRKGIH imunized with a prime-b -4 weeks later boosted a is a pSC11-based VV vo the pJW4303 vector wi boost, hybridomas were rmined with an Env from either de D vaccine isolated frozere characterized from sel pler epitopes were conce ). It to be proximal to heav	22005 (UG, clade D) and was recogned portion of two 15 mers that were both a IGPG) cost strategy involving three HIV-1 again with purified protein in Freuncetor with the first 38 amino acids of the a CMV promotor, and the purified made and tested for IL-2 production one of two clades: HIV-1 1007, a commuganda in 1992 through the WE six mice entrated in 5 distinct regions within tily glycosylated regions of the Envidifferential antigen processing and	d's adjuvant ontributed by BH10 and the rest of g ed protein is expressed from the pJW on using either B6 spleen cells or H- lade B strain isolated from an indivi	the not determined of the hybridoma with DNA given i.m., 3-4 weeks later appl 20 and gp41 by the vaccine strain, 74303 vector transfected into 2 IAb transfected L cells as targets dual from Memphis Tennesee, and onses in V2, 26 in C2, 22 in V3, 23 rands of the protein. The
gp160 (298–319)	coli (mLT)  • Epitope name: Peptide  • Helper T-cell proliferat gp120. Promiscuously with regions of local strequency of immunogeneous production of the pro	28 ive responses to gp120 vimmunodominant peptic ructural disorder in proxenic sequences.	rain: 89.6 HIV component: gp120 raccines in 2 mouse strains, CBA/J les were identified in both mice stra	murine  Adjuvant: R192G mutant heat-la  and BALB/c, were mapped using 47  and that were located in the outer do  ng 3-D protein structure influences	overlapping peptides that span of gp120 and were associated
gp160 (301–325)	gp120 (IIIB)  Vaccine Vector/Type: I  The env response is whe Intramuscular versus nation of the Ignumber of Ignumber of Ignumber of Ignumber	NNTRKSIRIORGPG IGKIGN DNA <i>Strain:</i> IIIB <i>HI</i> at is being sought, but consal vaccination with DN	RAFVT – Vaccine  V component: ENV, REV Adjuva o-expression of rev is required  VA vaccine with a QS-21 adjuvant v via Th1 cytokines IFNγ and IL-2 ar	was studied	Sasaki1998 TH) in response to the V3 peptide was

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
gp160 (302–315)	** *	NTRKSIRIQRGPGR  ptide Strain: IIIB HIV comp  Th epitopes that can stimulate a	Vaccine onent: V3 un antibody response in peptide-imm	murine nunized mice	Goodman-Snitkoff1990
gp160 (302–321)	gp120 (302–321 IIIB)	NTRKRIRIQRGPGRAFVTI- G?	HIV-1 infection	human	Geretti1994
	<ul> <li>After 12 months, most remonths, as did 5/15 non-</li> </ul>	ls. 10 of the responding patients esponses were lost or diminished responders. Hore sensitive and well-preserved	recognized three or more peptide poly, and specific responses fluctuated. It measure of Th function than prolife	ools. 4/10 of the responders at ba	
gp160 (302–327)	Hypervariable epitope co- degenerative peptide coo-	constructs (HECs) are degenerative extra containing 64 distinct peptises than the MN V3 peptide alon	Vaccine  onent: V3 Adjuvant: Montainde Is the peptide cocktails that are made in ides, NTRK-[SR]-I-[HR]-IGPG-[RQ the in BALB/c mice immunized and be	a single peptide synthesis i 2]-AFY-[AT]-TG-[DE]-IG-	[DN]-IRQ, elicited broader and
gp160 (305–321)	gp120 (312–329)  • Used as positive control	(CG) KSIRIQRGPGRAFVT- IG in study examining T-cell respon		human	Adams1997
gp160 (308–319)			HIV-1 infection (GPGQ) was incorporated into ISCC enhanced by the presentation in the I		-
gp160 (308–321)	• Epitope name: SP10	RIHIGPGRAFYTTK eptide Strain: MN HIV compositivates IL-4 and IL-6 in a dose outes to this response		murine (H-2 <sup>d</sup> )	Klinman1995
gp160 (308–322)	peptide • 1/18 unexposed-uninfect	RIHIGPGRAFYTTKN I individuals in this study had a p ted controls could recognize this I as IIIB sequence - most likely l		human e, but only 1/11 exposed-un	Furci1997 infected individuals recognized thi
gp160 (308–322)	gp120 (315–329 IIIB)  Vaccine Vector/Type: pe  • Epitope name: P18	RIQRGPGRAFVTIGK	Vaccine	Rhesus macaque	Nehete1993

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
				es a proliferative response in mice as observed in 3 rhesus monkeys	2
gp160 (308–322)	gp120 (315–329 IIIB) • Epitope name: P18	RIQRGPGRAFVTIGK	HIV-1 infection	human	Wasik1997
	<ul> <li>The breadth and intensity</li> <li>IL-2 and γ IFN production</li> <li>IL-4 production from The</li> <li>The HIV-1+ children with</li> </ul>	on from Th1 cells correlated wit 2 cells was inversely correlated h strong CTL responses had lev	th the CTLp frequency agains with the CTLp frequency rels of anti-CD3 MAb inducti	ed in seven rapidly progressing H st HIV-1 Gag, Env, Nef and Pol ion of Th1 cells comparable to un mbers of Th1 relative to Th2 cells	infected children
gp160 (308–322)	children with AIDS sym	ptoms, but increased with age in	n children with slowly progre	human ere undetectable at less than 1 mo essive disease to the child's ability to make Th1	-
gp160 (308–322)	<ul><li>gp120 (315–329 IIIB)</li><li>Epitope name: P18</li><li>CTL activity analyzed in</li></ul>	RIQRGPGRAFVTIGK  parallel with Th reactivity in ex	xposed but uninfected health	human care workers	Pinto1995
gp160 (308–322)	gp120 (315–329 MN) • Epitope name: P18 • CTL activity analyzed in	RIHIGPGRAFYTTKN parallel with Th reactivity in ex	xposed but uninfected health	human care workers	Pinto1995
gp160 (308–322)	gp120 (315–329 IIIB) • Epitope name: P18 • IL-2 production detectio	RIQRGPGRAFVTIGK n of Th lymphocytes from asym	HIV-1 infection	human	Clerici1989
gp160 (308–322)	gp120 (315–329 IIIB) • Epitope name: P18 • Peptides stimulate Th ce	RIQRGPGRAFVTIGK	HIV-1 infection	human	Clerici1991a
gp160 (308–322)	• Epitope name: P18	RIQRGPGRAFVTIGK combinant protein <i>Strain:</i> IIIE ndividuals with rgp160 results i	-	human  does natural infection	Clerici1991b
gp160 (308–322)	gp120 (315–329 IIIB)  • Epitope name: P18  • Cell-mediated immune r	RIQRGPGRAFVTIGK esponse to HIV-1 peptides in HI	IV-1 exposed seronegative me	human	Clerici1992
gp160 (308–322)	gp120 (315–329 IIIB) • Epitope name: P18 • used in a study of the inf	RIQRGPGRAFVTIGK luence of pentoxifylline on HIV	HIV-1 infection  7 specific T-cells	human	Clerici 1997

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
gp160 (308–322)	gp120 (MN) • Epitope P18 MN: Cell-n	RIHIGPGRAFYTTKN nediated immune response to HI	V-1 peptides in HIV-1 exposed seron	human negative men	Clerici1992
gp160 (308–322)	gp160 (315–329 IIIB)	RIQRGPGRAFVTIGK	HIV-1 infection, HIV-1 exposed seronegative	human	Wasik1999
	<ul><li>age 6 months</li><li>In both uninfected and in responses to P18</li></ul>	nfected infants of HIV-positive n	on were detectable at birth in the maj nothers, responses to the T1 peptide oner mutation rate due to its location is	(KQIINMWQEVGKAN	<u>-</u>
gp160 (308–322)	gp120 (315–329 IIIB)	RIQRGPGRAFVTIGK	HIV-1 infection	human	Kaul1999
	cases) and mucosal geni	tal tract anti-HIV IgA (16/21 cas	and to frequently have HIV-env pepti ses) lously described [Clerici1989], and v	•	• •
gp160 (308–322)	gp120 (315–329 IIIB)	RIQRGPGRAFVTIGK	HIV-1 infection, HIV-1 exposed seronegative	human	Kuhn2001
	<ul> <li>(measured by a bioassay epitopes P18 MN, P18 II</li> <li>The mothers were predo based on B subtype reag</li> <li>3/33 infants with cord bl with cord blood that was</li> </ul>	measuring IL2 production in a r IIB, T1, T2, and TH4 minantly infected with subtype 0 ents. ood T help responses to Env wer unresponsive to Env peptide sti	C, but the T help response was detected in utero, 2/33 were lost to	a proliferation assay) ag table in a number of cor o follow up, and 28/33 w ry, and 8/47 contracted	ainst a peptide cocktail containing Th d blood samples despite using peptides were not infected. 6/53 of the infants HIV intrapartum or via breast-feeding.
1(0 (208, 222)	with a protective natural	immunity that helps block moth	ner-infant transmission of HIV-1.		
gp160 (308–322)	<ul> <li>(measured by a bioassay epitopes P18 MN, P18 II</li> <li>The mothers were predo based on B subtype reag</li> <li>3/33 infants with cord bl with cord blood that was</li> <li>Measurable HIV specific</li> </ul>	measuring IL2 production in a rank IIB, T1, T2, and TH4 minantly infected with subtype cents.  ood T help responses to Env were unresponsive to Env peptide stip T help responses elicited in the	C, but the T help response was detected in utero, 2/33 were lost to	a proliferation assay) ag table in a number of cor o follow up, and 28/33 w ry, and 8/47 contracted	ainst a peptide cocktail containing Th d blood samples despite using peptides were not infected. 6/53 of the infants HIV intrapartum or via breast-feeding.

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
gp160 (308–322)	gp120 (315–329 IIIB) • Epitope name: P18 • Linked HIV-1 T1 and P1	RIQRGPGRAFVTIGK  8 peptides to anti-HLA-DR and	HIV-1 infection  IgD Fab fragments to enhance uptak	human (DR) e by antigen presenting cel	Baier1995  Is thus increase immunogenicity
gp160 (308–322)	• Epitope name: P18	RIQRGPGRAFVTIGK ccinia Strain: IIIB HIV comp		murine (H-2 A <sup>d</sup> )	Takahashi1990
gp160 (308–322)	gp120 (315–329 IIIB) • Epitope name: P18 • Binds Class II H-2 I-A <sup>d</sup>	RIQRGPGRAFVTIGK requiring riqrgPgRaFvti, and Cla	Peptide-HLA interaction ass I H-2 $D^d$ , requiring iGPgRaFvtI	murine (H-2 I-A <sup>d</sup> )	Takeshita1995
gp160 (308–322)	<ul><li>Epitope name: P18</li><li>MIP-1a expression plasn response as measured by</li></ul>	nid co-inoculated with a DNA va a CTL test against using V3 pep	Vaccine  2: IIIB HIV component: gp160, RE  3: Iccine consisting of HIV-1 pCMV160  4: bit de pulsed targets, and a DTH test to of MIP-1 alpha, suggesting it pref	DIIIB and pcREV enhanced o V3 peptide.	the HIV-specific T-cell immune
gp160 (308–327)	<ul> <li>Tandem peptides are tho</li> </ul>		g to class II molecule and therefore bugh improved recruiting of CD4 to		
gp160 (309–323)	gp120 (309–323 IIIB, B10) • 12 gag and 18 env peptic	EQRGPGRAFVTIGKI	HIV-1 infection  nmonly evoke T-cell responses.	human	Wahren1989b, Wahren1989a
gp160 (309–325)	<ul><li>activation antigens CD25</li><li>The ability to express act</li><li>This study investigated C</li></ul>	5 and CD71 tivation markers in response to H	HIV-1 infection s show reduced ability to proliferate in HIV is retained, but the response to te HIV from patients at various stages s, or p17 and p24	tanus toxoid recall antigen	is lost
gp160 (310–328)	coli (mLT) • Epitope name: Peptide 2 • Helper T-cell proliferativ gp120. Promiscuously ir	9 ve responses to gp120 vaccines in nmunodominant peptides were id actural disorder in proximal N-ter	Vaccine HIV component: gp120 Adjuvan 2 mouse strains, CBA/J and BALB, dentified in both mice strains that we rminal segments, suggesting 3-D pro	/c, were mapped using 47 or re located in the outer dom	werlapping peptides that span ain of gp120 and were associated

<b>HXB2</b> Location	<b>Author's Location</b>	Sequence	Immunogen	Species (HLA)	References
	This peptide was react:	ve in 2/10 BALB/c m	ice tested, and in 8/10 CBA/J mice.		
gp160 (311–319)	<ul> <li>gp120 encoding DNA GMCSF cloned into th</li> <li>The bicistronic gp120/ increase in IL-2, IL-4, enhanced proliferative</li> </ul>	co-injected with a pla e same vector and exp GM-CSF vaccine indo IL-10, IFN-gamma ar responses were substa onic DNA vaccines in	Vaccine  HIV component: gp120 Adjuvant: smid carrying GMCSF gave meager Claresed from the same promoter. aced an approximately 10-fold increased GM-CSF production, compared to inantiated by CD4+ T-cell Elispot. duced similar CTL responses directed are responses.	D4+ T-cell responses in BALB/c report of CD4+ T cell proliferative respondentiation with the monocistron	onses to gp120, as well as a significantic pVIJ-gp120 with GMCSF. The
gp160 (311–320)			Vaccine notor <i>Strain:</i> IIIB <i>HIV component:</i> In plasmid in addition to DNA vaccine		
gp160 (311–320)	<ul> <li>Intranasal immunization the serum IgG1 to IgG</li> </ul>	on with IL-15 expression with IL-15 expression That is a second of the contract of the contrac	Vaccine notor Strain: IIIB HIV component: on plasmid in addition to DNA vaccine type 1 (Th1) cell-mediated immunity 1 response to the vaccine, but they to d	e increases DTH response and CT	L activity to the antigen, and decrease
gp160 (311–320)	<ul><li>CD40L expression inc.</li><li>Elispot assay indicated cells</li></ul>	reases DTH, and Th1- co-injection with hC	Vaccine notor Strain: IIIB HIV component: dependent responses based on enhance D40L resulted in greater numbers of IF and Th2 cells, and such a pattern of income	ed IgG2a titers, with no lowering of N-gamma producing Th1cells, as	of IgG1 titers well as increased IL-4 producing Th2
gp160 (311–322)	• The timing of delivery	of the pGM-CSF exp	Vaccine notor Strain: IIIB HIV component: ression plasmid for intramuscular DNA or to the DNA vaccine, and Th1 respon	pCMV160IIIB/REV vaccination	impacts the Th response, maximizing
gp160 (314–328)	gp120 (314–328 IIIB, B10) • 12 gag and 18 env pep	GRAFVTIGKIGN	MRQ HIV-1 infection hat could commonly evoke T-cell response	human onses.	Wahren1989b, Wahren1989a
gp160 (314–341)	There was a great brea	ISRAKWNAT recombinant protein dth of proliferative re	MRQAHCN— Vaccine  Strain: NL43 HIV component: gp12 sponse to env peptides in 19 HIV-1 infe on index of greater than 5 to this peptid	ected rgp160 and 17 HIV-1 infecte	Sitz1999 d rgp120 vaccine recipients

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References					
gp160 (315–328)	Env (UG92005)  Vaccine Vector/Type: I adjuvant	RAYYTTNIVGNIRQ DNA, vaccinia, recombinant p	Vaccine protein Strain: 1007 (clade l	murine (H-2 IA <sup>b</sup> ) B), UG92005 (clade D) HIV compon	Surman2001 nent: gp140 Adjuvant: Freund's					
		in the V3 region of UG92005	5 (UG, clade D) and was recog	gnized by two hybridomas with V $oldsymbol{eta}$ us	sage not determined, but one used					
	• C57BL/6 mice were im		strategy involving three HIV- with purified protein in Freur	1 Env antigens: Mice were primed wind's adjuvant	th DNA given i.m., 3-4 weeks later					
	• The vaccinia construct is a pSC11-based VV vector with the first 38 amino acids contributed by BH10 and the rest of gp120 and gp41 by the vaccine strain, the DNA construct is in the pJW4303 vector with a CMV promotor, and the purified protein is expressed from the pJW4303 vector transfected into CHO-K1 cells									
	and $V\beta$ usage was dete	<ul> <li>Ten days after the final boost, hybridomas were made and tested for IL-2 production using either B6 spleen cells or H-2 IA<sup>b</sup> transfected L cells as targets and Vβ usage was determined</li> </ul>								
	HIV-1 92UG005, a clac	de D vaccine isolated from U	ganda in 1992 through the W	clade B strain isolated from an individ HO	dual from Memphis Tennesee, and					
				n the Env sequence (2 clonotype respo	onses in V2, 26 in C2, 22 in V3, 23					
	<ul> <li>Epitope hotspots tended non-uniform localization</li> </ul>	d to be proximal to heavily gl		sequence, in exposed, non-helical str d the glycosylation site proximity may						
gp160 (317–331)	gp160 (324–338 IIIB)	FVTIGKIGNMRQAHC	Vaccine	murine $(H-2^k, H-2^d)$	Berzofsky1991b, Berzofsky1991a					
				0 Adjuvant: Freund's adjuvant						
	<ul> <li>B10.BR (H-2A<sup>k</sup>, E<sup>k</sup>) and B10.D2 (H-2A<sup>d</sup>, E<sup>d</sup>) mice immunized with rec gp160 showed a proliferative response to this peptide</li> <li>FVTIGKIGNMRQAHCNISRAKWNNTLKQIDSKL encompasses several murine Th epitopes including FVTIGKIGNMRQAHC and is referred to as a "multideterminant region" or cluster peptide</li> </ul>									
gp160 (317–331)	Vaccine Strain: IIIB	FVTIGKIGNMRQAHC  HIV component: gp160 elper T-cell regions are recog	Vaccine gnized by mice of three or four	murine (H-2 <sup>k,d</sup> )	Hale1989					
gp160 (317–336)	gp120 (321–340 MN)  Vaccine Vector/Type: p  • Epitope name: 1987	YTTKNIIGTIRQAHCNS protein, DNA Strain: MN		guinea pig juvant: complete Freund's adjuvant (	Chattergoon2002 CFA)					
	<ul> <li>Hartley guinea pigs we (DTH) responses after</li> <li>A total of 7 gp120 pept gp120. The vaccine del</li> </ul>	vaccination, which are related ides elicited a delayed type h livery system, DNA versus re	d to Th1 T-cell responses. CF, sypersensivity (DTH) response to protein, resulted in the reco	or plasmid expressed gp120 and monit A did not augment responses in animals after vaccination, out of a set of 60 continuous of distinct peptides.  1/6 vaccinated with plasmid gp120 DN	als vaccinated with plasmid.  overlapping peptides that spanned					

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
gp160 (317–349)	gp160 (324–356 IIIB)	FVTIGKIGNMRQAHCNISR- AKWNNTLKQIDSKL	,	human, murine (H- $2^k$ , H- $2^d$ )	Berzofsky1991b, Berzofsky1991a
			HIV component: gp160 Adjuvan compasses several murine Th epitope		nultideterminant region" or cluster
		ion cluster peptides were evaluat	ted Th responses in different MHC/H	ILA backgrounds after vac	cination of mice with gp160, or in
	this region stimulated H-	$2^k$ , H- $2^d$ , H- $2^b$ and H- $2^s$ respons	Is from B10.BR mice (H-2A <sup><math>k</math></sup> , E <sup><math>k</math></sup> ) and sees in 58% (21/36) of asymptomatic HIV		<sup>d</sup> ), but shorter peptides from within
gp160 (319–338)	coli (mLT)	-	Vaccine HIV component: gp120 Adjuvan	murine t: R192G mutant heat-labi	Dai2001 le toxin from enterotoxigenic E.
	gp120. Promiscuously in with regions of local stru frequency of immunoger  This peptide was highly a	re responses to gp120 vaccines in mmunodominant peptides were ic actural disorder in proximal N-ten- nic sequences. reactive in 7/10 BALB/c mice ten-	n 2 mouse strains, CBA/J and BALB/dentified in both mice strains that we rminal segments, suggesting 3-D protected, and in 7/10 CBA/J mice and wa HCNISRAKW, NNTLQQIVIKLREK	re located in the outer dom tein structure influences That as consider one of the 3 imi	ain of gp120 and were associated an antigen processing and the munodominant peptides identified
gp160 (319–338)	<ul> <li>Promiscuous immunodor in the outer domain, prox</li> <li>This peptide was recogni immunodominant</li> </ul>	minant epitopes in gp120 were maint to regions of structural disc	HIV component: gp120 Adjuvan napped by overlapping peptides in CI order indicated by the crystal structur LB/c mice with SI $> 4$ , averaging 6.	BA/J H- $2^k$ and BALB/c H-re or by sequence divergence	$2^d$ mice, and all were found to be ce.
gp160 (321–336)		RIIGDIRKAHCNISRY BMC from non-infected individu t always induce T-cells that recog		human	Manca1995b
gp160 (322–336)	<ul> <li>adjuvant</li> <li>This epitope is located in</li> <li>C57BL/6 mice were imm boosted with VV, and 3-4</li> <li>The vaccinia construct is</li> </ul>	n the V3 region of 1007 (US, clac nunized with a prime-boost strate 4 weeks later boosted again with a pSC11-based VV vector with	Vaccine in Strain: 1007 (clade B), UG9200: de B) and was recognized by three hy egy involving three HIV-1 Env antige purified protein in Freund's adjuvant the first 38 amino acids contributed by promotor, and the purified protein is	which $\nabla \beta$ usage vens: Mice were primed with to by BH10 and the rest of gp	$V\beta$ 6 and not determined in DNA given i.m., 3-4 weeks later 120 and gp41 by the vaccine strain,

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
	<ul> <li>and Vβ usage was dete</li> <li>Mice were immunized HIV-1 92UG005, a cla</li> <li>80 unique clonotypes v</li> <li>H-2 IA<sup>b</sup> restricted T-he in V4C4, and 7 in gp4</li> <li>Epitope hotspots tende non-uniform localizati</li> </ul>	ermined with an Env from either of the D vaccine isolated from the end of the Environment	one of two clades: HIV-1 1007, a c in Uganda in 1992 through the WF ix mice intrated in 5 distinct regions within by glycosylated regions of the Env differential antigen processing and	lade B strain isolated from an indi	
gp160 (322–336)	<ul> <li>adjuvant</li> <li>This epitope is located</li> <li>C57BL/6 mice were in boosted with VV, and the DNA construct is in CHO-K1 cells</li> <li>Ten days after the final and Vβ usage was detended with the HIV-1 92UG005, a classification with the S0 unique clonotypes of H-2 IA<sup>b</sup> restricted The in V4C4, and 7 in gp4</li> <li>Epitope hotspots tended non-uniform localization</li> </ul>	in the V3 region of UG92 munized with a prime-bo 3-4 weeks later boosted agains a pSC11-based VV veon the pJW4303 vector with a boost, hybridomas were ermined with an Env from either of the D vaccine isolated from were characterized from silelper epitopes were concestable to be proximal to heavily	ant protein Strain: 1007 (clade E 2005 (UG, clade D) and was recog cost strategy involving three HIV-1 gain with purified protein in Freun ctor with the first 38 amino acids c h a CMV promotor, and the purified made and tested for IL-2 production one of two clades: HIV-1 1007, a c in Uganda in 1992 through the WF ix mice intrated in 5 distinct regions within by glycosylated regions of the Env lifferential antigen processing and	nized by three hybridomas with V, Env antigens: Mice were primed d's adjuvant ontributed by BH10 and the rest of ed protein is expressed from the pJ on using either B6 spleen cells or F lade B strain isolated from an inditio	I-2 IA <sup>b</sup> transfected L cells as targets vidual from Memphis Tennesee, and ponses in V2, 26 in C2, 22 in V3, 23 strands of the protein. The
gp160 (322–336)	Env (UG92005)  Vaccine Vector/Type: adjuvant  This epitope is located C57BL/6 mice were in boosted with VV, and The vaccinia construct the DNA construct is i CHO-K1 cells	IVGNIRQAHCNVSKA DNA, vaccinia, recombina in the V3 region of UG92 nmunized with a prime-bo 3-4 weeks later boosted as is a pSC11-based VV vec n the pJW4303 vector with	Vaccine A Vaccine Ant protein Strain: 1007 (clade E 2005 (UG, clade D) and was recog cost strategy involving three HIV-1 gain with purified protein in Freun ctor with the first 38 amino acids c h a CMV promotor, and the purific	nized by three hybridomas with V, Env antigens: Mice were primed d's adjuvant ontributed by BH10 and the rest of ed protein is expressed from the pJ	Surman2001 Soment: gp140 Adjuvant: Freund's B usage V $\beta$ 6, 8.1, and not determined with DNA given i.m., 3-4 weeks later Egp120 and gp41 by the vaccine strain, W4303 vector transfected into

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
	<ul> <li>HIV-1 92UG005, a clad</li> <li>80 unique clonotypes w</li> <li>H-2 IA<sup>b</sup> restricted T-helin V4C4, and 7 in gp41</li> <li>Epitope hotspots tended</li> </ul>	le D vaccine isolated from a lere characterized from a lere epitopes were concol.  It to be proximal to heaven may be influenced by	m Uganda in 1992 through the Wisix mice entrated in 5 distinct regions within the glycosylated regions of the Envillemental antigen processing and	НО	
gp160 (322–341)	<ul> <li>After 12 months, most i months, as did 5/15 non</li> </ul>	T?  ses were studied in 36 as ols. 10 of the responding responses were lost or di-responders.  nore sensitive and well-	patients recognized three or more iminished, and specific responses for preserved measure of Th function	ductuated. 4/10 of the responders at	
gp160 (324–336)	<ul> <li>adjuvant</li> <li>This epitope is located if the epitope described in (IVGNIRQAHCNVSK)</li> <li>C57BL/6 mice were im boosted with VV, and 3</li> <li>The vaccinia construct is in CHO-K1 cells</li> <li>Ten days after the final and Vβ usage was detered in Mice were immunized white HIV-1 92UG005, a clade 80 unique clonotypes were in V4C4, and 7 in gp41</li> <li>Epitope hotspots tended</li> </ul>	in the V3 region of UG9 here is the region of over A and GNIRQAHCNV; munized with a prime-based as a pSC11-based VV vote the pJW4303 vector with a primed with an Env from either the D vaccine isolated from the proper epitopes were concluded by the proximal to heaven may be influenced by	2005 (UG, clade D) and was recognap of two 15 mers that were both SKAKW) oost strategy involving three HIV- gain with purified protein in Freur octor with the first 38 amino acids of the CMV promotor, and the purification and tested for IL-2 production one of two clades: HIV-1 1007, a community of the Uganda in 1992 through the White with the contracted in 5 distinct regions within the gly glycosylated regions of the Envilled III glycosylated III glycosy	gnized by two hybridoma with $V\beta$ usuable to stimulate IL-2 production from an antigens: Mice were primed with a distributed by BH10 and the rest of ed protein is expressed from the properties of the protein is expressed from the protein using either B6 spleen cells of the protein is expressed from an individual of the protein is expressed from an individual of the protein in the protein is expressed from an individual of the protein in the protein is expressed from an individual of the protein in the protein is expressed from an individual of the protein in the protein is expressed from an individual of the protein in the protein is expressed from an individual of the protein in the protein in the protein is expressed from the protein in t	om the hybridoma with DNA given i.m., 3-4 weeks later gp120 and gp41 by the vaccine strain, W4303 vector transfected into G-2 IA <sup>b</sup> transfected L cells as targets widual from Memphis Tennesee, and ponses in V2, 26 in C2, 22 in V3, 23 strands of the protein. The

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
gp160 (324–338)	<ul> <li>adjuvant</li> <li>This epitope is located it determined – a Vβ 8.1's</li> <li>C57BL/6 mice were imit boosted with VV, and 3-</li> <li>The vaccinia construct it the DNA construct is in CHO-K1 cells</li> <li>Ten days after the final band Vβ usage was deter</li> <li>Mice were immunized whIV-1 92UG005, a clad</li> <li>80 unique clonotypes where in V4C4, and 7 in gp41)</li> <li>Epitope hotspots tended non-uniform localization</li> </ul>	In the V3 region of UG92005 (Us and V $\beta$ 8.2 also were shown to munized with a prime-boost strategy at the pJW4303 vector with a CM proof, hybridomas were made a mined with an Env from either one of the D vaccine isolated from Ugar ere characterized from six mice per epitopes were concentrated to be proximal to heavily glycon.		eleven hybridomas with $V\beta$ $V\alpha$ 2 gens: Mice were primed with the laby BH10 and the rest of grain is expressed from the pJW ither B6 spleen cells or H-2 ain isolated from an individual equence (2 clonotype response) in exposed, non-helical str	usage V $\beta$ 5, 7, 8.1, 8.2, 11 and not th DNA given i.m., 3-4 weeks later of 120 and gp41 by the vaccine strain, 4303 vector transfected into IA $^b$ transfected L cells as targets ual from Memphis Tennesee, and the nses in V2, 26 in C2, 22 in V3, 23 ands of the protein. The
gp160 (327–341)	Vaccine Vector/Type: re	RQAHCNISRAKWNNT combinant protein Strain: HZ	Vaccine XB2 HIV component: gp120 CTL clone that recognizes the N-tern	murine $(I-A^d)$ minal flank of the V3 loop	Warren1992
gp160 (327–346)	<ul> <li>Epitope name: 1988</li> <li>Hartley guinea pigs wer (DTH) responses after v</li> <li>A total of 7 gp120 pepti gp120. The vaccine deli</li> </ul>	e intradermally injected with ei accination, which are related to des elicited a delayed type hypo very system, DNA versus rec p	V Vaccine W component: gp120 Adjuvant: continuous component: gp120 Adjuvant: continuous component: gp120 Adjuvant: continuous contin	expressed gp120 and moniting ugment responses in animal cination, out of a set of 60 of distinct peptides.	ored for delayed type hypersensivity ls vaccinated with plasmid. verlapping peptides that spanned
gp160 (330–350)	<ul> <li>After 12 months, most r months, as did 5/15 non</li> </ul>	ls. 10 of the responding patient esponses were lost or diminished responders.	natic HIV-1+ patients. PBMC from 1: ts recognized three or more peptide poed, and specific responses fluctuated.	ools. 4/10 of the responders at ba	

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
	• 3/15 responders recogniz	zed this peptide, average $SI = 5.5$			
gp160 (331–345)		CNISRAQWNNTLEQI BMC from non-infected individu t always induce T-cells that recog		human	Manca1995b
gp160 (332–354)	• There was a great breadt	EQFG combinant protein <i>Strain:</i> NL4	3 HIV component: gp120, gp160 peptides in 19 HIV-1 infected rgp16	human 0 and 17 HIV-1 infected rg	Sitz1999 p120 vaccine recipients
gp160 (335–349)	• B10.BR (H- $2A^k$ , $E^k$ ), B1	$(0.A(5R) (H-2A^b, E^b))$ and B10.S NISRAKWNNTLKQIDSKL end	Vaccine  HIV component: gp160 Adjuvan (9R) (H-2A <sup>s</sup> , E <sup>s</sup> ) mice immunized w compasses several murine Th epitope	rith rec gp160 showed a pro	
gp160 (335–349)	gp120 (342–356 IIIB)  Vaccine Strain: IIIB H  • Six multideterminant hel		Vaccine  I by mice of three or four MHC types	murine (H- $2^{k,t4,i5}$ )	Hale1989
gp160 (337–356)	<ul> <li>Epitope name: 1989</li> <li>Hartley guinea pig were (DTH) responses after va</li> <li>A total of 7 gp120 peptic gp120. The vaccine deliv</li> </ul>	intradermally injected with eithe accination, which are related to T des elicited a delayed type hypers very system, DNA versus rec pro	Vaccine component: gp120 Adjuvant: com r recombinant protein or plasmid exp Th1 T-cell responses. CFA did not au sensivity (DTH) response after vaccin tein, resulted in the recognition of di H to this peptide, and 2/6 responded t	oressed gp120 and monitoregment responses in animal nation, out of a set of 60 over the stinct peptides.	ed for delayed type hypersensivity s vaccinated with plasmid. erlapping peptides that spanned
gp160 (339–359)	coli (mLT)  • Epitope name: Peptide 3  • Helper T-cell proliferative gp120. Promiscuously in with regions of local strue frequency of immunoger  • This peptide was reactive.	2 //e responses to gp120 vaccines in mmunodominant peptides were ic actural disorder in proximal N-ten ic sequences. e in 6/10 BALB/c mice tested, an	Vaccine HIV component: gp120 Adjuvan a 2 mouse strains, CBA/J and BALB/ dentified in both mice strains that we rminal segments, suggesting 3-D pro ad in 4/10 CBA/J mice and was consi ISRAKW, NNTLQQIVIKLREKFRI	c, were mapped using 47 or re located in the outer dom tein structure influences The der one of the 3 immunodo	verlapping peptides that span ain of gp120 and were associated antigen processing and the pominant peptides identified that
gp160 (339–359)	gp120 (340–359 89.6)	NNTLQQIVIKLREKFRNKTI		murine $(H-2^k, H-2^d)$	Dai2001

HXB2 Location	<b>Author's Location</b>	Sequence	Immunogen	Species (HLA)	References
	<ul><li>in the outer domain, pro</li><li>This peptide was recognimmunodominant</li></ul>	oximal to regions of s nized by 4/10 CBA/J	p120 were mapped by overlapping per tructural disorder indicated by the crys and $6/10$ BALB/c mice with SI > 4, av d to be in the inner domain of the prote	tal structure or by sequence diverging 4.9 and 5.5 and is cons	_
gp160 (341–356)	gp120 (IIIB)  • Peptide stimulation of F  • Peptide priming does no			human	Manca1995b
gp160 (342–361)	<ul> <li>After 12 months, most r</li> <li>months, as did 5/15 non</li> </ul>	F?  ses were studied in 36 ols. 10 of the responderesponses were lost of the responders.  shore sensitive and we	GNNKTII- HIV-1 infection  6 asymptomatic HIV-1+ patients. PBMiling patients recognized three or more prediminished, and specific responses fluctures are preserved measure of Th function through SI = 6.0.	peptide pools. actuated. 4/10 of the responders	
gp160 (344–357)	gp120 (346–359) • Conjugation of HIV pep	QIVKKLREQFGN otides to liposomes a	NK HIV-1 infection nd rIL-2 stimulation may enhance cell-	human mediated responses	Krowka1990
gp160 (349–368)	<ul> <li>coli (mLT)</li> <li>Epitope name: Peptide :</li> <li>Helper T-cell proliferati gp120. Promiscuously i with regions of local str frequency of immunoge</li> </ul>	ve responses to gp12 mmunodominant per uctural disorder in prenic sequences.	Strain: 89.6 HIV component: gp120 0 vaccines in 2 mouse strains, CBA/J a	nd BALB/c, were mapped using that were located in the oute	g 47 overlapping peptides that span r domain of gp120 and were associated
gp160 (350–370)	<ul> <li>After 12 months, most r</li> <li>months, as did 5/15 non</li> </ul>	PE?  ses were studied in 36  ols. 10 of the respond responses were lost o -responders.  nore sensitive and we	KQSSGGD- HIV-1 infection  6 asymptomatic HIV-1+ patients. PBMoling patients recognized three or more per diminished, and specific responses fluctures are perfectly properly that the property of the property	peptide pools. actuated. 4/10 of the responders	
gp160 (353–360)	gp120 (355–362 IIIB)  • C3 region minimal epito	FGNNKTII	SHIV infection	Rhesus macaque	Lekutis1997a

HXB2 Location	<b>Author's Location</b>	Sequence	Immunogen	Species (HLA)	References		
	Cell line was lost prior to	o confirmation of MHC requirem	ents				
gp160 (363–372)	gp120 (368–377 LAI) • Stimulates T-cell prolifer	QSSGGDPEIV ration in HIV-infected donors	HIV-1 infection	human	Schrier1989		
gp160 (364–378)	gp120 (364–378 IIIB, B10)	SSGGKPEIVTHSFNC	HIV-1 infection	human	Wahren1989b, Wahren1989a		
gp160 (369–383)	gp120 (369–383 IIIB, B10)	PEIVTHSFNCGGEFF  les were identified that could con	HIV-1 infection	human	Wahren1989b, Wahren1989a		
gp160 (380–393)	<ul> <li>gp120 (380–393 IIIB) GEFFYCNSTQLFNS? HIV-1 infection human Geretti1994</li> <li>Epitope name: G4</li> <li>Th proliferative responses were studied in 36 asymptomatic HIV-1+ patients. PBMC from 15/36 patients responded to stimulation with gp120 synthetic overlapping peptide pools. 10 of the responding patients recognized three or more peptide pools.</li> <li>After 12 months, most responses were lost or diminished, and specific responses fluctuated. 4/10 of the responders at baseline had new responses at 12 months, as did 5/15 non-responders.</li> <li>IL-2 production was a more sensitive and well-preserved measure of Th function than proliferation.</li> <li>Five peptides were recognized most frequently: C2 (aa 142-161), C3 (aa 152-171), C5 (aa 172-191), E5 (aa 272-291) and G4 (aa 380-393). The first three were in or near V2, the other two were proximal to the V3 and V4 loops.</li> <li>4/15 responders recognized this immunodominant peptide, average SI = 4.4.</li> </ul>						
gp160 (381–395)	*	EFFYCNTTQLFNNTW BMC from non-infected individu t always induce T-cells that recog		human	Manca1995b		
gp160 (392–411)	<ul> <li>Peptide priming does not always induce T-cells that recognize whole protein</li> <li>gp120 (392–411 IIIB) NSTWFNSTWSTEGSNNTEG- HIV-1 infection human Geretti1994</li> <li>Epitope name: G5</li> <li>Th proliferative responses were studied in 36 asymptomatic HIV-1+ patients. PBMC from 15/36 patients responded to stimulation with gp120 synthetic overlapping peptide pools. 10 of the responding patients recognized three or more peptide pools.</li> <li>After 12 months, most responses were lost or diminished, and specific responses fluctuated. 4/10 of the responders at baseline had new responses at 12 months, as did 5/15 non-responders.</li> <li>IL-2 production was a more sensitive and well-preserved measure of Th function than proliferation.</li> <li>1/15 responders recognized this peptide, SI = 9.3.</li> </ul>						
gp160 (394–408)	gp120 (394–408 IIIB, B10) • 12 gag and 18 env peptic	TWFNSTWSTKGSNNT	HIV-1 infection  nmonly evoke T-cell responses.	human	Wahren1989b, Wahren1989a		
gp160 (396–411)		FNNTWRLNHTEGTKGC BMC from non-infected individu t always induce T-cells that recog		human	Manca1995b		

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
gp160 (399–413)	gp120 (399–413 IIIB, B10)	TWSTKGSNNTEGSDT	HIV-1 infection	human	Wahren1989b, Wahren1989a
	• 12 gag and 18 env pepti	des were identified that could cor	nmonly evoke T-cell respon	nses.	
gp160 (404–423)	coli (mLT)	•		murine  Adjuvant: R192G mutant heat-labi	Dai2001 le toxin from enterotoxigenic E.
	gp120. Promiscuously is with regions of local strafequency of immunoge  This peptide was reactive	we responses to gp120 vaccines in mmunodominant peptides were in uctural disorder in proximal N-ten nic sequences. The in 8/10 BALB/c mice tested, ar	dentified in both mice strain rminal segments, suggesting and in 6/10 CBA/J mice, and	and BALB/c, were mapped using 47 on that were located in the outer doming 3-D protein structure influences The was consider one of the 3 immunod LREKFRNKTI, GTNGTEGNDIITL	ain of gp120 and were associated an antigen processing and the ominant peptides identified that
gp160 (404–423)	<ul> <li>Promiscuous immunodo in the outer domain, pro</li> <li>This peptide was recogn immunodominant</li> </ul>	ominant epitopes in gp120 were n ximal to regions of structural disc	HIV component: gp120 napped by overlapping pept order indicated by the cryst LB/c mice with SI > 4, average of the component	murine (H-2 <sup>k</sup> , H-2 <sup>d</sup> )  Adjuvant: mutant R192G heat-labitides in CBA/J H-2 <sup>k</sup> and BALB/c Hallor structure or by sequence divergence araging 4.9 and 5.5 and is considered in	$2^d$ mice, and all were found to be ce.
gp160 (405–420)	<ul> <li>adjuvant</li> <li>This epitope is located it determined – one of the</li> <li>C57BL/6 mice were immunities boosted with VV, and 3-</li> <li>The vaccinia construct it the DNA construct is in CHO-K1 cells</li> <li>Ten days after the final thand Vβ usage was deter</li> <li>Mice were immunized with the specific of the same value of the same value</li></ul>	In the V4C4 region of 1007 (US, $\alpha$ V $\beta$ 8.2 was shown to utilize V $\alpha$ munized with a prime-boost strate 4 weeks later boosted again with a pSC11-based VV vector with the pJW4303 vector with a CMV poost, hybridomas were made and mined	clade B) and was recognize 2 egy involving three HIV-1 I purified protein in Freund' the first 38 amino acids con promotor, and the purified tested for IL-2 production to clades: HIV-1 1007, a cla	ntributed by BH10 and the rest of gp protein is expressed from the pJW4 using either B6 spleen cells or H-2 and B strain isolated from an individual	$V\beta$ 4, 7, 8.1, 8.2, 10, 12 and not a DNA given i.m., 3-4 weeks later 120 and gp41 by the vaccine strain, 303 vector transfected into $IA^b$ transfected L cells as targets

• H-2 IA<sup>b</sup> restricted T-helper epitopes were concentrated in 5 distinct regions within the Env sequence (2 clonotype responses in V2, 26 in C2, 22 in V3, 23

• 80 unique clonotypes were characterized from six mice

in V4C4, and 7 in gp41).

<b>HXB2</b> Location	<b>Author's Location</b>	Sequence	Immunogen	Species (HLA)	References
	non-uniform localization		sylated regions of the Env sequence, tial antigen processing and the glycos		
gp160 (410–429)	-	GSDTITLPCRIKQFINMWQE senting natural variants were us	E HIV-1 infection ed to test for recognition in the contex	human (DR4) xt DR4	Callahan1990
gp160 (410–429)		GSDTITLPCRIKQFINMWQEnes lyse recombinant vaccinia v	E HIV-1 infection irrus-infected cells that synthesize env	human (DR4(Dw10)) velope gp160	Polydefkis1990
gp160 (412–431)	gp120 (412–431 IIIB)	DTITLPCRIKQIINMWQKV- G?	- HIV-1 infection	human	Geretti1994
	<ul> <li>• After 12 months, most remonths, as did 5/15 non-</li> </ul>	ls. 10 of the responding patients esponses were lost or diminished responders.  ore sensitive and well-preserved.	natic HIV-1+ patients. PBMC from 15 recognized three or more peptide pod, and specific responses fluctuated. 4 d measure of Th function than prolife	ols. 4/10 of the responders at ba	
gp160 (416–431)		LPCRIKQIINMWQEVY BMC from non-infected individ t always induce T-cells that reco		human	Manca1995b
gp160 (418–436)	Env (417–435)  • HIV-infected chimpanze Env	CRIKQIINMWQGVGKAMYA es and HIV-positive patients sh	HIV-1 infection ow positive proliferative responses to	human, chimpanzee multiple peptides from fiv	Nehete1998b e conserved regions of the HIV-1
gp160 (421–436)	defined epitope	KQFINMWQEWGKAMYA exposed-uninfected individuals with this epitope as opposed	s in this study had a proliferative resp to V in the sequence.	human onse to a C5 peptide, but n	Furci1997 none reacted with this previously
gp160 (421–436)	children with AIDS sym	ptoms, but increased with age in	HIV-1 infection  I in HIV-1 infected infants were unden children with slowly progressive disensity year of life was related to the children with slowly progressive disensity year of life was related to the children was related	sease	_
gp160 (421–436)	<ul> <li>IL-2 and γ IFN production</li> <li>IL-4 production from Th</li> </ul>	on from Th1 cells correlated wi 2 cells was inversely correlated	HIV-1 infection  ype of Th response was studied in seventh the CTLp frequency against HIV-1 with the CTLp frequency wels of anti-CD3 MAb induction of The state o	Gag, Env, Nef and Pol	

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
gp160 (421–436)	• Epitope name: T1	KQIINMWQEVGKAMYA accinia <i>Strain:</i> IIIB <i>HIV comp</i> T1 and T2 peptides in 14 immur		human	Berzofsky1988
gp160 (421–436)	gp120 (428–443 IIIB)  Vaccine Vector/Type: pe  Epitope name: T1  Goats immunized with p	•	Vaccine ific neutralizing determinants couple	goat ed to T1	Palker1989
gp160 (421–436)	gp120 (428–443 IIIB) • Epitope name: T1 • IL-2 production detection	KQIINMWQEVGKAMYA	HIV-1 infection ptomatic HIV-positive individuals	human	Clerici1989
gp160 (421–436)	gp120 (428–443 IIIB) • Epitope name: T1 • Peptides stimulate Th ce	KQIINMWQEVGKAMYA	HIV-1 infection imilar patient populations	human	Clerici1991a
gp160 (421–436)	• Epitope name: T1	KQIINMWQEVGKAMYA combinant protein <i>Strain:</i> IIIB individuals with rgp160 results in	Vaccine HIV component: gp160  a stronger Th response than does nat	human ural infection	Clerici1991b
gp160 (421–436)	gp120 (428–443 IIIB) • Epitope name: T1 • Cell-mediated immune r	KQIINMWQEVGKAMYA response to HIV-1 peptides in HI	V-1 exposed seronegative men	human	Clerici1992
gp160 (421–436)		KQIINMWQEVGKAMYA acteriophage coat protein Strain red into a filamentous bacterioph	Vaccine a: MN HIV component: V3 age coat protein, and the Th epitope	murine stimulated Ab production	diMarzo Veronese1994 to the V3 loop
gp160 (421–436)	gp120 (428–443 IIIB)  Vaccine Vector/Type: pe  Epitope name: T1  Hybrid T1-V3 peptide in		Vaccine e fusogenic domain of gp41 was add	chimpanzee	Haynes1993
gp160 (421–436)	gp120 (428–443 IIIB)  • Epitope name: T1  • Used in a study of the in	KQIINMWQEVGKAMYA fluence of pentoxifylline on HIV	HIV-1 infection  specific T-cells	human	Clerici1997
gp160 (421–436)	gp120 (428–443 IIIB) • Epitope name: T1 • CTL activity analyzed in	KQIINMWQEVGKAMYA  n parallel with Th reactivity in ex	posed but uninfected health care wo	human	Pinto1995
gp160 (421–436)	gp160 (428–433 IIIB)  • Epitope name: T1	KQIINMWQEVGKAMYA	HIV-1 infection, HIV-1 exposed seronegative	human	Wasik1999

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HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
	<ul><li>age 6 months</li><li>T1 peptide: In both unir (RIQRGPGRAFVTIGK</li></ul>	nfected and infected infants of	HIV-positive mothers, responses	to the T1 peptide were more f	
160 (101 106)			igher mutation rate due to its loca		
gp160 (421–436)	cases) and mucosal geni	ital tract anti-HIV IgA (16/21			Kaul1999 s detected by an IL-2 assay (11/20 bed in [Kaul1999]
gp160 (421–436)	<ul> <li>Epitope name: T1</li> <li>C4-V3 PV (polyvalent I one of four different No</li> <li>This was a pilot phase I</li> </ul>	rth American strains study involving vaccination of		vere HLA-B7-positive	Bartlett1998  em with a V3 loop CTL epitope from responses in 4/8 vacinees
gp160 (421–436)	gp120	KQIINMWQEVGKAMYA	HIV-1 infection, HIV-1 exposeronegative	osed human	Kuhn2001
	<ul> <li>(measured by a bioassay epitopes P18 MN, P18 I</li> <li>The mothers were predobased on B subtype reag</li> <li>3/33 infants with cord b with cord blood that wa</li> <li>Measurable HIV specifi</li> </ul>	y measuring IL2 production in IIB, T1, T2, and TH4 pminantly infected with subtypents.  lood T help responses to Env so sunresponsive to Env peptide c T help responses elicited in the subtype in the su	be C, but the T help response was were infected <i>in utero</i> , 2/33 were stimulation were infected before	with a proliferation assay) aga detectable in a number of core lost to follow up, and 28/33 w delivery, and 8/47 contracted wborn, possibly in response t	ers produced T-helper responses ainst a peptide cocktail containing The d blood samples despite using peptides there not infected. 6/53 of the infants HIV intrapartum or via breast-feeding. In the infants of in the infants are associated.
gp160 (421–436)	immunogenicity of its' (RKSITKGPGRVIYATO)  • As a free peptide, the T gp120, and a nonnative	T helper (KQIINMWQEVGK G). 1 segment, a T-helper epitope is conformation may account for coil conformations, and it is so	the inability of free T1 peptide to	L (SITKGPGRVIYATG) and I ith nascent helical conformation o elicit antibody responses, in	

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
gp160 (421–436)	gp120 (428–443 IIIB) • Epitope name: T1 • Linked HIV-1 T1 and P immunogenicity	KQIINMWQEVGKAMYA	HIV-1 infection d anti-IgD Fab fragments to	human (DR) enhance uptake by antigen presenting	Baier1995 ng cells and thus increase
gp160 (421–436)	<ul> <li>Epitope name: T1</li> <li>BALB/c and A.AL were</li> <li>Substitution of Glu (wt) responding Th cells, and thus enhance CTL respondence CTL respondenc</li></ul>	to Ala, kqiinmwqAvgkamya, ca d shifted the response towards T conses. T1A, elicited stronger protection	le vaccine construct containi aused increased affinity for M h1. Increased Th responses	murine (Ek)  ng the CTL epitope P18IIIB and a TMHC class II Ek. This resulted in the stimulated DCs to produce higher leviral challenge with vaccinia expres	e upregulation of CD40L in the evels of IL-12, and B7-1 and B7-2,
gp160 (421–436)	<ul> <li>EαEβ<sup>b</sup> – the nature of</li> <li>Alanine substitutions ac 435Q, 439K), however sinteraction and for main</li> </ul>	ed for immunization in the study the T1 class II molecular interactors peptide did not negatively a substitutions with larger side chataining T-cell receptor specificity observed when 436E was replace	ction was thoroughly explored affect MHC binding or effect ains often diminished activity	murine (H- $2E\alpha E\beta^k$ ) icularly good T1 responders – T1 cannot be seen that the presentation of epitope, except $y$ – only a few amino acids were for abstitutions in positions that interference $z$	at three critical residues (432N, and to be critical for class II
gp160 (421–436)	gp120 (428–443 IIIB)  Vaccine Vector/Type: po  Epitope name: T1  Hybrid T1-V3 peptide a	KQIINMWQEVGKAMYA eptide Strain: IIIB activates IL-4 and IL-6 in a dose	Vaccine dependent manner	murine (H-2 <sup>d</sup> )	Klinman1995
gp160 (421–436)	• B10.BR (H- $2A^k$ , $E^k$ ), B	IYAPPISGQIR encompasses sev	$(H-2A^s, E^s)$ mice immur	murine (H-2 <sup>k</sup> , H-2 <sup>s</sup> , H-2 <sup>d</sup> )  Adjuvant: Freund's adjuvant nized with rec gp160 showed a problem KQIINMWQEVGKAMYA	
gp160 (421–436)	gp120 (428–443 IIIB, B10) • Epitope name: T1	KQIINMWQEVGKAMYA	computer prediction	murine (H- $2^{k,d,s}$ )	Cease1987

HXB2 Location	<b>Author's Location</b>	Sequence	Immunogen	Species (HLA)	References
gp160 (421–436)	gp120 (428–443 IIIB)  Vaccine Strain: IIIB   Epitope name: T1  Six multidaterminant ha	KQIINMWQEVGKAMYA  HIV component: gp160  lper T-cell regions are recognize	Vaccine	murine (H-2 <sup>k,d,t4</sup> )	Hale1989
gp160 (421–436)	gp120 (428–443 IIIB)  Vaccine Vector/Type: pe  Epitope name: T1  first identified Th epitop  Alanine at position 436  Vaccines with a CTL ep  T1 peptide linked to CT.	KQIINMWQEVGKAMYA eptide Strain: IIIB HIV comp	Vaccine  ponent: polyepitope  nces MHC binding and antigenic lper epitope yielded greatly enharucts used to immunize mice: K	murine (H-2 <sup>k</sup> )  city of peptide by several orders anced CTL response relative to QIINMWQEVGKAMYAPPISO	the wildtype helper epitope GQIRRIQRGPGRAFVTIGK,
gp160 (421–444)	KQIINMWQAVGKAM gp160 (428–451 IIIB)  Vaccine Vector/Type: re KQIINMWQEVGKAM Six multideterminant reg infected people This cluster peptide elici B10.A(5R) mice (H-2A)	KQIINMWQEVGKAMYAPPI- SGQIR combinant protein <i>Strain:</i> IIIE IYAPPISGQIR encompasses sev	HIV-1 infection, Vaccine  3 HIV component: gp160 Adveral murine Th epitopes and is rated Th responses in different Mells from all H-2 haplotypes tested 2As, Es)	human, murine $(H-2^k, H-2^b, H-2^b, H-2^s, H-2^d)$ ljuvant: Freund's adjuvant referred to as a "multidetermina IHC/HLA backgrounds after valed: B10.BR mice $(H-2A^k, E^k)$ , and the sum of the sum	Berzofsky1991b, Berzofsky1991a  nt region" or cluster peptide ccination of mice with gp160, or in
gp160 (421–444)	gp120 (428–451 IIIB)  Vaccine Vector/Type: pe  Epitope name: T1  Linked to a CTL epitope	KQIIMNWQEVGKAMYAPPI- SGQIR eptide <i>Strain:</i> IIIB		murine $(H2^d)$	Shirai1996a
gp160 (423–440)	<ul><li>activation antigens CD2.</li><li>The ability to express ac</li><li>This study investigated 0</li></ul>	5 and CD71 etivation markers in response to 1	HIV is retained, but the response PBMC from patients at various st	e to tetanus toxoid recall antiger	Caruso1997 n, but retain the ability to express the n is lost g the response to in vitro stimulation
gp160 (424–438)	gp120 (424–438 IIIB, B10) • 12 gag and 18 env peptic	INMWQEVGKAMYAPP	HIV-1 infection	human	Wahren1989b, Wahren1989a

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
gp160 (425–439)	gp160 (432–446 IIIB)	NMWQEVGKAMYAPPI	Vaccine	murine (H-2 <sup>s</sup> )	Berzofsky1991b, Berzofsky1991a
	• B10.S(9R) (H-2A <sup>s</sup> , E <sup>s</sup> ) 1	mice immunized with rec gp160 YAPPISGQIR encompasses sever	HIV component: gp160 Adjuva showed a proliferative response to the eral murine Th epitopes including N	this peptide	nd is referred to as a
gp160 (425–439)	gp120 (432–446 IIIB)  Vaccine Strain: IIIB H  Six multideterminant he		Vaccine  I by mice of three or four MHC typ	murine (H- $2^{t4}$ ) es	Hale1989
gp160 (426–441)		MWQEVGKAMYAPPIGC BMC from non-infected individu t always induce T-cells that recog		human	Manca1995b
gp160 (430–444)	gp160 (437–451 IIIB)	VGKAMYAPPISGQIR	Vaccine	murine $(H-2^k, H-2^b, H-2^s, H-2^d)$	Berzofsky1991b, Berzofsky1991a
	• This peptide elicited pro (H-2A <sup>b</sup> , E <sup>b</sup> ), and B10.Se	liferative responses in cells from (9R) mice (H-2A <sup>s</sup> , E <sup>s</sup> ) YAPPISGQIR encompasses seve		mice (H-2A $^k$ , E $^k$ ), B10.D2	mice (H-2A $^d$ , E $^d$ ), B10.A(5R) mice is referred to as a "multideterminant
gp160 (430–444)	gp120 (437–451 IIIB)  Vaccine Strain: IIIB F  • Six multideterminant he		Vaccine  I by mice of three or four MHC typ	murine (H- $2^{k,d,i5,t4}$ ) es	Hale1989
gp160 (430–453)	gp120 (430–453)	VGKAMYAPPISGQIRCSSN- ITGLL	Vaccine	murine (H-2 <sup>b</sup> )	Sjolander1996
	<ul><li>Study demonstrates that</li><li>Peptide stimulation of an</li></ul>	n in vitro proliferative response re	nent: gp160 roteins can depend on the glycosyla equired in vivo priming with glycos tope, but may be important for epit	sylated protein	
gp160 (432–451)	gp120 (432–451 IIIB)	KAMYAPPISGQIRCSSNIT- G?	HIV-1 infection	human	Geretti 1994
	<ul> <li>After 12 months, most remonths, as did 5/15 non-</li> </ul>	ls. 10 of the responding patients esponses were lost or diminished responders. Hore sensitive and well-preserved	tic HIV-1+ patients. PBMC from 1 recognized three or more peptide portion, and specific responses fluctuated.  measure of Th function than prolif	ools. 4/10 of the responders at b	

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References				
gp160 (433–447)	adjuvant	•		murine (H-2 IA <sup>b</sup> ) B), UG92005 (clade D) HIV composing gnized by ten hybridomas with V $\beta$ us	-				
	determined – among the	e ND V $\beta$ set, three V $\alpha$ s were in	identified, $V\alpha$ 2, 8, and 11	-1 Env antigens: Mice were primed wi	- '				
	boosted with VV, and 3	-4 weeks later boosted again w	vith purified protein in Freu	nd's adjuvant					
	the DNA construct is in CHO-K1 cells	<ul> <li>The vaccinia construct is a pSC11-based VV vector with the first 38 amino acids contributed by BH10 and the rest of gp120 and gp41 by the vaccine strain, the DNA construct is in the pJW4303 vector with a CMV promotor, and the purified protein is expressed from the pJW4303 vector transfected into CHO-K1 cells</li> </ul>							
	and $V\beta$ usage was deter	rmined		cion using either B6 spleen cells or H-2					
	HIV-1 92UG005, a clad	with an Env from either one of le D vaccine isolated from Uga ere characterized from six mic	anda in 1992 through the W	clade B strain isolated from an individ THO	dual from Memphis Tennesee, and				
		lper epitopes were concentrate		in the Env sequence (2 clonotype respo	onses in V2, 26 in C2, 22 in V3, 23				
	non-uniform localizatio			v sequence, in exposed, non-helical str d the glycosylation site proximity may					
gp160 (436–451)		APPIGGQISCSSNITY PBMC from non-infected indivot always induce T-cells that re		human	Manca1995b				
gp160 (438–460)	gp120 (443–465 NL43)	PISGQIRCSSNITGLLLT:	R- Vaccine	human	Sitz1999				
	There was a great bread	ecombinant protein Strain: N	env peptides in 19 HIV-1 in	nfected rgp160 and 17 HIV-1 infected	rgp120 vaccine recipients				
gp160 (439–448)	HIV-1 specific T-cell lin	ecombinant protein Strain: V	negative volunteer vaccinate	human p120 Adjuvant: QS21/MPL adjuvant ed with rgp120 and a QS21/MPL adjuv s IGGOIRCSSN					
		first reactive peptide, EVGKA		s a single substitution and induces pro	liferation as well as the original				
gp160 (446–461)	•	SSNITGLLLTRDGGTC PBMC from non-infected indivot always induce T-cells that re		human	Manca1995b				

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References				
gp160 (452–471)	gp120 (452–471 IIIB)	LLLTRDGGNSNNESEIFRP- G?	HIV-1 infection	human	Geretti1994				
	<ul> <li>Epitope name: I1</li> <li>Th proliferative responses were studied in 36 asymptomatic HIV-1+ patients. PBMC from 15/36 patients responded to stimulation with gp120 synthetic overlapping peptide pools. 10 of the responding patients recognized three or more peptide pools.</li> <li>After 12 months, most responses were lost or diminished, and specific responses fluctuated. 4/10 of the responders at baseline had new responses at 12 months, as did 5/15 non-responders.</li> <li>IL-2 production was a more sensitive and well-preserved measure of Th function than proliferation.</li> <li>2/15 responders recognized this peptide, average SI = 3.5.</li> </ul>								
gp160 (456–470)		RDGGTNVTNDTEVFRC  BMC from non-infected individuate talways induce T-cells that recognized that recognized the street that the control of the street that the control of the street that the control of the street that the st		human	Manca1995b				
gp160 (459–473)	gp120 (459–473 IIIB, B10) • 12 gag and 18 env peptio	GNSNNESEIFRPGGG  des were identified that could con	HIV-1 infection	human	Wahren1989b, Wahren1989a				
gp160 (468–483)	gp120 (466–481)	FRPGGGDMRDNWRSEL	HIV-1 infection ulation may enhance cell-mediated	human	Krowka1990				
gp160 (472–491)	gp120 (472–491 IIIB)	GGDMRDNWRSELYKYKVVK- I?	HIV-1 infection	human	Geretti1994				
	<ul> <li>Epitope name: I3</li> <li>Th proliferative responses were studied in 36 asymptomatic HIV-1+ patients. PBMC from 15/36 patients responded to stimulation with gp120 synthetic overlapping peptide pools. 10 of the responding patients recognized three or more peptide pools.</li> <li>After 12 months, most responses were lost or diminished, and specific responses fluctuated. 4/10 of the responders at baseline had new responses at 12 months, as did 5/15 non-responders.</li> </ul>								
		for sensitive and well-preserved and this peptide, average $SI = 7.2$ .	measure of Th function than prolife .	ration.					
gp160 (474–488)	gp120 (474–488 IIIB, B10)	DMRDNWRSELYKYKV	HIV-1 infection	human	Wahren1989b, Wahren1989a				
160 (456 400)		des were identified that could con	•	· arek rres	P. Cl. 10011				
gp160 (476–490)	gp160 (483–497 IIIB)	RDNWRSELYKYKVVK	Vaccine	murine $(H-2^k, H-2^s)$	Berzofsky1991b, Berzofsky1991a				
	<ul> <li>Vaccine Vector/Type: recombinant protein Strain: IIIB HIV component: gp160 Adjuvant: Freund's adjuvant</li> <li>This peptide elicited proliferative responses in B10.BR mice (H-2A<sup>k</sup> and B10.S(9R) mice (H-2A<sup>s</sup>, E<sup>s</sup>)</li> <li>RDNWRSELYKYKVVKIEPLGVAPT encompasses several murine Th epitopes including RDNWRSELYKYKVVK and is referred to as a "multideterminant region" or cluster peptide</li> </ul>								
gp160 (476–490)	gp120 (483–497 IIIB) Vaccine Strain: IIIB H	RDNWRSELYKYKVVK IIV component: gp160	Vaccine	murine (H- $2^{d,t4}$ )	Hale1989				

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
	Six multideterminant helps	lper T-cell regions are recognized	d by mice of three or four MH	C types	
gp160 (476–499)	gp160 (483–506 IIIB)  Vaccine Vector/Type: rec	RDNWRSELYKYKVVKIEPL- GVAPT combinant protein Strain: IIIB	,	human, murine $(H-2^k, H-2^b, H-2^s, H-2^d)$ Adjuvant: Freund's adjuvant	Berzofsky1991b, Berzofsky1991a
	<ul> <li>RDNWRSELYKYKVV</li> <li>Six multideterminant reginfected people</li> <li>This cluster peptide elici B10.A(5R) mice (H-2A<sup>L</sup></li> </ul>	KIEPLGVAPT encompasses sev gion cluster peptides were evalua	eral murine Th epitopes and is ted Th responses in different I ls from all H-2 haplotypes tes $A^s$ , $E^s$ )	s referred to as a "multideterminal MHC/HLA backgrounds after vacted: B10.BR mice (H- $2A^k$ , $E^k$ ), E	cination of mice with gp160, or in
gp160 (479–498)	<ul> <li>Epitope name: 2013</li> <li>Hartley guinea pigs were (DTH) responses after v.</li> <li>A total of 7 gp120 peptic gp120. The vaccine delivered to the control of th</li></ul>	e intradermally injected with eith accination, which are related to des elicited a delayed type hypervery system, DNA versus rec pro	rer recombinant protein or plas fh1 T-cell responses. CFA did sensivity (DTH) response afte stein, resulted in the recognition	not augment responses in animal or vaccination, out of a set of 60 or	ored for delayed type hypersensivity s vaccinated with plasmid. Verlapping peptides that spanned
gp160 (482–501)	HIV-1 env DNA vaccine	ELYKYKVVKIEPLGVAPTKA NA Strain: IIIB HIV compone induced Th cell response to this by both monkeys used in this stu	ent: ENV epitope in a rhesus monkey	Rhesus macaque	Lekutis1997b
gp160 (482–501)	<ul> <li>overlapping peptide pool</li> <li>After 12 months, most remonths, as did 5/15 non-</li> <li>IL-2 production was a month of the second of the second</li></ul>	ls. 10 of the responding patients esponses were lost or diminished	ntic HIV-1+ patients. PBMC for recognized three or more pept, and specific responses fluctumeasure of Th function than	ated. 4/10 of the responders at ba	
gp160 (483–502)	coli (mLT) • Epitope name: Peptide 4 • Helper T-cell proliferativ gp120. Promiscuously in	46 we responses to gp120 vaccines in mmunodominant peptides were in actural disorder in proximal N-te	HIV component: gp120 A  1 2 mouse strains, CBA/J and dentified in both mice strains	murine Adjuvant: R192G mutant heat-lab BALB/c, were mapped using 47 of that were located in the outer dom B-D protein structure influences The	overlapping peptides that span ain of gp120 and were associated

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
	• This peptide was reactive	e in 7/10 BALB/c mice tested, ar	nd in only 1/10 CBA/J mice.		
gp160 (484–496)	gp120 (484–496 HXB2)	YKYKVVKIEPLGV	Vaccine	Rhesus macaque (DR*W201)	Lekutis1998
	<ul> <li>Variants of this epitope HIV-1 env-specific CD4</li> </ul>		(K) retained ability to bind to MHC	class II, but failed to induc	e proliferation/cytokine secretion in
gp160 (484–498)	gp120 (484–498 IIIB, B10) • 12 gag and 18 env peption	YKYKVVKIEPLGVAP  des were identified that could cor	HIV-1 infection  mmonly evoke T-cell responses.	human	Wahren1989b, Wahren1989a
gp160 (484–499)	gp120 (492–506 IIIB)  Vaccine Strain: IIIB F  Six multideterminant he		Vaccine d by mice of three or four MHC type	murine (H- $2^{d,k,t4,i5}$ )	Hale1989
gp160 (485–499)	gp160 (492–506 IIIB)	KYKVVKIEPLGVAPT	Vaccine	murine $(H-2^k, H-2^b, H-2^s, H-2^d)$	Berzofsky 1991b, Berzofsky 1991a
	• This peptide elicited pro (H-2A <sup>b</sup> , E <sup>b</sup> ), and B10.S	liferative responses in cells from (9R) mice (H-2A <sup>s</sup> , E <sup>s</sup> ) KIEPLGVAPT encompasses sev	HIV component: gp160 Adjuvan all H-2 haplotypes tested: B10.BR rear murine Th epitopes including K	nice $(H-2A^k, E^k)$ , B10.D2	
gp160 (485–500)		KYKVIKIEPLGIAPTC BMC from non-infected individuot always induce T-cells that recognitions.		human	Manca1995b
gp160 (486–494)	gp120 (486–494 IIIB)	YKVVKIEPL	SHIV infection	Rhesus macaque (DRB*W201)	Lekutis1997a
-	C5 region minimal epito	ppe determined through fine epito	ppe mapping		
gp160 (487–512)	gp120 (494–518 IIIB)	KVVKIEPLGVAPTKAKRRV- VQREKRC	Vaccine	murine	Goodman-Snitkoff1990
	<ul><li>Vaccine Vector/Type: pe</li><li>Identification of putative</li></ul>	-	ntibody response in peptide immuniza	ed mice	
gp160 (492–512)	gp120 (492–512 IIIB)	EPLGVAPTKAKRRVVQREK- RA?	HIV-1 infection	human	Geretti1994
	overlapping peptide poo • After 12 months, most remonths, as did 5/15 non-	ls. 10 of the responding patients esponses were lost or diminished responders.	atic HIV-1+ patients. PBMC from 15 recognized three or more peptide pool, and specific responses fluctuated. 4 measure of Th function than prolifer	ols. /10 of the responders at ba	

<b>HXB2</b> Location	<b>Author's Location</b>	Sequence	Immunogen	Species (HLA)	References		
	• 1/15 responders recogn	ized this peptide, SI = 4.9.					
gp160 (493–511)	coli (mLT)	PIGVAPTRAKRRTVQREKR ecombinant protein Strain: 89.6	Vaccine HIV component: gp120	murine  Adjuvant: R192G mutant heat-la	Dai2001 bile toxin from enterotoxigenic E.		
	gp120. Promiscuously with regions of local str frequency of immunoge	ive responses to gp120 vaccines in immunodominant peptides were ic ructural disorder in proximal N-ter	dentified in both mice strains rminal segments, suggesting	s that were located in the outer do 3-D protein structure influences	main of gp120 and were associated		
gp160 (499–511)	gp120 (IIIB)  Thought to be a mimic Response to this epitop Presentation of epitope	TKAKRRVVEREKR  of a HLA class II DR β chain vari e may cause a breakdown of self-t induced autoreactive T-cell lines i ation to soluble antigens by the CI	in vitro stimulation iable region olerance n PBMC from uninfected do	human (DR)	Wilson1997b observed		
gp160 (519–543)		FLGFLGAAGSTMGAASLTL- TVQARC peptide ed from conserved region of the H o this peptide was observed in 3/3	IV-1 envelope that stimulate		Nehete1993 , and in rhesus monkeys		
gp160 (519–543)	Env (519–543)	FLGFLGAAGSTMGAASLTL- TVQARQ	HIV-1 infection	human, chimpanzee	Nehete1998b		
	<ul> <li>HIV-infected chimpanz</li> <li>Env</li> </ul>	ees and HIV-positive patients show	w positive proliferative response	onses to multiple peptides from five	ve conserved regions of the HIV-1		
gp160 (519–543)	gp41 (519–543)	FLGFLGAAGSTMGAASLTL- TVQARC	Vaccine	murine (H- $2^{bxk,sxd}$ )	Sastry1991		
	<ul> <li>Vaccine Vector/Type: peptide</li> <li>Peptides induced T-cell proliferative response to immunizing peptide and to gp160</li> </ul>						
gp160 (547–561)	gp41 (547–561 IIIB, B10)	GIVQQQNNLLRAIEA	HIV-1 infection	human	Wahren1989b, Wahren1989a		
	• 12 gag and 18 env peptides were identified that could commonly evoke T-cell responses.						
gp160 (562–576)	gp41 (562–576 IIIB, B10)	QQHLLQLTVWGIKQL	HIV-1 infection	human	Wahren1989b, Wahren1989a		
	• 12 gag and 18 env pept	ides were identified that could con	nmonly evoke T-cell respons	ses.			
gp160 (572–591)	gp41 (572–591) <b>Vaccine</b> <i>Vector/Type:</i> p	GIKQLQARILAVERYLKDQQ peptide	Vaccine	murine $(H-2^{d,b})$	Brown1995		
		d immunogen in BALB/c and CBA	A mice, producing a strong p	proliferative response			

• At least one of the four residues GIKQ enhances stimulation, and in CBA mice these residues influence the ability to prime T-cells in vivo

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References		
		ulated the greatest in vitro T-cell minimal reactive sequence recogn					
gp160 (576–591)	gp41 (576–591) Vaccine Vector/Type: pe	•	Vaccine	murine (H- $2^{d,b}$ )	Brown1995		
		immunogen in BALB/c and CBA	mice used in this experiment, produ	ucing a weak proliferative r			
gp160 (578–608)	gp41 (585–615 IIIB)	ARILAVERYLKDQQLLGIW- GCSGKLICTTAV	Vaccine	murine	Goodman-Snitkoff1990		
	<ul><li>Vaccine Vector/Type: pe</li><li>Identification of putative</li></ul>		n antibody response in peptide immu	unized mice			
gp160 (579–601)	gp41 (579–601)	RILAVERYLKDQQLLGGIW- GCSGK	Vaccine	murine (H- $2^{d,b}$ )	Brown1995		
		immunogen in BALB/c and CBA					
		Q than to immunizing peptide	strains which was more responsive t	towards GIKQLQARILAVI	ERYLKDQQ and		
gp160 (579–604)	gp41 (584–609 LAI)	RILAVERYLKDQQLLGIWG- CSGKLIC	HIV-1 infection	human	Schrier1989		
	Stimulates T-cell proliferation in HIV-infected donors						
gp160 (586–597)	Env (586–598)  • HIV-infected chimpanze Env	YLRDQQLLGIWG ees and HIV-positive patients show	HIV-1 infection w positive proliferative responses to	human, chimpanzee multiple peptides from five	Nehete1998b conserved regions of the HIV-1		
gp160 (586–598)		ed from conserved region of the H	Vaccine  IV-1 envelope that stimulates a prolimmunized rhesus monkeys, with a				
gp160 (593–604)	gp41 (593–604 IIIB) • Elicits T-cell proliferation	LGIWGCSGKLIC on and B cell responses, but only of	HIV-1 infection during the asymptomatic phase of H	human IV infection	Bell1992		
gp160 (593–604)	gp41 (598–609 LAV-1) • Murine T-dependent B-o	LGLWGCSGKLIC cell response – 7/29 had a prolifer	Vaccine rative response to this peptide	murine (H2 <sup>d</sup> )	Schrier1988		
gp160 (594–603)	• Immunization with a p2	4-VLP virus-like particle did not VLP did not increase the prolifer	HIV-1 infection [Bell1992], but in Bell <i>et al.</i> it was disignificantly impact CD4+ lymphocative response to this gp41 epitope,	yte count, viral load, or p24	antibody titre		
gp160 (594–604)	gp41 (consensus) • Core region of peptides	GIWGCSGKLIC that can stimulate proliferative re-	HIV-1 infection sponses from seronegative and serop	human positive people	Mutch1994		

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
gp160 (598–609)	gp41 (603–614 LAI) • Stimulates T-cell prolifer	CSGKLICTTAVP ration in HIV-infected donors	HIV-1 infection	human	Schrier1989
gp160 (604–615)	gp41 (609–620 LAI) • Stimulates T-cell prolifer	CTTAVPWNASWS ration in HIV-infected donors	HIV-1 infection	human	Schrier1989
gp160 (606–620)	adjuvant  ■ This gp140 epitope of U		Vaccine in Strain: 1007 (clade B), UG9200 egnized by five hybridomas with $V\beta$		
	<ul> <li>boosted with VV, and 3-</li> <li>The vaccinia construct is the DNA construct is in the CHO-K1 cells</li> <li>Ten days after the final beand Vβ usage was determed to the Mice were immunized with HIV-1 92UG005, a clade 80 unique clonotypes were H-2 IA<sup>b</sup> restricted T-help in V4C4, and 7 in gp41)</li> <li>Epitope hotspots tended</li> </ul>	4 weeks later boosted again with a pSC11-based VV vector with the pJW4303 vector with a CMV vector, hybridomas were made and mined with an Env from either one of two ED vaccine isolated from Ugand are characterized from six mice per epitopes were concentrated in to be proximal to heavily glycos a may be influenced by differentiated.	egy involving three HIV-1 Env antigon purified protein in Freund's adjuvant the first 38 amino acids contributed of promotor, and the purified protein is different to clades: HIV-1 1007, a clade B strata in 1992 through the WHO in 5 distinct regions within the Env second antigen processing and the glycostal antigen processing and the glycostal in the second in the	by BH10 and the rest of grains expressed from the pJW4 ther B6 spleen cells or H-2 in isolated from an individual equence (2 clonotype responsible exposed, non-helical strains).	ol 120 and gp41 by the vaccine strain, 1303 vector transfected into  IA <sup>b</sup> transfected L cells as targets and from Memphis Tennesee, and the ses in V2, 26 in C2, 22 in V3, 23 ands of the protein. The
gp160 (609–616)	gp41 (consensus)	PWNASWSN	HIV-1 infection esponses from seronegative and seron	human positive people	Mutch1994
gp160 (611–620)	adjuvant  This gp41 epitope is con were vaccinated with dif  The epitope described he (T[TN]VPWNASWSNK and UG92005 has an N i  C57BL/6 mice were imm boosted with VV, and 3-  The vaccinia construct is	NA, vaccinia, recombinant prote served in 1007 (US, clade B) an ferent clades – the $V\beta$ usage was the is the region of overlap of two	o 15 mers that were both able to stim NN) – the only difference between 10	recognized by two hybridor nulate IL-2 production from 007 and UG92005 for these ens: Mice were primed with the by BH10 and the rest of gp	mas from two different mice that the hybridoma the two proteins is that 1007 has a T th DNA given i.m., 3-4 weeks later to 120 and gp41 by the vaccine strain,

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
	<ul> <li>and Vβ usage was dete</li> <li>Mice were immunized HIV-1 92UG005, a class</li> <li>80 unique clonotypes v</li> <li>H-2 IA<sup>b</sup> restricted T-he in V4C4, and 7 in gp41</li> <li>Epitope hotspots tende</li> </ul>	ermined with an Env from either de D vaccine isolated for were characterized from elper epitopes were cort).  d to be proximal to head on may be influenced by	ncentrated in 5 distinct regions within the avily glycosylated regions of the Env sec by differential antigen processing and the	le B strain isolated from an individual e Env sequence (2 clonotype resquence, in exposed, non-helical s	vidual from Memphis Tennesee, and ponses in V2, 26 in C2, 22 in V3, 23 strands of the protein. The
gp160 (614–629)	gp41 (IIIB)  • Peptide stimulation of  • Peptide priming does n			human	Manca1995b
gp160 (634–649)	gp41 (IIIB)  • Peptide stimulation of  • Peptide priming does n			human	Manca1995b
gp160 (647–661)	gp41 (647–661 IIIB, B10) • 12 gag and 18 env pept	EESQNQQEKNEQE	HIV-1 infection at could commonly evoke T-cell respons	human ses.	Wahren1989b, Wahren1989a
gp160 (650–662)	gp41 (655–667 LAI) • Stimulates T-cell prolif	QNQQEKNEQELLE		human	Schrier1989
gp160 (667–681)	gp41 (667–681 IIIB, B10) • 12 gag and 18 env pept	ASLWNWFNITNWI	HIV-1 infection at could commonly evoke T-cell respons	human ses.	Wahren1989b, Wahren1989a
gp160 (682–696)	gp41 (682–696 IIIB, B10) • 12 gag and 18 env pept	IKLFIMIVGGLVC	GLR HIV-1 infection at could commonly evoke T-cell respons	human ses.	Wahren1989b, Wahren1989a
gp160 (724–745)	<ul> <li>A gp41 peptide was ex</li> </ul>	DRS peptide in cowpea mospressed in a cowpea mulate anti-gp41 antiboo	EGGERDR – Vaccine  aic virus (CPMV) HIV component: gp osaic virus (CPMV) and mice were vacc dies and an in vitro proliferative response ggesting a Th1 response	cinated with a purified chimeric	
gp160 (732–744)	gp41 (737–749 LAI) • Stimulates T-cell prolif	GIEEEGGERDRDF eration in HIV-infected		human	Schrier1989

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References					
gp160 (780–794)	gp160 (787–801 IIIB)	RIVELLGRRGWEALK	Vaccine	murine $(H-2^k, H-2^d, H-2^s)$	Berzofsky1991b, Berzofsky1991a					
	<ul><li>This peptide elicited pro</li><li>RIVELLGRRGWEALK</li></ul>	liferative responses in cells from YWWNLLQYWSQELKNSAV	HIV component: gp160 Adjuva B10.BR mice (H-2A $^k$ , E $^k$ ), B10.D2 S encompasses several murine Th enger peptide only stimulates cells from	mice (H-2A $^d$ , E $^d$ ), and B1 bitopes including RIVELLO	0.S(9R) mice (H-2A <sup>s</sup> , E <sup>s</sup> ) GRRGWEALK and is referred to as					
gp160 (780–794)	gp41 (787–801 IIIB)  Vaccine Strain: IIIB    • Six multideterminant he		Vaccine  1 by mice of three or four MHC type	murine (H- $2^{d,k,t4}$ )	Hale1989					
gp160 (780–813)	gp160 (787–820 IIIB)	RIVELLGRRGWEALKYWWN- LLQYWSQELKNSAVS	HIV-1 infection, Vaccine	murine (H-2 <sup>k</sup> )	Berzofsky1991b, Berzofsky1991a					
	<ul> <li>RIVELLGRRGWEALK cluster peptide</li> </ul>	Vaccine Vector/Type: recombinant protein Strain: IIIB HIV component: gp160 Adjuvant: Freund's adjuvant  • RIVELLGRRGWEALKYWWNLLQYWSQELKNSAVS encompasses several murine Th epitopes and is referred to as a "multideterminant region" or								
	$(H-2A^b, E^b)$ , or B10.S(9	$(R)$ mice $(H-2A^s, E^s)$	ls from only B10.BR mice (H- $2A^k$ , in 59% (17/29) of asymptomatic H		mice (H-2A $^d$ , E $^d$ ), B10.A(5R) mice					
gp160 (794–808)	gp160 (801–815 IIIB)	KYWWNLLQYWSQELK	Vaccine	murine $(H-2^k, H-2^d, H-2^s)$	Berzofsky1991b, Berzofsky1991a					
	<ul><li>This peptide elicited pro</li><li>RIVELLGRRGWEALK</li></ul>	liferative responses in cells from YWWNLLQYWSQELKNSAV	HIV component: gp160 Adjuva B10.BR mice (H-2A <sup>k</sup> , E <sup>k</sup> ), B10.D2 S encompasses several murine Th el longer peptide only stimulates cells	mice (H-2A $^d$ , E $^d$ ), and B1 bitopes including KYWW						
gp160 (794–808)	gp41 (801–815 IIIB)  Vaccine Strain: IIIB F  Six multideterminant he		Vaccine  I by mice of three or four MHC type	murine (H-2 <sup>k</sup> )	Hale1989					
gp160 (799–813)	gp160 (806–820 IIIB)	LLQYWSQELKNSAVS	Vaccine	murine $(H-2^k, H-2^d, H-2^s)$	Berzofsky1991b, Berzofsky1991a					
	<ul><li>This peptide elicited pro</li><li>RIVELLGRRGWEALK</li></ul>	liferative responses in cells from YWWNLLQYWSQELKNSAV	HIV component: gp160 Adjuva. B10.BR mice (H-2A $^k$ , E $^k$ ), B10.D2 S encompasses several murine Th enger peptide only stimulates cells from	mice (H-2A $^d$ , E $^d$ ), and B1 bitopes including LLQYWS	·					
gp160 (799–813)	gp41 (806–820 IIIB)  Vaccine Strain: IIIB H  Six multideterminant he		Vaccine  I by mice of three or four MHC type	murine $(H-2^{k,d,t^4})$	Hale1989					

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
gp160 (799–813)	gp41 (806–820 IIIB)  Vaccine Strain: IIIB  Six multideterminant he		Vaccine and by mice of three or four MHC type	murine (H- $2^{k,d,t^4}$ )	Hale1989
gp160 (814–829)		WLNATAIAVTEGTDRC PBMC from non-infected individent always induce T-cells that reco		human	Manca1995b
gp160 (821–835)	gp160 (828–842 IIIB)	AVAEGTDRVIEVVQG	Vaccine	murine (H- $2^k$ , H- $2^b$ , H- $2^s$ )	Berzofsky 1991b, Berzofsky 1991a
	This peptide elicited pr	oliferative responses in cells from GAYRAIRHIPRRIRQGLER enco	B HIV component: gp160 Adjuvant B10.BR mice (H-2A <sup>k</sup> , E <sup>k</sup> ), B10.A(compasses several murine Th epitopes	5R) mice (H-2A $^b$ , E $^b$ ), and	
gp160 (821–835)	gp41 (828–842 IIIB)  Vaccine Strain: IIIB  • Six multideterminant he		Vaccine d by mice of three or four MHC type	murine (H-2 <sup>k</sup> )	Hale1989
gp160 (821–838)	<ul><li>activation antigens CD2</li><li>The ability to express a</li><li>This study investigated</li></ul>	25 and CD71 ctivation markers in response to I	HIV-1 infection Is show reduced ability to proliferate HIV is retained, but the response to to BMC from patients at various stages es, or p17 and p24	etanus toxoid recall antiger	is lost
gp160 (821–853)	gp160 (828–860 IIIB)	AVAEGTDRVIEVVQGAYRA- IRHIPRRIRQGLER	HIV-1 infection, Vaccine  HIV component: gp160 Adjuva.	human, murine $(H-2^k, H-2^b, H-2^s, H-2^d)$	Berzofsky1991b, Berzofsky1991a
	<ul> <li>AVAEGTDRVIEVVQC peptide</li> <li>Six multideterminant rein infected people</li> <li>This cluster peptide elic B10.A(5R) mice (H-2A)</li> </ul>	GAYRAIRHIPRRIRQGLER encorgion cluster peptides were evaluated proliferative responses in ce $(b, E^b)$ , and B10.S(9R) mice (H-2	ompasses several murine Th epitopes ated for Th responses in different ME alls from all four MHC types tested: 1	s and is referred to as a "muHC/HLA backgrounds after B10.BR mice $(H-2A^k, E^k)$ ,	vaccination of mice with gp160, or
gp160 (827–835)	gp41 (834–842 IIIB)  Vaccine Strain: IIIB  • Suggested H-2 <sup>k</sup> epitope	DRVIEVVQG  HIV component: gp160 based on region of overlap	Vaccine	murine (H-2 <sup>k</sup> )	Hale1989
gp160 (827–841)	• Epitope name: TH4		Vaccine Strain: IIIB HIV component: gp1 response to gp160 immunization	Rhesus macaque 60	Hosmalin1991

<b>HXB2</b> Location	<b>Author's Location</b>	Sequence	Immunogen	Species (HLA)	References
	• Called Th4.1 and TH4				
gp160 (827–841)	gp41 (834–848 IIIB) • Epitope name: TH4 • used in a study of the in	DRVIEVVQGAYRAIR  Ifluence of pentoxifylline on HIV	HIV-1 infection	human	Clerici 1997
gp160 (827–841)	gp41 (834–848 IIIB) • Epitope name: TH4	DRVIEVVQGAYRAIR	posed but uninfected health care wo	human	Pinto1995
gp160 (827–841)	gp41 (834–848 IIIB)  • Epitope name: TH4  • Peptides stimulate Th c  • Called Th4.1 and TH4	DRVIEVVQGAYRAIR ell function and CTL activity in si	HIV-1 infection	human	Clerici 1991a
gp160 (827–841)	• Epitope name: TH4	DRVIEVVQGAYRAIR ecombinant protein Strain: IIIB individuals with rgp160 results in	Vaccine HIV component: gp160  a stronger Th response than does nat	human tural infection	Clerici1991b
gp160 (827–841)	gp41 (834–848 IIIB)  • Epitope name: TH4  • Cell-mediated immune  • Called Th4.1 and TH4	DRVIEVVQGAYRAIR response to HIV-1 peptides in HI	V-1 exposed seronegative men	human	Clerici 1992
gp160 (827–841)	gp41 (834–848 IIIB)  • Epitope name: TH4  • IL-2 production detection  • Called Th4.1 and TH4	DRVIEVVQGAYRAIR on of Th lymphocytes from asymp	HIV-1 infection ptomatic HIV-positive individuals	human	Clerici 1989
gp160 (827–841)	cases) and mucosal gen	ital tract anti-HIV IgA (16/21 cas	HIV-1 infection  and to frequently have HIV-env pepties) ously described [Clerici1989], and v		
gp160 (827–841)	gp41	DRVIEVVQGAYRAIR	HIV-1 infection, HIV-1 exposed seronegative	human	Kuhn2001
	• Enitone name: TH4 Th	4.1			

- Epitope name: TH4, Th4.1
- In a S. African perinatal transmission study, 33% (33/86) of cord blood samples from infants with seropositive mothers produced T-helper responses (measured by a bioassay measuring IL2 production in a murine cell line and confirmed with a proliferation assay) against a peptide cocktail containing Th epitopes P18 MN, P18 IIIB, T1, T2, and TH4
- The mothers were predominantly infected with subtype C, but the T help response was detectable in a number of cord blood samples despite using peptides based on B subtype reagents.

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
	<ul><li>with cord blood that was</li><li>Measurable HIV specific</li></ul>	s unresponsive to Env peptide sti c T help responses elicited in the	re infected <i>in utero</i> , 2/33 were lost mulation were infected before deliving immunologically immature newboar-infant transmission of HIV-1.	very, and 8/47 contracted HI	V intrapartum or via breast-feeding.
gp160 (827–841)	gp160 (834–848 IIIB)	DRVIEVVQGAYRAIR	Vaccine	murine $(H-2^k, H-2^b)$	Berzofsky1991b, Berzofsky1991a
			HIV component: gp160 Adjuve B10.BR mice (H-2A $^k$ , E $^k$ ) and B1		·
gp160 (827–841)	gp41 (834–848 IIIB)  Vaccine Strain: IIIB F  Epitope name: TH4	DRVIEVVQGAYRAIR HIV component: gp160	Vaccine	murine (H-2 <sup><i>k</i>,<i>i</i>5</sup> )	Hale1989
		lper T-cell regions are recognize	d by mice of three or four MHC typ	pes	
gp160 (829–843)	gp160 (836–850 IIIB)	VIEVVQGAYRAIRHI	Vaccine	murine $(H-2^k, H-2^b)$	Berzofsky1991b, Berzofsky1991a
			HIV component: gp160 Adjuvent B10.BR mice (H-2A <sup>k</sup> , E <sup>k</sup> ) and B1		
gp160 (834–841)	gp41 (841–848 IIIB)  Vaccine Strain: IIIB F  Suggested H-2 <sup>k</sup> epitope	QGAYRAIR HIV component: gp160 based on region of overlap	Vaccine	murine (H-2 <sup>i5</sup> )	Hale1989
gp160 (834–848)	gp160 (841–855 IIIB)	QGAYRAIRHIPRRIR	Vaccine	murine $(H-2^k, H-2^b, H-2^d, H-2^d, H-2^s)$	Berzofsky1991b, Berzofsky1991a
			HIV component: gp160 Adjuvent B10.BR mice (H- $2A^k$ , $E^k$ ), B10.A	ant: Freund's adjuvant	•
gp160 (834–848)	gp41 (841–855 IIIB) <b>Vaccine</b> <i>Strain:</i> IIIB <i>H</i> • Six multideterminant he		Vaccine d by mice of three or four MHC typ	murine (H-2 <sup>d,t4,i5</sup> )	Hale1989
gp160 (839–848)	gp41 (846–855 IIIB) <b>Vaccine</b> Strain: IIIB F  • Suggested H-2 <sup>d,t4</sup> epitop	AIRHIPRRIR HIV component: gp160 pe based on region of overlap	Vaccine	murine (H- $2^{d,t^4}$ )	Hale1989
gp160 (839–853)	gp160 (828–842 IIIB)	AIRHIPRRIRQGLER	Vaccine	human, murine $(H-2^k, H-2^b, H-2^s)$	Berzofsky1991b, Berzofsky1991a
			HIV component: gp160 Adjuve B10.BR mice (H- $2A^k$ , $E^k$ ), B10.A	ant: Freund's adjuvant	•
gp160 (839–853)	gp41 (846–860 IIIB) Vaccine Strain: IIIB F	AIRHIPRRIRQGLER HIV component: gp160	Vaccine	murine (H-2 <sup>d,t4</sup> )	Hale1989

HXB2 Location	<b>Author's Location</b>	Sequence	Immunogen	Species (HLA)	References
	Six multideterminant h	elper T-cell regions are recogn	nized by mice of three or four M	HC types	
gp160 (842–856)	gp41 (842–856 IIIB, B10)	HIPRRIRQGLERILL	HIV-1 infection	human	Wahren1989b, Wahren1989a
	• 12 gag and 18 env pept	ides were identified that could	l commonly evoke T-cell respon	ses.	
gp160	gp120 (IIIB)		HIV-1 infection	human	Geretti 1994
	overlapping peptide po	ols. 10 of the responding patie	ents recognized three or more pe	ptide pools.	
	<ul> <li>After 12 months, most months, as did 5/15 nor</li> <li>IL-2 production was a result.</li> </ul>	responses were lost or diminis n-responders.	shed, and specific responses fluctived measure of Th function that	tuated. 4/10 of the responders a	at baseline had new responses at 12

## III-B-15 Env Helper T-Cell Epitopes

HXB2 Location	<b>Author's Location</b>	Sequence	Immunogen	Species (HLA)	References
Env	<ul> <li>DNA vaccinations of interferon and IL-2, w</li> <li>An intramuscular rout</li> </ul>	BALBc mice with a gp with little or no IL-4, as we te of inoculation gave a	Vaccine HIV component: gp120, gp160 120 or gp160 DNA vaccine elicited a strowell as antigen specific gp120 Abs stronger proliferative response than intra all lymph tissues tested: spleen, PBMC,	dermal	,
Env		e, when delivered in cor	Vaccine t: gp160, GAG, POL Adjuvant: CD86 njunction with the plasmid encoding the		Kim1997d , gives an increase in the proliferative
Env	gp120 • Sequences flanking he	elper T-cell immunogen	ic domains can be important for immuno	human genicity	De Berardinis1997
Env	gp120 • A strong proliferative	response to p24 and gp	HIV-1 infection 160 was found in a healthy long term sur	human vivor	Rosenberg1997
Env	• A strong proliferative	response against gp160	HIV-1 infection and clear the infection within 6 months, with IL-4 production, indicating a Th2 r produces both IL-4 and $\gamma$ interferon, indicating	response, was found with 4 wee	eks of infection
Env	<ul> <li>Vaccination of Macaca response, and type-spo</li> </ul>	a mulatta (rhesus monkecific neutralizing antib	Vaccine 0 boost Strain: HXBc2 HIV componeys) with a HXBc2 env DNA prime and sodies XB2 were protected from infection		Letvin1997 proliferative response, a CTL
Env	An HIV DNA env and	d rev vaccine given to 15	HIV-1 infection, Vaccine HIV component: ENV, REV 5 asymptomatic HIV+ individuals at thre rative response after vaccination	human e different dosages, 30, 100 or	MacGregor1998 300 μg, was safe
Env	<ul><li>seronegative individua</li><li>Exposed-uninfected part</li></ul>	als, and only 1/50 low-rander of the roduced more IL-2 and	ive partners of HIV-positive individuals – isk controls less IL-10 then HIV-infected individuals sponse to Env peptides had concomitantl		
Env	Env • Patients from later sta	ges of infection given H	HIV-1 infection IAART do not show restoration of HIV-1	human specific Th proliferative respo	Plana1998 nses

HXB2 Location	<b>Author's Location</b>	Sequence	Immunogen	Species (HLA)	References
Env			HIV-1 infection and to test Th proliferative responses after IL2 specific proliferative responses	human 2 therapy – while IL2 therapy	Kelleher1998a y causes an increase in CD4+
Env			HIV-1 infection, Vaccine HIV component: gp160 immunoproliferative responses in individua	human als who were immunized ever	Ratto-Kim1999  ry 2 months for 5 years starting early
Env	<ul> <li>27 HIV subtype B, 4 s rgp160 immunized ind</li> <li>gp120 was prepared fr least one additional su</li> <li>This study shows that</li> </ul>	ubtype C, 2 D and one lividuals showed increa om A, B, C, D, and E s btype in addition to B s cross-subtype HIV-spec	HIV-1 infection, Vaccine HIV component: gp160 of each subtype E, F, G infected individuals sed proliferation responses to the B clade in ubtype virions and used as antigenic stimule subtype, while a placebo recipient did not re cific T-cell proliferative responses can be sti ubtype B immunogen, but many developed	nmunizing antigen rgp160. us – 7 of 10 tested individual spond to any gp120 mulated in patients already in	s responded to native gp120 from at
Env		responses were induce	Vaccine 0 boost <i>Strain:</i> MN <i>HIV component:</i> gpd by MN rgp160 as measured by proliferation		Gorse1999a e release – this response could be
Env	<ul> <li>Vaccinated monkeys w ISCOM strategy gave</li> </ul>	with the highest level of more potent anti -gp12 nallenged 4 months afte	Vaccine as Strain: SF2 HIV component: gp120 Th1 and Th2 responses and the highest level responses than the Fowl pox strategy r boost, those that maintained high levels of		
Env	<ul> <li>A DNA vaccine contain</li> </ul>	ining env and rev was to	HIV-1 infection, Vaccine HIV component: ENV, REV ested for safety and immune response in 15 els of MIP-1 alpha were detected in multipl		Boyer1999 uals
Env			Vaccine  HIV component: gp160 Adjuvant: GM- n a vaccinia vector elicits a higher HIV-spec		Rodríguez1999  ponse than when native env is used
Env			Vaccine nia boost Strain: LAI HIV component: I ing with a vaccinia construct induced greate		Kent1998 nity than either vaccine alone

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
		ean SI for HIV Gag and	ter the DNA vaccination had a mean SI of d Env. The T help response happened de- was also enhanced		
Env	challenge. Protection of ISCOM vaccines were	strategies were evaluate correlated with the mage tested. the highest NAb titers,	Vaccine ke particle, ISCOM ed for their ability to protect from infecti gnitude of NAb responses, beta-chemoki Th1 and Th2 responses, was the only va	nes, and a balanced Th response	. DNA, protein+adjuvant, VLP and
Env	• This study followed 10	0 HLA-A2 asymptoma	HIV-1 infection, Vaccine HIV component: gp160 ttic HIV+ individuals as they received Maresponse but this did not impact viral loa	0.1	Kundu1998a o year period.
Env	<ul> <li>16 rhesus Macaques w ISCOMs</li> <li>DNA vaccination elici induced both kinds of</li> </ul>	ted a weak Th type 1 r Th cells, and a strong ged with SF13 SHIV. I	Vaccine otein, ISCOM Strain: SF2 HIV comp ther an epidermal SF2 gp120 DNA vacci response and low antibody response, rgp1 humoral response. Early induction of Th type 1 and type 2 re	ne, rgp120 with a MF59 adjuvar 20/MF59 triggered a strong ant	nt, or rgp120 incorporated into ibody response, and rgp120/ISCOM
Env	<ul> <li>Co-stimulatory molecular</li> </ul>	ules co-expressed with	Vaccine  HIV component: GAG, POL, ENV Adj an HIV-1 immunogen in a DNA vaccine Env and Gag/Pol specific CTL and Th pr	used to enhance the immune re	
Env			Vaccine IN, LAI HIV component: gp120, gp41, g MN gp120 and LAI gp41/gag/protease	_	Salmon-Ceron1999 coproliferative response in healthy
Env	<ul> <li>Rhesus macaques were finger in the nucleocap</li> <li>Env and Gag specific 0</li> <li>2/4 monkeys (MM146</li> </ul>	e vaccinated by i.m. in osid to prevent packagi CTL but no antibody ro and MM143) produce nated monkeys produce	Vaccine HIV component: complete genome jection with naked plasmid DNA carryinng esponses were induced in 2/4 vaccinated antibodies against p24 and/or gp160, bed IFNγ, in response to HIV-1 gp160, incomplete the second s	monkeys (MM145 and MM153 out no CTL response was detected	) ed

<b>HXB2</b> Location	<b>Author's Location</b>	Sequence	Immunogen	Species (HLA)	References
	detection limit		plasma viral loads of both MM145 and M N plasma viral loads of both MM146 and	·	
Env		-	HIV-1 infection p24, p55 and gp120 were tested in 27 pat response was detected in only one patient	_	Zhang2001b prous responses directed at Gag were
Env		alloantigen, and PHA	HIV-1 infection potent anti-retroviral therapy did not allow A did develop in many HIV+ patients, and		
Env	CD4 proliferative resp	onses and were able to	HIV-1 infection fection (three with sustained therapy, two o maintain a CTL response even with und tive responses and lost their CTL response	etectable viral load - three pati	ients that had delayed initiation of
Env	<ul> <li>Proliferative responses boosted with a recomb</li> </ul>	s in PBMC of uninfect sinant gp120 subunit v	Vaccine rgp120 boost HIV component: gp120 red individuals that were vaccinated with accine gave a Th1 and Th2 proliferative red also produced IL-2, IL-6, IL-4 and IL-5	response upon stimulation with	
Env	<ul> <li>16/29 HIV-1 infected a individuals, none had on in the absence of lymp</li> <li>No 48 hour DTH response</li> </ul>	and 24/30 vaccinated in detectable proliferative hoproliferation. Onses were detected as	HIV-1 infection, Vaccine  Strain: MN HIV component: gp120  ndividuals had DTH reactions within 48 le responses. Thus skin testing may be a semong uninfected volunteers, although 10/ter 7-12 days, that may be indicative of process.	hours after an intradermal rec gensitive way to identify people 35 (40%) of the high risk and 1	with Th recall responses to vaccines, of 11/32 (34%) of the low risk individuals
Env	<ul><li>Vigorous HIV-1 specif borderline responses. I</li><li>None of the progressor</li></ul>	ic responses to p24, N IL-2 production was sors (0/5) had HIV-1 spe	HIV-1 infection responses, but not responses to other antigues and gp120 with SI between 8-99 were een in all cases, and IL-4 production was ecific proliferative responses, or IL-2 or II Staphylococcus enterotoxin B, tetanus tox	seen in 6/7 long term non-progalso evident many responses4 induction.	gressors (LTNP), the seventh had a
Env	IFNgamma producing.		HIV-1 infection re responses (SIs) were inversely correlate arely observed (only 4 cases).	human ed with viral load in 21 ARV na	Kalams1999a aive patients. The responses were Th1,

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
Env	<ul> <li>A phase I clinical trial monitored. The constructor responses, but not CD</li> <li>With a 300 ug dose, 4</li> <li>With a 1000 ug dose, Rev.</li> <li>No responses to three</li> </ul>	of a HIV-1 Env and Re ruct was modified for sai 8 T-cell responses. Rev /6 individuals had a lym 4/6 individuals had a LF	Vaccine stor Strain: MN HIV component: E v DNA vaccine with a CMV promoter fety and included no LTRs or packagin elicited strong Th responses, and is a e phocyte proliferation (LP) responses to p and 2/6 had IFNgamma Elispot responses vere observed by Elispot in individuals	was conducted and Th proliferating signals. The vaccine strategy warly produced protein so may control of pp120, 3/6 to Rev.  nses to gp160; 3/6 had LP, and 4/2	as safe, and elicited strong CD4-T cell offer advantages. 6 had IFNgamma Elispot responses to
Env	immune responses, ii) HAART at least 12 m • HAART naïve patient over the two year stud naïve group at time ze • Short-term HAART p	newly treated patients fronths prior to the study. It is had strongest proliferately period against HIV-1 pro, but increased the most atients showed a significant strong treater than the strong trea	HIV-1 infection ar study of chronically HIV-1 infected is followed for 24 months after initiation of tive responses at time zero, but long-tegp160, influenza, and Candida. Similar ost in the long-term HAART treated particular improvement in their CD4+ T cell g-term HAART patients.	of HAART, iii) and long-term HA rm HAART patients the most signly, IL-2 and IFN $\gamma$ production in tients.	AART patients who had been on nificant increase in specific responses responses to gp160 was highest in the
Env	<ul> <li>(HAART failures and patient groups with ac</li> <li>gp160 proliferation re for HIV seronegative</li> <li>No differences in the</li> </ul>	HAART naive). Patient tive HIV-1 replication, s sponses were apparent i controls.	HIV-1 infection HIV-1 infected patients with HAART so s with HAART suppression showed str suggesting active viral replication in vir n 7/32 donors tested, but weaker overal fic CD4+ T-cells that were positive for o e viral replication.	onger p24- and p66-specific proloson specifically reduces proliferatiall, with a median value for the su	iferative responses compared to on responses. ppressed group not above that found
Env	<ul> <li>viremia but had progre</li> <li>In a comparison of reshigher for non-progresusing p24 peptides that</li> </ul>	essive CD4+ T-cell declesponses to HIV-1 protein ssors and immunologica an native p24. Native p2	HIV-1 infection 10 clinical non-progressors, and 3 imm ine) were analyzed for their T-helper co as based on 10 non-progressors, 3 imm lly discordant than progressors. Amon 4, Nef, gp120 proteins, and Remune (g ssors, Nef and gp120 responses were s	ell responses to p24 and cytokine unologically discordant, and 70 p g the non-progressors, the respon p120 depleted HIV-1, p24 is sub	profile. progressors, SIs were always much uses to different antigens were greater type G), had roughly comparable
Env	<ul> <li>Of 5 mouse inbred lin proliferative responses</li> </ul>	es tested: DBA/2 (H-2d s to HIV proteins (gp160	Vaccine  in: BRU HIV component: whole viru, Ad, Ed), B10.A(4R) (H-2h4, Ak) and D, gp120, p17, p24, Nef and RT), after and Ab) had weaker responses.	B10.A(5R) (H-2i5) showed part	icularly good CD4+ T cell

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
Env	<ul> <li>Co-stimulatory molec</li> </ul>	ules co-expressed with a	Vaccine T: GAG, POL, ENV Adjuvant: IL-2 an HIV-1 immunogen in a DNA vacconses and enhanced CTL responses		
Env	Helicobacter pylori in	duces Th1 responses ear	Vaccine  HIV component: gp160  rly, but predominantly Th2 responses to HIV gp160-vaccinia vaccination		
Env	<ul> <li>BALB/c mice were gi gp120 and Pr55gag</li> <li>High dose-independent carrying vaccinia expression</li> </ul>	ven intraperitoneal imm nt humoral responses we ressed gp120 and Gag.	Vaccine  ain: gp120 A clade UG5.94UG018, lunization in the absence of adjuvants are elicited against both gp120 and p2  T cell proliferative responses in vitro	s with virus-like particles (VLPs) ex 24 peptides, and CTL responses we	spressing recombinant subtype A
Env	<ul> <li>Mice were intranasall enterotoxin produced</li> <li>Adjuvant LT(R192G) peptide-specific CTL</li> </ul>	y immunized with 20 ug by E. coli was required for stimul- responses	Vaccine rotein Strain: IIIB HIV componer g of HIV-gp160 and 5 ug of peptide E ation of antigen-specific IgG1, IgG2 ne production specific to gp160 was	7 (RIHIGPGRAFYAARK) with th antibodies, and Th1 and Th2 cytoki	e adjuvant LT(R192G), a heat-labil ines responses to gp160, and
Env	<ul> <li>The CMV promotor r CMV-based DNA vac</li> <li>8 Br-cAMP increased</li> </ul>	esponds to the intracelluscine both intranasally as serum IgG responses, F	Vaccine otor Strain: IIIB HIV component: alar level of cAMP, and 8 Br-cAMP c and intramuscularly HIV-specific CTL, DTH and Th1 resp as due to CMV promotor activation	an increase transgene expression so	o it was co-administered with a

## III-B-16 Nef Helper T-Cell Epitopes

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References	
Nef (1–20)	Stronger, broader respectively.	onses were observed in ar	component: NEF, TAT, REV cimals vaccinated with DNA epic	murine (H-2 <sup>d</sup> )	Hinkula1997 protein	
	Proliferative response	to vaccination was observ	ed to peptides throughout Nef ar			
Nef (1–20)	Nef (1–20 HXB2) MGGKWSKSSVIGWPTVRERM HIV-1 infection (H-2 <sup>d</sup> ) Peng2001  • Deletion of the 19 N-terminal amino acids from Nef including the myristolation signal eliminates Nef-induced down-regulation of MHC class I and molecules. Such a construct has the potential to serve as a more potent immunogen. The known T-cell epitopes that that would be disputed by this are minimal, a murine H-2d Th epitope in the peptide MGGKWSKSSVIGWPTVRERM, and a HLA-B8 CTL epitope, WPTVRERM.					
Nef (16–35)	Stronger, broader respectively.	onses were observed in ar	component: NEF, TAT, REV	murine $(H-2^d)$ lermally rather than with intramuscular Nef and Tat, less for Rev	Hinkula1997 protein	
Nef (31–50)	Stronger, broader respectively.	onses were observed in ar	component: NEF, TAT, REV	murine $(H-2^d)$ lermally rather than with intramuscular Nef and Tat, less for Rev	Hinkula1997 protein	
Nef (45–69)	**		n boost <i>Strain:</i> BRU <i>HIV con</i>	chimpanzee, rat  nponent: Nef Ab response to Nef protein immunizatio	Estaquier1992	
Nef (45–69)	Nef (45–69)  Vaccine Vector/Type:	SSNTAATNAACAWL EEVGFP peptide <i>Adjuvant:</i> no ad	EAQEE - Vaccine juvant, aluminum hydroxide	rat rative responses at low doses with no a	Rouaix1994	
			aduction of detectable Th respon		guvani in Zouvii iato, to a weater	
Nef (46–65)	Stronger, broader respectively.	onses were observed in ar	component: NEF, TAT, REV	murine $(H-2^d)$ lermally rather than with intramuscular Nef and Tat. less for Rev	Hinkula1997 protein	
Nef (56–68)	Nef (56–68 HXB2)	AWLEAQEEEEVGF	Vaccine	murine (DQ2, DQ3, DQ5, DQ6, DQ7, DQ8,)	Pancré2002	
	<ul> <li>This highly conserved</li> </ul>		ous HLA-DQ class II binding po	otential. It has a can bind to 6 different l nity, and with DQ7 with low affinity.	HLA-DQ alleles, but did not bind	

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• DQ transgenic mice (in particular DQ8) mounted strong cellular and humoral responses after immunization with this peptide.

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
	cytokine production. I production was observ	FNgamma production red.	was stimulated in 7/14 cases, both I	) with this peptide presented on auto FNgamma and IL-2 in 6/14, and just monstrated a preference for TCR VI	
Nef (61–80)	Stronger, broader resp	DNA Strain: LAI In onses were observed in	QVPLRPMT Vaccine HIV component: NEF, TAT, REV a animals vaccinated with DNA epid as observed to peptides throughout	murine $(H-2^b)$ ermally rather than with intramuscu Nef and Tat, less for Rev	Hinkula1997 lar protein
Nef (66–97)	<ul><li>administered in a phas</li><li>A CD4+ T cell prolife</li></ul>	VDLSHFLKEKGG. lipopeptide vaccine consisting of s se I trial rative response to at lea CTL responses to at lea	ix long peptides derived from Nef, Cast one of the six peptides was obserast one of the six peptides, each of the six peptides was observed.	human  Gag and Env HIV-1 proteins modifie  ved in 9/10 vaccinees – 5/10 reacted  the six peptides elicited a CTL respo	to this Nef peptide
Nef (76–95)	<ul> <li>Stronger, broader resp</li> </ul>	DNA Strain: LAI In onses were observed in	SHFLKEKG Vaccine HIV component: NEF, TAT, REV a animals vaccinated with DNA epid as observed to peptides throughout	murine $(H-2^b)$ ermally rather than with intramuscu Nef and Tat, less for Rev	Hinkula1997 lar protein
Nef (91–110)	<ul> <li>Stronger, broader resp</li> </ul>	DNA Strain: LAI In onses were observed in	SQRRQDIL Vaccine HIV component: NEF, TAT, REV a animals vaccinated with DNA epid as observed to peptides throughout	murine (H-2 <sup>b</sup> ) ermally rather than with intramuscu Nef and Tat, less for Rev	Hinkula1997 lar protein
Nef (98–112)			Vaccine tein boost Strain: BRU HIV con s in the absence of carrier protein – 1		Estaquier1992
Nef (104–123)	<ul><li>A strong T helper prol background – the resp</li><li>Mice were immunized</li></ul>	D? DNA Strain: HXB3 iferative response agai onse was weak by 4 woll with nef DNA under t	eeks post immunization he control of a CMV promotor, coat	murine (H-2 <sup>b</sup> )  weeks after immunization of HLA- ed on gold particles delivered to aborticating a response to multiple epitop	lominal skin by a gene gun
Nef (106–125)	Stronger, broader resp	DNA Strain: LAI In onses were observed in	QGYFPDWQ Vaccine HIV component: NEF, TAT, REV a animals vaccinated with DNA epid as observed to peptides throughout	murine $(H-2^b)$ ermally rather than with intramuscu Nef and Tat, less for Rev	Hinkula1997 lar protein

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
Nef (117–147)	Nef (117–147 LAI)	TQGYFPDWQNYTPGPGVRY- PLTFGWCYKLVP	Vaccine	human	Gahery-Segard2000
	<ul><li>administered in a phase</li><li>A CD4+ T cell prolifer</li></ul>	vaccine consisting of six long pept e I trial ative response to at least one of th CTL responses to at least one of th	e six peptides was observed	g and Env HIV-1 proteins modified d in 9/10 vaccinees – 1/10 reacted six peptides elicited a CTL respon	to this Nef peptide
Nef (121–140)	Stronger, broader responser.	FPDWQNYTPGPGVRYPLTFG  ONA Strain: LAI HIV componences were observed in animals value onse to vaccination was observed	nent: NEF, TAT, REV ccinated with DNA epiderr	murine $(H-2^b)$ mally rather than with intramuscul f and Tat, less for Rev	Hinkula 1997 ar protein
Nef (136–155)	Stronger, broader responser.	PLTFGWCYKLVPVEPDKVEE DNA Strain: LAI HIV componences were observed in animals value onse to vaccination was observed	nent: NEF, TAT, REV ccinated with DNA epiderr	murine $(H-2^d)$ mally rather than with intramuscul f and Tat, less for Rev	Hinkula1997 ar protein
Nef (151–170)	Stronger, broader responser.	DKVEEANKGENTSLLHPVSL DNA Strain: LAI HIV compon onses were observed in animals va- tionse to vaccination was observed	nent: NEF, TAT, REV ccinated with DNA epiderr	murine $(H-2^d)$ mally rather than with intramuscul f and Tat, less for Rev	Hinkula1997 ar protein
Nef (164–183)	<ul> <li>A strong T helper proli background – the respo</li> <li>Mice were immunized</li> </ul>	onse was weak by 4 weeks post im with nef DNA under the control o	conent: Nef f protein was observed 2 w munization f a CMV promotor, coated	murine $(H-2^b)$ eeks after immunization of HLA- $\mu$ on gold particles delivered to abdeting a response to multiple epitope	
Nef (166–185)	Stronger, broader responser	HPVSLHGMDDPEREVLEWRF DNA Strain: LAI HIV componences were observed in animals value to vaccination was observed	nent: NEF, TAT, REV ccinated with DNA epiderr	murine $(H-2^{b,d})$ mally rather than with intramuscul f and Tat, less for Rev	Hinkula1997 ar protein
Nef (179–198)	<ul> <li>A strong T helper proli background – the respo</li> <li>Mice were immunized</li> </ul>	onse was weak by 4 weeks post im with nef DNA under the control o	conent: Nef f protein was observed 2 w munization f a CMV promotor, coated	murine (H-2 <sup>b</sup> )  eeks after immunization of HLA-A  on gold particles delivered to abde ting a response to multiple epitope	

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References		
Nef (181–205)	Nef (181–205 LAI)	LEWRFDSRLAFHHVARELH- PEYFKN	Vaccine	murine $(H-2^d)$	Hinkula1997		
		DNA Strain: LAI HIV compon					
		onses were observed in animals vac			lar protein		
	Some proliferative resp	ponse to vaccination was observed	to peptides throughout Nef	and Tat, less for Rev			
Nef (182–205)	Nef (182–205 LAI)	EWRFDSRLAFHHVARELHP- EYFKN	Vaccine	human	Gahery-Segard2000		
	<ul> <li>Vaccine Vector/Type: 1</li> <li>Anti-HIV lipopeptide vadministered in a phase</li> </ul>	vaccine consisting of six long pept	ides derived from Nef, Gag	and Env HIV-1 proteins modifie	d by a palmitoyl chain was		
		rative response to at least one of the					
		CTL responses to at least one of the nad an IgG response to this peptide		ix peptides elicited a CTL respo	nse in at least one individual		
Nef (185–200)	Nef (183–198) • T-cell response to this	FDSRLAFHHVARELHP epitope persisted after seroreversion	HIV-1 infection on	human	Ranki1997		
Nef (186–206)	Nef(p27) (185–205 BRU)	DSRLAFHHVARELHPEYFK-NC		chimpanzee	Bahraoui1990		
	adjuvant (Syntex)	recombinant protein Strain: BRU	HIV component: gp160,	p25, Nef, p17 and p24 Gag Aa	ljuvant: muramyl-dipeptide base		
	• Epitope name: PF63	immunized with rec vaccinia virus	eas (VV) avarassing HIV 1	an 160. Gag, and Nef			
		ed persistent T-helper proliferative			ted at the C-term end of Nef.		
Nef	Nef (LAI)		HIV-1 infection	human	daSilva1998		
1101	* *	ne level of variation in Nef CTL ep			dusiivaiyyo		
					ints in the regions where CTL epitope		
Nef	Nef		Vaccine	human	Calarota1999		
	Vaccine Vector/Type: DNA HIV component: Nef, Rev Tat						
	• 9/9 HIV-1+ subjects were given one of three DNA vaccinations for nef, rev or tat, and novel proliferative and CTL responses were generated						
	<ul> <li>The nef DNA immunization induced the highest and most consistent CTLp activity, IFN-gamma production, and IL-6 and IgG responses</li> <li>Highly active antiretroviral treatment (HAART) did not induce new HIV-specific CTL responses but reduced viral load, while DNA vaccination induced</li> </ul>						
		s but did not reduce viral load – the					
Nef	Nef		HIV-1 infection, Vaccine	human	Calarota2001		
		DNA HIV component: Nef, Rev,	Tat Adjuvant: CpG motif				
	<ul> <li>This review discusses t vaccine boosting of CT</li> </ul>	he cellular immune response, and	comments on CpG inductio	n of Th1 cytokines and enhance	d immune responses, and HIV-1 DNA		

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
Nef	CD4 proliferative resp	onses and were able to	HIV-1 infection ection (three with sustained therapy, two maintain a CTL response even with under responses and lost their CTL response	detectable viral load – three pati	ents that had delayed initiation of
Nef	<ul> <li>Vigorous HIV-1 specific borderline responses. I</li> <li>None of the progressor</li> </ul>	ic responses to p24, Ne L-2 production was sec s (0/5) had HIV-1 spec	HIV-1 infection sponses, but not responses to other anti f and gp120 with SI between 8-99 were in all cases, and IL-4 production was ific proliferative responses, or IL-2 or I aphylococcus enterotoxin B, tetanus to	e seen in 6/7 long term non-prog s also evident many responses. IL-4 induction.	gressors (LTNP), the seventh had a
Nef	<ul><li>BALB/c mice were im</li><li>High Ab titers (predon 5-fold higher than Nef</li></ul>	munized with Nef alon ninantly IgG1) against lalone.	Vaccine  Strain: BRU HIV component: Nef A e, Nef with Freund's adjuvant, or Nef e Nef were retained for seven months in the ed, and cytokine profiles indicated this	encapsulated in poly(DL-lactide- the mice infected with Nef-PLG	-co-glycolide) PLG microparticles.
Nef	<ul> <li>viremia but had progre</li> <li>In a comparison of reshigher for non-progres using p24 peptides that</li> </ul>	ssive CD4+ T-cell decl ponses to HIV-1 protein sors and immunologican n native p24. Native p2	HIV-1 infection 10 clinical non-progressors, and 3 imm ine) were analyzed for their T-helper co as based on 10 non-progressors, 3 imm illy discordant than progressors. Amon 4, Nef, gp120 proteins, and Remune (g assors, Nef and gp120 responses were s	ell responses to p24 and cytokin unologically discordant, and 70 g the non-progressors, the respo p120 depleted HIV-1, p24 is sul	e profile. progressors, SIs were always much unses to different antigens were greater btype G), had roughly comparable
Nef	<ul> <li>Of 5 mouse inbred line proliferative responses</li> </ul>	es tested: DBA/2 (H-2d to HIV proteins (gp16	Vaccine in: BRU HIV component: whole viru , Ad, Ed), B10.A(4R) (H-2h4, Ak) and 0, gp120, p17, p24, Nef and RT), after and Ab) had weaker responses.	B10.A(5R) (H-2i5) showed par	ticularly good CD4+ T cell
Nef	<ul> <li>IFN-gamma levels</li> <li>Antigen stimulation in</li> <li>IL-4 production was no</li> <li>Cross-clade CTL activ</li> </ul>	B/c mice immunized v creased IFN-gamma pr ot significantly changed ity was also observed:	Vaccine  York, Vpu, Nef  Yorkh pVVN-P DNA were incubated with pVVN-P DNA were incubated with oduction in pVVN-P immunized mice, after antigen stimulation compared to A, B clade, CRF01(AE) clade antigens timulate a CTL response, but was expr	indicating a Th1 response control levels could serve as targets for the B	clade immunization stimulated CTL –

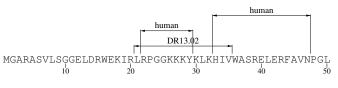
# III-B-17 HIV-1 Helper T-Cell Epitopes

HXB2 Location	<b>Author's Location</b>	Sequence	Immunogen	Species (HLA)	References
HIV-1	and HIV-1 specific CT	L in some. It is unknow	HIV-1 infection eir mothers results in HIV-1 specific T-l n whether these responses are associated eding mothers. Summary tables are pro-	d with lack of infection, but th	ere is some evidence that HIV-1 T-ce
HIV-1	<ul><li>Incomplete Freund adj</li><li>No benefit was observ vaccinated with placet</li></ul>	juvant (IFA) ed in terms of progression	HIV-1 infection, Vaccine 2321 (REMUNE(TM)) Strain: Z321 on free survival for HIV-1 patients on A no statistically different outcome in HI counts.	RT given vaccinations with HI	(V-1 antigen (N=1,262) versus those
HIV-1	<ul><li>Incomplete Freund adj</li><li>15 HIV-1+ patients on</li></ul>	juvant (IFA) ARV given vaccinations	HIV-1 infection, Vaccine 2321 (REMUNE(TM)) Strain: Z321 s with HIV-1 antigen versus vaccinated antigen increased in HAART treated pat	with placebo. Lymphocyte pro	
HIV-1	<ul><li>Incomplete Freund ad</li><li>HIV-1 specific stimula</li></ul>	juvant (IFA)	HIV-1 infection, Vaccine 2321 (REMUNE(TM)) Strain: Z321 on, and beta-chemokines (RANTES) an -1 immunogen.		-
HIV-1	<ul><li>Incomplete Freund ad</li><li>Long-term follow up of immunogen had a bett</li></ul>	juvant (IFA) of HIV-1+ individuals giv er clinical outcome. Of t	HIV-1 infection, Vaccine 2321 (REMUNE(TM)) Strain: Z321 ven HIV-1 immunogen, suggesting those welve who developed DTH-responsives H-nonresponsive, 9 (69%) progressed to	e patients who became HIV-Diness, one got an opportunistic	TH-responsive in response to the HIV infection and died, and one develope
HIV-1	A dose response study	of HIV immunogen in I	Vaccine iuvant: Incomplete Freund adjuvant (IFFA was conducted. Doses of 50, 100, 20 munogen was well tolerated, and the m	00, or 400 micrograms (total p	
HIV-1			HIV-1 infection idea that T-helper cell dysfunction resul CTL memory through therapy and impr		
HIV-1			HIV-1 infection, Vaccine 2321 (REMUNE(TM)), recombinant pronone, Thymosin alpha-1.	human otein, virus-like particle, canar	Imami2002a ypox, adenovirus, DNA Adjuvant:

HXB2 Location	Author's Location	Sequence	Immunogen	Species (HLA)	References
	response. The loss of a	anti HIV-1 proliferative	npy and therapeutic immunization to he responses early after infection is reviegiven with or without vaccination.		
HIV-1	Review of the important	nce of balanced Th1 and	HIV-1 infection d Th2 HIV-specific CD4 T-cell respons	human ses in control of infection and for	Heeney2002 r vaccination strategies.
HIV-1			HIV-1 infection the dynamics of HIV-1 infection and p lower viral fitness, and with AIDS resu		
HIV-1	counter-balancing effectivirus had a low replicated reduce viral set point v	cts in a new infection: a tion rate, then CTLp an with observed replicatio	d CD4 helper cells could control an in	help but also more target cells. I fection. Only a vaccine that coul	The model indicates that if the infecting
HIV-1	peripheral blood and th		HIV-1 infection  V infection and progression that includ as the effects of HAART. Increasing v is model.		
HIV-1	(HZ321) Vaccine murine Ayash-Rashkovsky2002  Vaccine Vector/Type: gp120 depleted virus HZ321 (REMUNE(TM)) Strain: HZ321 Adjuvant: CpG, incomplete Freund's adjuvant (IFA)  Parasitic helminthic infections in humans, common in parts of Africa and Asia, can shift immune responses to Th2 responses. To model this, BALB/c mi were infected with the parasite Schistosoma mansoni, and the infected mice showed a dominant Th2 immune response. Vaccination with gp120-depleted HIV-1 viral particles and incomplete Freund's adjuvant induced Th2 responses in these mice, but this could be shifted towards a Th1 profile when CpG oligodeoxynucleotide was added to the vaccine as an immunostimulatory agent.				Freund's adjuvant (IFA) esponses. To model this, BALB/c mice se. Vaccination with gp120-depleted
HIV-1	<ul><li>absolute numbers of H an proliferation respon</li><li>These results indicate a</li></ul>	IV-specific memory CI uses to HIV Remune and a control of viral replica	HIV-1 infection  and on HAART, while 14 elected not to go to 4+ T-cells were observed in untreated tigen (gp120 depleted vaccine).  ation in therapy-naive patients may be contribute to viral rebound.	patients than patients receiving	HAART therapy, tested by stimulation
HIV-1	a weak response in a sj Stimulation of PBMC	TREC assay indicating with multiple recall ant		tients not on steroids had clear p ad mitogens, and revealed that in	Pido-Lopez2002 receiving steroid treatment therapy had ositive sjTREC readings after HAART. the patient treated with steroids there

# **III-C** Maps of T-Helper Epitope Locations Plotted by Protein

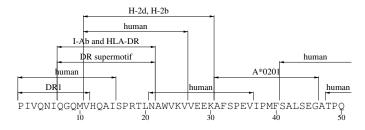
Linear helper T cell epitopes less than twenty-two amino acids long are III-C-1 p17 T-Helper Epitope Map

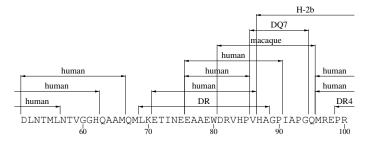


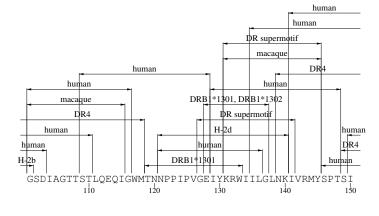


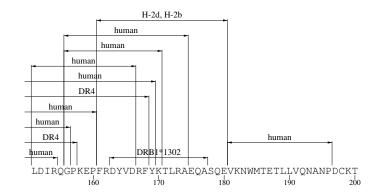


#### III-C-2 p24 T-Helper Epitope Map



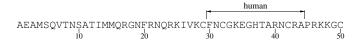


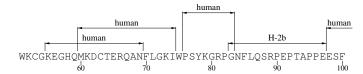


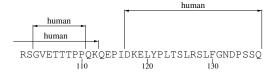


ILKALGPAATLEEMMTACQGVGGPGHKARVL 210 220 230

#### III-C-3 p2p7p1p6 T-Helper Epitope Map





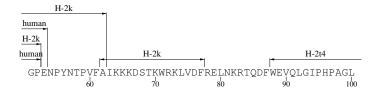


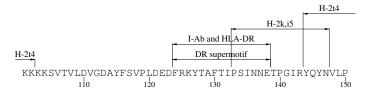
#### III-C-4 Protease T-Helper Epitope Map

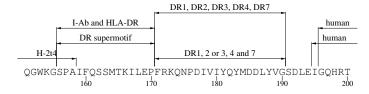
PQVTLWQRPLVTIKIGGQLKEALLDTGADDTVLEEMSLPGRWKPKMIGGI

#### III-C-5 RT T-Helper Epitope Map

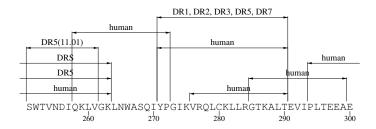


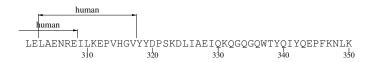




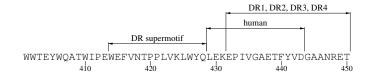


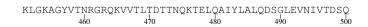


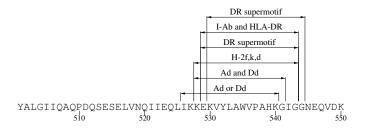






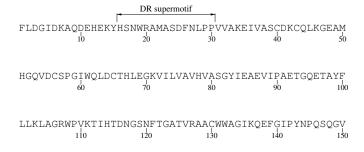


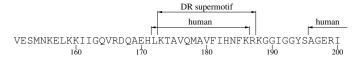


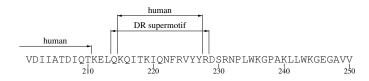


LVSAGIRKVL 560

#### III-C-6 Integrase T-Helper Epitope Map

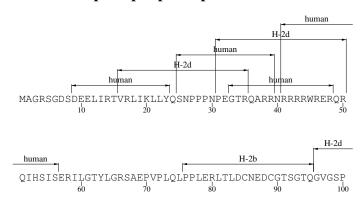




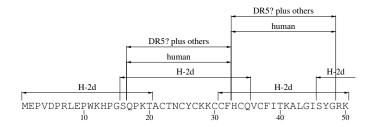


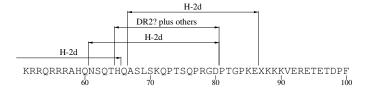
IQDNSDIKVVPRRKAKIIRDYGKQMAGDDÇVASRQDED 260 270 280

# III-C-7 Rev T-Helper Epitope Map



#### III-C-8 Tat T-Helper Epitope Map





D 101

#### III-C-9 Vif T-Helper Epitope Map

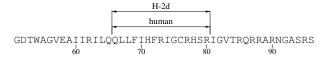
 $\underset{10}{\text{MENRWQVMIVWQVDRMRIRTWKSLVKHHMYVSGKARGWFYRHHYESPHPR}} \underset{10}{\text{MENRWQVMIVWQVDRMRIRTWKSLVKHHMYVSGKARGWFYRHHYESPHPR}} \underset{50}{\text{MENRWQVMIVWQVDRMRIRTWKSLVKHHMYVSGKARGWFYRHHYESPHPR}} \underset{10}{\text{MENRWQVMIVWQVDRMRIRTWKSLVKHHMYVSGKARGWFYRHHYESPHPR}} \underset{10}{\text{MENRWQVMIVWQVDRMRIRTWKSLVKHHMYVSGKARGWFYRHHYESPHPR}} \underset{10}{\text{MENRWQVMIVWQVDRMRIRTWKSLVKHHMYVSGKARGWFYRHHYESPHPR}} \underset{10}{\text{MENRWQVMIVWQVDRMRIRTWKSLVKHHMYVSGKARGWFYRHHYESPHPR}} \underset{10}{\text{MENRWQVMIVWQVDRMRIRTWKSLVKHHMYVSGKARGWFYRHHYESPHPR}} \underset{10}{\text{MENRWQVMIVWQVDRMRIRTWKSLVKHHMYVSGKARGWFYRHHYESPHPR}} \underset{10}{\text{MENRWQVMIVWQVDRMRIRTWKSLVKHHMYVSGKARGWFYRHHYESPHPR}} \underset{10}{\text{MENRWQVMIVWQVDRMRIRTWKSLVKHHMYVSGKARGWFYRHHYESPHPR}} \underset{10}{\text{MENRWQVMIVWQVDRMRIRTWKSLVKHHMYVSGKARGWFYRHHYESPHPR}} \underset{10}{\text{MENRWQVMIVWQVDRMRIRTWKSLVKHMYVSGKARGWFYRHHYESPHPR}} \underset{10}{\text{MENRWQVMIVWQVDRMRIRTWKSLVKHMYVSGKARGWFYRHHYESPHPR}} \underset{10}{\text{MENRWQVMIVWQVDRMRIRTWKSLVKHMYVSGKARGWFYRHHYESPHPR}} \underset{10}{\text{MENRWQVMIVWQVDRMRIRTWKSLVKHMYVSGKARGWFYRHHYESPHPR}} \underset{10}{\text{MENRWQVMIVWQVDRMRIRTWKSLVKHMYVSGKARGWFYRHHYESPHPR}} \underset{10}{\text{MENRWQVMIVWQVDRMRIRTWKSLVKHMYVSGKARGWFYRHYESPHPR}} \underset{10}{\text{MENRWQVMIVWQVDRMRIRTWKSLVKHMYVSGKARGWFYRHYESPHPR}} \underset{10}{\text{MENRWQVMIVWQVDRMRIPTWKSLVKHMYVSGKARGWFYRHYESPHPR}} \underset{10}{\text{MENRWQVMIVWQVDRMRIPTWKSLVKHMYVSGKARGWFYRHYESPHPR}} \underset{10}{\text{MENRWQVMIVWQVDRMRIPTWKSLVKHMYVSGKARGWFYRHYESPHPR}} \underset{10}{\text{MENRWQVMIVWQVDRMRIPTWKSLVKHMYVSGKARGWFYRHYESPHPR}} \underset{10}{\text{MENRWQVMIVWQVDRMRIPTWKSLVKHMYVSGKARGWFYRHYESPHPR}} \underset{10}{\text{MENRWQVMIVWQVDRMRIPTWKSLVKHMYVSGKARGWFYRHYESPHPR}} \underset{10}{\text{MENRWQVMIVWQVDRMRIPTWKSLVKHMYVSGKARGWFYRHYESPHPR}} \underset{10}{\text{MENRWQVMIVWQVDRMRIPTWKSLVKHMYVSGKARGWFYRHYESPHPR}} \underset{10}{\text{MENRWQVMIVWQVDRMRIPTWKSLVKHMYVSGKARGWFYRHYESPHPR}} \underset{10}{\text{MENRWQVDRMRIPTWKSLVKHMYVSGKARGWFYRHYESPHPR}} \underset{10}{\text{MENRWQVDRMRIPTWKSLVKHMYVSGKARGWFYRHYESPHPR}} \underset{10}{\text{MENRWQVDRMRIPTWKSLVKHMYVSGKARGWFYRHYESPHPR}} \underset{10}{\text{MENRWQVDRMRIPTWKSLVKHMYVSGKARGWFYRHYESPHPR}} \underset{10}{\text{MENRWQVDRMRIPTWKSLVKHMYVSGKARGWFYRHYESPHPR}} \underset{10}{\text{MENRWQVDRMRIPTWKSLVKHMYVSGKARGWFYRHYESPHPR}} \underset{10}{\text{MENRWQVDRMRIPTWKSLVKHYWSGKARGWFYRHYES$ 



AALITPKKIKPPLPSVTKLTEDRWNKPQKTKGHRGSHTMNGH

#### III-C-10 Vpr T-Helper Epitope Map

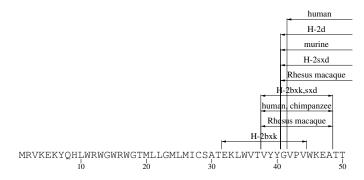


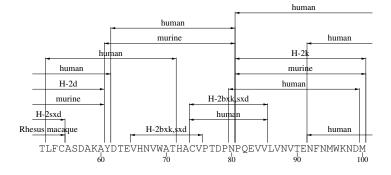


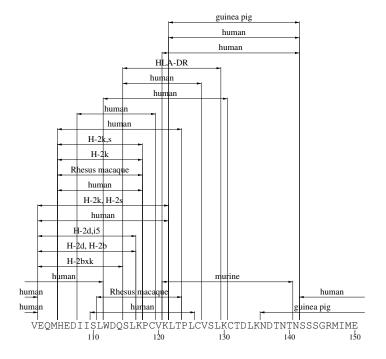
#### III-C-11 Vpu T-Helper Epitope Map

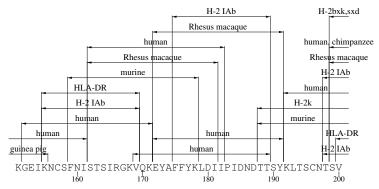
EDSGNESEGEISALVEMGVEMGHHAPWDVDDL 60 70 80

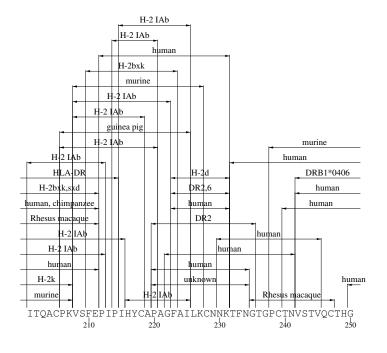
#### III-C-12 gp160 T-Helper Epitope Map

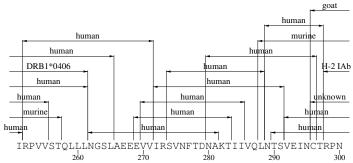


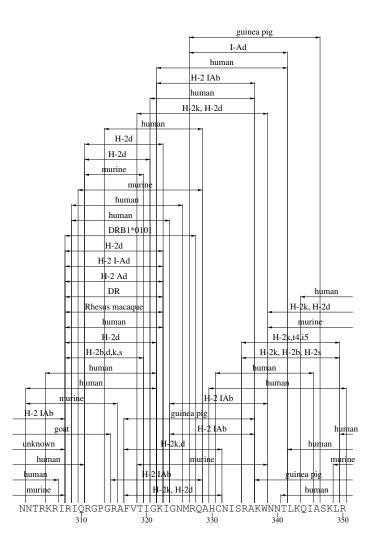


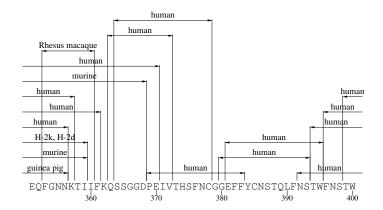


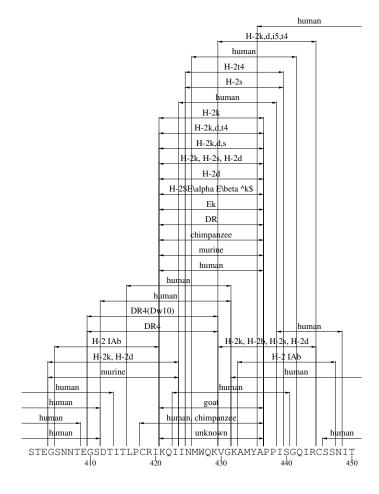


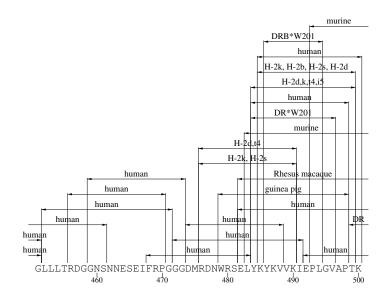


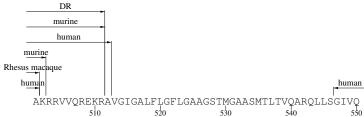


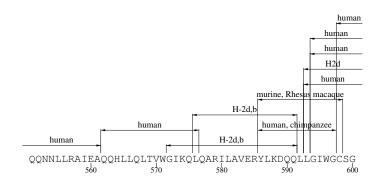


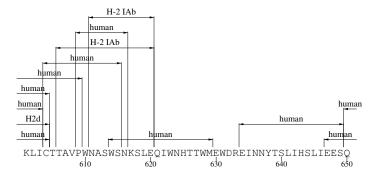


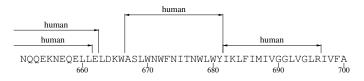




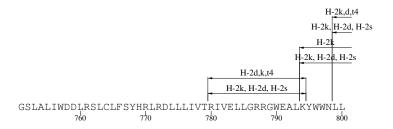




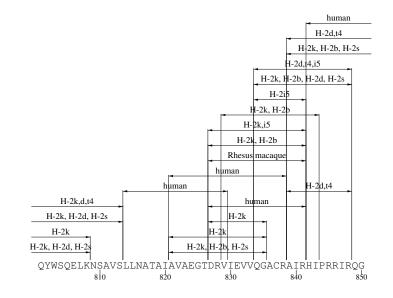






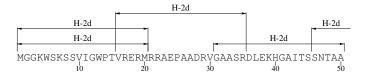


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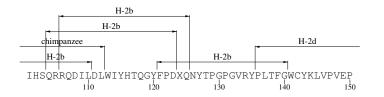


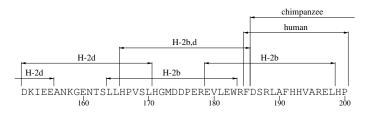


# III-C-13 Nef T-Helper Epitope Map











# Part IV HIV Antibody Binding Sites

# **IV-A Summary**

Part IV section summarizes HIV-specific antibodies (Abs) arranged sequentially according to the location of their binding domain, organized by protein. We attempted to make this section as comprehensive as possible. For the monoclonal (MAbs) capable of binding to linear peptides, we require that the binding site be contained within a region of 30 or so amino acids to define the epitope, but not that the precise boundaries be defined. MAbs that do not bind to defined linear peptides are grouped by category at the end of each protein. Antibody categories, for example CD4 binding site (CD4BS) antibodies, are also noted in the index at the beginning of this section. Studies of polyclonal Ab responses are also included. Responses that are just characterized by binding to a protein, with no known specific binding site, are listed at the end of each protein. For more recent updates, epitope sequence alignments, and search capabilities, please see our web site: http://hiv-web.lanl.gov/immunology.

#### IV-A-1 Indices

Three indices are provided. The first provides a concise list of anti-HIV-1 MAbs by cross-competition category, with both discontinuous epitopes (for example, CD4BS) and some well known linear epitopes (for example, cluster I) summarized. The second lists the MAb's IDs in alphabetical order so one can find their location in the table. The third is a listing by order of appearance in the tables.

#### IV-A-2 Tables

Each MAb has an ten-part basic entry:

**Number:** Order of appearance in this table.

**MAb ID:** The name of the monoclonal antibody with synonyms in parentheses. MAbs often have several names. For example, punctuation can be lost and names are often shortened (M-70 in one paper can be M70 in another). Polyclonal responses are listed as "polyclonal" in this field.

**HXB2 Location:** Position of the Ab binding site relative to the viral strain HXB2 (GenBank Accession Number K03455), which is used as a reference strain throughout this publication. The numbering in this table corresponds to

the protein maps. Because of HIV-1 variation the epitope may not actually be present in HXB2, rather the position in HXB2 indicates the position aligned to the epitope. HXB2 was selected as the reference strain because so many studies use HXB2, and because crystal structures for HXB2-related proteins are often available. The precise positions of an epitope on the HXB2 reference strain can be readily obtained using the interactive position locator at our web site: http://hiv-web.lanl.gov/content/hiv-db/LOCATE\_SEQ/locate.html.

Author Location: The amino acid positions of the epitope boundaries and the reference sequence used to define the epitope are listed as given in the primary publication. Frequently, these positions as published are imprecise, and do not truly correspond to the numbering of the sequence, but they provide a reasonable guide to the peptide's approximate location in the protein. Also, in many cases, position numbers were provided but the reference sequence identification was not. Because of HIV-1's variability, position numbers require a reference strain to be meaningful. Binding sites that cannot be defined through peptide binding or interference studies are labeled as discontinuous. The approximate location on the protein, sequence number, and reference sequence are listed.

Sequence: The amino acid sequence of the binding region of interest, based on the reference strain used in the study defining the binding site. On occasions when only the position numbers and not the actual peptide sequence was specified in the original publication, we tried to fill in the peptide sequence based on the position numbers and reference strain. If the sequences were numbered inaccurately by the primary authors, or if we made a mistake in this process, we may have misrepresented the binding site's amino acid sequence. Because of this uncertainty, epitopes that were not explicitly written in the primary publication, that we determined by looking up the reference strain and the numbered location, are followed by a question mark in the table.

**Neutralizing:** L: neutralizes lab strains. P: neutralizes at least some primary isolates. **no**: does not neutralize. No information in this field means that neutralization was either not discussed or unresolved in the primary publications referring to the MAb.

**Immunogen:** The antigenic stimulus of the original B cell response. Often this is an HIV-1 infection. If a vaccine was used as the original antigenic stimulation, not a natural infection, this is noted on a separate line, and additional information about the vaccine antigen is provided as available.

**Species**(**Isotype**): The host that the antibody was generated in, and the isotype of the antibody.

References: All publications that we could find that refer to the use of a specific monoclonal antibody. First is a list of all references. Additional details for some of older references can be found in Part V, although we have tried to keep the entries self-contained since 1997. The "donor" field is meant to serve as a potential guide to a source of information about an antibody or how to obtain it, as well as to provide credit.

**Notes:** Describe the context of each study, and what was learned about the antibody in the study.

#### **IV-A-3** HIV Protein Binding Site Maps

The names of MAbs and the location of well characterized linear binding sites of 21 amino acids or less are indicated relative to the protein sequences of the HXB2 clone. This map is meant to provide the relative location of epitopes on a given protein, but the HXB2 sequence may not actually bind to the MAb of interest, as it may vary relative to the sequence for which the epitope was defined. Above each linear binding site, the MAb name is given followed by the species in parentheses. Human is represented by 'h', non-human primate by 'p', mouse by 'm', and others by 'o'. More precise species designations for any given MAb can be found using the web search interface or in the tables in this section.

## IV-A-4 Alignments

To conserve space, no epitope alignments are provided in this book, but they can be generated using the MAb search tool at http://hiv-web.lanl.gov/immunology. All epitopes are aligned to the HXB2 sequence, with the sequence used to define the epitope indicated directly above it. Sequences are sorted by their subtype and country of origin.

The master alignment files from which the epitope alignments were created are available at our web site (http://hiv-web.lanl.gov/ALIGN\_CURRENT/ALIGN-INDEX.html). The alignments were modified in some

cases to optimize the alignment relative to the defined epitope and minimize insertions and deletions; epitope alignments are generated by anchoring on the C-terminal residue. A dash indicates identity to the consensus sequence, and a period indicates an insertion made to maintain the alignment. Stop codons are indicated with a \$, and frameshifts by a #, or ambiguous codons (nucleotide was r, y, or n) by an x; they are inserted to maintain the alignments. In consensus sequences an upper case letter indicates the amino acid was present in all sequences, a lower case letter indicates the amino acid was present in most sequences in a given position, and a question mark indicates two or more amino acids were represented with equal frequency.

# **IV-B** Cross Reference Listing of MAbs

## IV-B-1 MAbs by binding type

Cross reference by protein and binding type of MAb names and their order of appearance in the tables.

Binding type	MAb ID (No.)
p17	
C-term	sc-FV p17 (33)
p24	
C-term	13B5 (115)
Protease	
N-term	1696 (170)
flap region	F11.2.32 (172)
RT	
palm domain	6B9 (193)
thumb domain	5F (194), 5G (195), 7C4 (196)
Integrase	
Integrase DNA binding	5D9 (213), 2-19 (216), 8-22 (217), 4-20 (218), 6-19 (219)
domain	
Integrase catalytic core	7-16 (210), 4F6 (211)
N-term	1C4 (197), 2C11 (198), 2E3 (199), 3E11 (200), 3F9 (201), 5F8 (202), 6G5 (203), 7B6 (204), 7C6 (205), 6C5 (206), 4D6 (209)
Pol	
C-term	33 (244)
Vif	
C-term	TG001 (246)
Tat	
C-term	1D2F11 (252), 2D9E7 (253), 4B4C4 (254), 5G7D8 (255), NT2/4D5.24 (256), 2D9D5 (258)
N-term	NT3/2D1.1 (249), 1D9D5 (251)
Env (gp160)	
C-domain	polyclonal (601), 5B2 (669), 9G11 (670), TH-Ab1 (671), polyclonal (672), polyclonal (673), polyclonal (674), polyclonal
	(675)
C-term	105-306 (574), 750-D (576), 722-D (580), polyclonal (581), 1131-A (582), 858-D (583), 989-D (584), Z13 (677), 1575 (698), polyclonal (702), polyclonal (703), 1577 (705), polyclonal (706), 101-342 (853), 101-451 (854), 120-1 (855)

Binding type	MAb ID (No.)
C1	M85 (271), 7E2/4 (272), 4D4#85 (273), M92 (274), M86 (275), polyclonal (276), 133/237 (277), 133/290 (278), 133/11 (279), D/3G5 (280), D/6A11 (281), D/5E12 (282), L5.1 (283), 4A7C6 (284), 1D10 (285), B242 (286), 133/192 (287), 489.1(961) (288), 5B3 (289), B10 (290), B2 (291), C6 (292), MF49.1 (293), T1.1 (294), T7.1 (295), T9 (296), GV4D3 (297), B27 (298), B9 (299), B35 (300), D/4B5 (301), D/5A11 (302), D/6B2 (303), B18 (304), B20 (305), MF39.1 (306), 187.2.1 (307), 37.1.1(ARP 327) (308), 6D8 (309), M96 (310), MF119.1 (311), MF4.1 (312), MF53.1 (313), MF58.1 (314), MF77.1 (315), T2.1 (316), 11/65 (317), W1 (318), T11 (319), GV1A8 (320), 11 (321), 12G10 (322), 135/9 (323), 7C10 (324), C4 (325), MF46.1 (326), 212A (856), 522-149 (857), L19 (858), M90 (859), MAG 104 (860), MAG 45 (861), MAG 95 (862), MAG 97 (863), T9 (864), p7 (865)
C1-C2	L100 (866)
C1-C4	2/11c (867), A32 (868)
C1-C5	C11 (869), L81 (870)
C2	1006-30-D (367), 847-D (368), 213.1 (372), B12 (373), B13 (374), C13 (375), M89 (376), B21 (377), B23 (378), B24 (379), B25 (380), B3 (381), B26 (382), B29 (383), B36 (384), 110.E (385), 110.C (386)
C3	2H1B (340), 110.D (522), B32 (523), 2F19C (871), B2C (872), polyclonal (873)
C3, C4	ICR38.1a (533)
C4	5C2E5 (528), G3-211 (529), G3-537 (530), G3-299 (534), G3-42 (535), G3-508 (536), G3-519 (537), G3-536 (538), ICR38.8f (539), MO86/C3 (540), 13H8 (541), G45-60 (542), polyclonal (543), 1662 (544), 1663 (545), 1664 (546), 1697 (547), 1794 (548), 1804 (549), 1807 (550), 1808 (551), 1024 (874)
C5	9201 (556), 1C1 (557), 3F5 (558), 5F4/1 (559), 660-178 (560), 9301 (561), B221 (562), H11 (564), W2 (565), M38 (566), 1331A (569), 110.1 (570), 42F (571), 43F (572), RV110026 (573), GV1G2 (575), 450-D (577), 670-D (578), 23A (875), D7324 (876)
CD4BS	polyclonal (531), 1795 (532), 10/46c (877), 1027-30-D (878), 1125H (879), 120-1B1 (880), 1202-D (881), 1331E (882), 1570 (883), 1595 (884), 1599 (885), 15e (886), 205-43-1 (887), 205-46-9 (888), 21h (889), 28A11/B1 (890), 2G6 (891), 35F3/E2 (892), 38G3/A9 (893), 428 (894), 448-D (895), 44D2/D5 (896), 48-16 (897), 50-61A (898), 5145A (899), 558-D (900), 559/64-D (901), 55D5/F9 (902), 588-D (903), 654-D (904), 67G6/C4 (905), 729-D (906), 830D (907), 9CL (908), BM12 (909), D20 (910), D21 (911), D24 (912), D25 (913), D28 (914), D35 (915), D39 (916), D42 (917), D52 (918), D53 (919), D60 (920), DA48 (921), DO8i (922), F105 (923), F91 (924), GP13 (925), GP44 (926), GP68 (927), HF1.7 (928), HT5 (929), HT6 (930), HT7 (931), ICR 39.13g (932), ICR 39.3b (933), IgG1b12 (934), IgGCD4 (935), L28 (936), L33 (937), L41 (938), L42 (939), L52 (940), L72 (941), M12 (942), M13 (943), M6 (944), MAG 116 (945), MAG 12B (946), MAG 29B (947), MAG 3B (948), MAG 55 (949), MAG 72 (950), MAG 86 (951), MAG 96 (952), MTW61D (953), S1-1 (954), T13 (955), T49 (956), T56 (957), TH9 (958), anti-CD4BS summary (959), b11 (960), b13 (961), b14 (962), b3 (963), b6 (964), polyclonal (965)
CD4BS, C-term, N-term	D33 (966)
CD4BS, CD4i, V3, V2	(967)
CD4i	17b (968), 21c (969), 23e (970), 48d (971), 49e (972), X5 (973)
Env oligomer	T22 (974)
HIV-2 V3	anti-HIV-2 polyclonal (516)
Leucine zipper motif	(593), (594)

Binding type	MAb ID (No.)
N-HR, C-HR, and six-helix bundle	polyclonal (975)
N-term	polyclonal (602), 2A2 (976), AC4 (977), AD3 (978), AD3 (979), ID6 (980), ID6 (981)
V1	35D10/D2 (330), 40H2/C7 (331), 43A3/E4 (332), 43C7/B9 (333), 45D1/B7 (334), 46E3/E6 (335), 58E1/B3 (336), 64B9/A6 (337), 69D2/A1 (338), 82D3/C3 (339)
V1, V2, V3, V4, V5	polyclonal (552)
V1-V2	11/68b (982), 62c (983), CRA-6 (984), L15 (985), T52 (986), T54 (987)
V1-V2 and V3-V5	polyclonal (988)
V2	6D5 (327), B33 (328), 697-D (341), 11/4c (348), 8.22.2 (349), 12b (350), G3-136 (351), G3-4 (352), 1088 (989), 110-B (990), 1357 (991), 1361 (992), 1393A (993), 66a (994), 66c (995), 684-238 (996), 830A (997), CRA-3 (998), CRA-4 (999), L17 (1000), SC258 (1001)
V2-CD4BS	L25 (1002), L39 (1003), L40 (1004), L78 (1005)
V3	IIIB-V3-26 (387), IIIB-V3-21 (388), polyclonal (389), polyclonal (390), MO97/V3 (391), polyclonal (392), 55/11 (393), 8/38c (394), 8/64b (395), polyclonal (396), polyclonal (397), polyclonal (398), polyclonal (399), 9284 (400), polyclonal (401), polyclonal (402), polyclonal (403), polyclonal (404), MAG 109 (405), MAG 49 (406), MAG 53 (407), MAG 56 (408), 1324-E (409), polyclonal (410), MO99/V3 (411), C311E (412), 924 (414), polyclonal (415), polyclonal (416), 10F10 (417), 2C4 (418), 412-D (419), polyclonal (420), CGP 47 439 (421), polyclonal (422), 178.1 (423), 257-D (424), 311-11-D (425), 41148D (426), 391/95-D (427), Aw (428), Bw (429), DO142-10 (430), Dv (431), Fv (432), Gv (433), Hv (434), polyclonal (435), 50.1 (436), polyclonal (437), BAT123 (438), 838-D (439), 1006-15D (440), 782-D (441), 908-D (442), 1027-15D (443), F19.26-4 (444), F19.48-3 (445), F19.57-11 (446), M77 (447), SP.BAL114 (448), SP.SF2:104 (449), polyclonal (450), 19b (451), 4G10 (452), 5F7 (453), G3-523 (454), MN215 (455), Nea 9301 (456), 4117C (457), 419-D (458), 453-D (459), 504-D (460), 83.1 (461), 5023B (462), F58/D1 (463), P1/D12 (464), P4/D10 (465), IIIB-13 V3 (466), IIIB-34 V3 (467), A47/B1 (468), D59/A2 (469), G44/H7 (470), M096/V3 (471), μ5.5 (472), loop 2 (473), 268-D (474), 386-D (475), 5042A (476), 5042B (477), 418-D (478), 5021 (479), 5025B (480), 5042 (481), 110.3 (482), 110.4 (483), 110.5 (484), 58.2 (485), 537-D (487), 5020 (488), RC25 (489), 5023A (490), 110.6 (491), polyclonal (492), 10/36e (493), 10/54 (494), 11/85b (495), polyclonal (496), 0.5β (497), Cβ1, 0.5β (498), NM-01 (499), 1026 (500), 1034 (501), 59.1 (502), polyclonal (503), 10E3 (504), polyclonal (505), N11-20 (506), 5025A (507), N70-1.9b (508), 902 (509), 694/98-D (510), 9205 (514), 110.1 (515), IIIB-V3-01 (517), 447-52D (681), (1006), 110.J (1007), 1334-D (1008), 2182 (1009), 2191 (1010), 2219 (1011), 2412 (1012), 2442 (1013), 2456 (1014), 39F (1015), 55/68b (1016), 5G11 (1017), 6.1 (1018), 6.7 (1019), 8.27.3 (1020), 8E11/A8 (1021), 9305 (1022), AG1121 (102
	polyclonal (1030), polyclonal (1031), polyclonal (1032), polyclonal (1033), polyclonal (1034), polyclonal (1035), polyclonal (1036)
V3 discontinuous	11/75a/21/41 (1037), 41.1 (1038), 55/45a/11 (1039)
V3 mimotope	1108 (1040)
V3, V4	polyclonal (1041)
V3-C4	MO101/V3,C4 (511), polyclonal (1042)
V3-C5	MO101/V3,C4 (512), MO101/V3,C4 (513)
V3-CD4BS	D27 (1043), D56 (1044)

Binding type	MAb ID (No.)
V4	D/6D1 (518), 4D7/4 (519), 36.1(ARP 329) (520), C12 (521), polyclonal (524), B15 (525), B34 (526)
V5	polyclonal (553)
V5-C5	CRA1(ARP 323) (554), M91 (555), 8C6/1 (563)
adjacent to cluster II	2F5 (667)
alpha-helical C-HR, hairpin intermediate	98-6 (663)
carbohydrates at glycosylation residues in C2, C3, C4, and V4	2G12 (1045)
cluster I	50-69 (605), 246-D (623), 181-D (625), 240-D (627), F240 (628), D49 (629), D61 (630), T32 (631), T34 (632), 1367 (1046)
cluster II	D50 (660), 167-7 (664), ND-15G1 (665), 126-6 (1047), 1342 (1048), 1379 (1049), Fab D11 (1050), Fab D5 (1051), Fab G1
	(1052), Fab M10 (1053), Fab M12 (1054), Fab M15 (1055), Fab S10 (1056), Fab S6 (1057), Fab S8 (1058), Fab S9 (1059), Fab T3 (1060), Md-1 (1061)
cluster II, six-helix bundle	167-D (666), 1281 (1062)
cluster III	Fab A9 (1063), Fab G15 (1064), Fab G5 (1065), Fab L1 (1066), Fab L11 (1067), Fab L2 (1068)
cytoplasmic domain	Chessie 8 (1069)
gp120-CD4 complex	8F101 (1070), 8F102 (1071), CG-10 (1072), CG-25 (1073), CG-4 (1074), CG-76 (1075), CG-9 (1076)
immunodominant region	3D6 (658), 105-518 (1077)
p24+gp41	31A1 (1078), 39A64 (1079), 39B86 (1080), 9303 (1081)
six helix bundle	NC-1 (1082)
Nef	
C-term	AE6 (1116), AG11 (1117), EH1 (1118), AE6 (1123)

# IV-B-2 Alphabetical listing of MAbs

Cross reference	e of MAb	1025	714	111/073	55	1331E	882	1807	550
names and their o		1026	500	111/182	36	1334-D	1008	1808	551
pearance in the ta		1027-15D	443	112/021	37	1342	1048	181-D	625
phanumeric sortin		1027-30-D	878	112/047	38	135/9	323	183-H12-5C	135
bols, digits, upper		1034	501	1125H	879	1357	991	187.2.1	307
and lowercase lette		105-134	715	113/038	56	1361	992	1899	689
		105-306	574	113/072	74	1367	1046	19	215
MAb ID	No.	105-518	1077	1131-A	582	1379	1049	1907	690
	593	105-732	657	115.8	633	1393A	993	1908	691
	594	106/01	116	11C10B10	105	13B5	115	1909	692
	708	108/03	110	11D11F2	106	13E1	173	19b	451
	709	1088	989	11H9	24	13H8	541	1A1	585
	710	10E3	504	12	224	14	226	1A7	90
	711	10E7	171	12-B-4	102	14D4E11	50	1B1	720
	712	10E9	716	120-1	855	15-21	31	1B2C12	86
	967	10F10	417	120-16	662	1570	883	1B8.env	647
(544 504)	1006	11	321	120-1B1	880	1575	698	1C1	557
$\alpha(566-586)$	589	11-C-5	61	1202-D	881	1576	685	1C12B1	228
μ5.5	472	11/41e	345	126-50	717	1577	705	1C4	197
$0.5\beta$	497	11/4b	346	126-6	1047	1578	686	1D10	285
1-B-7	68	11/4c	348	1281	1062	1579	687	1D2F11	252
1-E-4	57	11/65	317	12G-A8g2	19	1583	688	1D4A3	188
1-E-9	58	11/68b	982	12G-D7h11	20	1595	884	1D9	27
1.152 B3	178	11/75a/21/41	1037	12G-H1c7	21	1599	885	1D9D5	251
1.153 G10	186	11/85b	495	12G10	322	15F8C7	45	1E8	177
1.158 E2	179	110-B	990	12H-D3b3	18	15e	886	1F11	595
1.160 B3	190	110.1	363	12H2	718	16	227	1F6	91
1.17.3	89	110.1	570	12I-D12g2	22	16/4/2	134	1F7	721
1.2	250	110.3	482	12b	350	1662	544	1G10	267
10-E-7	59	110.4	483	13	225	1663	545	1G5C8	51
10-G-9	60	110.5	484	13-102-100	76	1664	546	1G7	268
10.1	261	110.6	491	13.10	719	167-7	664	1H5	596
10/36e	493	110.C	386	13/035	1086	167-D	666	2-19	216
10/46c	877	110.D	522	13/042	1085	1696	170	2-E-4	62
10/54	494	110.E	385	13/058	1096	1697	547	2-H-4	63
10/76b	344	110.I	515	1324-E	409	17	208	2.2B	722
1006-15D	440	110.J	1007	133/11	279	178.1	423	2/11c	867
1006-30-D	367	110/015	111	133/192	287	1794	548	205-43-1	887
101-342	853	1108	1040	133/237	277	1795	532	205-46-9	888
101-451	854	1109/01	49	133/290	278	17b	968	21	229
102-135	713	111/052	46	1331A	569	1804	549	212A	856
1024	874				207		J.,		0.0

2182         1009         2H1B         340         3D3         43         4D2D5         896         522-149         875           21c         999         3-H-7         25         3D5         727         453-D         459         537-D         487           21c         999         3-H-7         25         3D5         727         453-D         459         537-D         487           21p         1011         800         93-375         83         3D6         68         45D-R7         334         5571         331-11         393           21A         875         31-11         32         3E11         13         47-2         52         558-6b         1016           23A5G5         93         311-11-D         425         3E6         1108         489-1(961)         288         559/64-D         901           23A5G5         93         31710B         74         3F10         223         486         971         352-559-D         900           23A5G5         93         31710B         74         3F10         223         3E6         3B6         1108         489.1(961)         288         559/64-D         901           240-D	213.1	372	2H12	1111	3D12	1092	448-D	895	5145A	899
1911   1910   3-B-7	2182	1009	2H1B	340	3D3	43	44D2/D5	896	522-149	857
21h         889         30.315         83         306         688         45D/B7         334         55/11         393           22p         1011         300         723         309         597         46B3H56         33         55/45/II         103           23A         875         31-11         32         3EH         13         47-2         52         55/68b         1016           23A5C4         92         3170B         110I         3BEI         1108         48-16         897         558-D         90           23A5C5         93         31L-11-D         425         3B6         1108         48-1061         288         59/64-D         901           240-D         627         31A1         1078         3F2         1091         499-156         362         55EHH         732           241-D         136         31D6         180         385         558         49B11/A1         730         56C4C8         733           241-D         136         31D6         180         385         558         49B11/A1         730         56C4C8         733           241-D         1013         32         230         3G12         210	2191	1010	3-B-7	69	3D3.B8	360	450-D	577	52G5/B9	731
2219         1011         30D         723         3DP         597         4683786         335         \$5548b         103           23A 5G4         875         31-11         32         3B11         13         47-2         \$2         5568b         1016           23A5G5         93         311-11-D         425         3B6         1108         489.1(961)         288         559/64-D         901           23A5G5         93         311-11-D         425         3B6         1108         489.1(961)         288         559/64-D         901           240-D         627         31A1         1078         3F2         1091         493-156         362         55E4/H1         732           241-D         136         3106         180         3F5         558         49B11/A1         73         56C4(28         733           241-D         136         3106         180         3F5         558         49B11/A1         73         56C4(28         733           241-D         136         3106         180         3F5         558         49B11/A1         73         56C4(28         481         741         732           241-D         131         32	21c	969	3-H-7	25	3D5	727	453-D	459	537-D	487
2219         1011         30D         723         3DP         597         46E3VE6         335         55/4sJul         1030           23A 5C4         92         31/03         1101         3E11         20         48-16         897         558-D         90           23A5C5         93         311-11-D         425         3E6         1108         489.1(961)         28         559/64-D         90           240-D         627         31A1         1078         3F2         1091         493-156         362         558/491         732           241-D         136         31D6         180         3F5         558         49B1I/AI         730         56C4(28         733           241-D         136         31D6         180         3F5         558         49B1I/AI         730         56C4(28         733           241-D         136         31D6         180         3F5         558         49B1I/AI         730         56C4(28         733           241-D         136         31D2         130         3612         1995         4A7C6         284         57H5D7         735           244-D         1012         340         340         266 <td>21h</td> <td>889</td> <td>30:3E5</td> <td>83</td> <td>3D6</td> <td>658</td> <td>45D1/B7</td> <td>334</td> <td>55/11</td> <td>393</td>	21h	889	30:3E5	83	3D6	658	45D1/B7	334	55/11	393
23A         875         31-11         32         3E11         13         47-2         52         55/68b         1016           23A5G5         93         31I-11-D         425         3E6         1108         48-16         897         58-B.D         900           23A5G5         93         31I-11-D         425         3E6         1108         48-10(91)         288         559/64-D         901           23A         970         3170B         724         3F10         233         48d         971         55D5/F9         902           240-D         627         31A1         1078         3F2         1091         49-116         362         55E4/H1         732           241-D         136         31D6         180         3F5         558         49B11/A1         730         56C4/C8         733           2412         1013         32         230         3G12         1095         4A7C6         284         57H5/D7         735           2456         1013         32/15.842         3         3H6         262         4BHC4         254         588-D         993           246-D         623         32/55.842         4         3H6	2219	1011	30D		3D9	597	46E3/E6	335	55/45a/11	1039
23A5G4         92         31/03         1101         3E11         200         48-16         897         558-D         900           23A5G5         93         311-11-D         425         3B6         1108         489.1(961)         288         559/64-D         901           240-D         627         31A1         1078         3F2         1091         493-156         362         55E4/H1         732           241-D         136         31D6         180         3F5         558         49B11/A1         730         56C4/C8         733           2412         1012         31G8         181         3F9         201         49e         972         57B6/F1         734           2442         1013         32         230         3G12         1095         4A7C6         284         57H5/F1         735           2456         1014         321/L24.89         11         3G4         266         483         598         58.2         485           246-D         623         325.842         4         3H6         728         4B1C4         254         588-D         90           25/03         158         3222.151         359         4	23A		31-11		3E11					1016
23A5C5         93         311-11-D         425         386         1108         489,1(961)         288         559/64-D         901           23e         970         31710B         724         3170         233         48d         971         5505/P9         902           240-D         627         31A1         1078         3F2         1091         49-156         362         55E4/H1         732           241-D         136         31D6         180         3F5         558         49B11/A1         730         56C4/C8         733           2412         1013         32         230         3G12         1095         4A7C6         284         57H5/D7         735           2456         1014         321/24.89         11         3G4         266         488         598         852         485           2460         623         32/5.842         3         3H6         262         484C4         254         85B-D         903           24G3         35/5.842         4         3H6         728         4C1LD8         361         58E1/B3         336           243         420         241         48C9         28         59.1 <t< td=""><td>23A5G4</td><td>92</td><td>31/03</td><td>1101</td><td>3E11</td><td>200</td><td>48-16</td><td>897</td><td>558-D</td><td>900</td></t<>	23A5G4	92	31/03	1101	3E11	200	48-16	897	558-D	900
23c         970         31710B         724         3F10         233         48d         971         55D5F9         002           240-D         627         31A1         1078         3F2         1091         493-156         362         55E4H1         732           241-D         136         31D6         180         3F5         558         49B11/A1         730         56C4C8         733           2412         1012         31G8         181         3F9         201         49c         972         57B6F1         734           2442         1013         32         230         3G12         1095         4A7C6         284         57H5D7         735           246-D         623         32/5.842         3         3H6         266         4B3         598         58.2         485           24G3         586         32/5.842         4         3H6         728         4CI1.D8         361         58E1/B3         336           25.3         75         322-151         359         4         234         4C9         28         59.1         502           25/03         1089         32-232K         112         4         650	23A5G5		311-11-D	425	3E6	1108	489.1(961)	288	559/64-D	901
240-D         627         31 A1         1078         3F2         1091         493-156         362         55E/HI1         732           241-D         136         31D6         180         3F5         558         49B11/A1         730         56C4/C8         733           2412         1012         31G8         181         3F9         201         49e         972         57B6/F1         734           2442         1013         32         230         3G12         1095         4A7C6         284         57H5/D7         735           246-D         623         32/5.8.42         3         3H6         262         4B4C4         254         588-D         903           24G3         586         32/5.8.42         4         3H6         728         4C11.D8         361         58E1/B3         336           25.3         75         322-151         359         4         234         4C9         28         59.1         502           25/03         1089         32-2151         339         4         234         4C9         28         59.1         502           25/10         1090         32-32K         112         4         409		970	31710B				48d		55D5/F9	902
2412         1012         31G8         181         3F9         201         49e         972         57B6/F1         734           2442         1013         32         230         3G12         1095         4A7C6         284         57H5/D7         735           2456         1014         32/1.24.89         11         3G4         266         4B3         598         58.2         485           2460         623         32/5.8.42         3         3H6         262         4B4C4         254         588-D         903           24G3         586         32/5.8.42         4         3H6         728         4C11.D8         361         58E/B1/B3         336           25.3         75         322-151         359         4         234         4C9         28         59.1         502           25/03         1089         32:32K         112         4         650         4D4         599         5B2         184           257-D         424         325         420         218         4D4#85         273         5B2         669           25C2         587         33         441         406/01         78         4D6         299							493-156			
2442         1013         32         230         3G12         1095         4A7C6         284         57H5/D7         735           2456         1014         32/1.24.89         11         3G4         266         4B3         598         58.2         485           246-D         623         32/5.8.42         3         3H6         262         4B4C4         254         588-D         903           24G3         586         32/5.8.42         4         3H6         728         4C11.D8         361         58E1/B3         336           25.3         75         322-151         359         4         234         4C9         28         59.1         502           25/03         1089         32:32K         112         4         606         4D4         599         5B2         184           257-D         424         32E7         182         4-20         218         4D4#85         273         5B2         669           26C2         587         33         244         406/01         78         4D6         209         5B3         289           26C92         1074         351         406         316         403         403 <td>241-D</td> <td>136</td> <td>31D6</td> <td>180</td> <td>3F5</td> <td>558</td> <td>49B11/A1</td> <td>730</td> <td>56C4/C8</td> <td>733</td>	241-D	136	31D6	180	3F5	558	49B11/A1	730	56C4/C8	733
2442         1013         32         230         3G12         1095         4A7C6         284         57H5/D7         735           2456         1014         32/1.24.89         11         3G4         266         4B3         598         58.2         485           246-D         623         32/5.8.42         3         3H6         262         4B4C4         254         588-D         903           24G3         586         32/5.8.42         4         3H6         728         4C11.D8         361         58E1/B3         336           25.3         75         322-151         359         4         234         4C9         28         59.1         502           25/03         1089         32:32K         112         4         606         4D4         599         5B2         184           257-D         424         32E7         182         4-20         218         4D4#85         273         5B2         669           26C2         587         33         244         406/01         78         4D6         209         5B3         289           26C92         1074         351         406         316         403         403 <td>2412</td> <td>1012</td> <td>31G8</td> <td>181</td> <td>3F9</td> <td>201</td> <td>49e</td> <td>972</td> <td>57B6/F1</td> <td>734</td>	2412	1012	31G8	181	3F9	201	49e	972	57B6/F1	734
246-D         623         32/5.8.42         3         3H6         262         4B4C4         254         588-D         903           24G3         586         32/5.8.42         4         3H6         728         4C11.D8         361         58E1/B3         336           25.3         75         322.151         359         4         234         4C9         28         59.1         502           25/03         1089         32:32K         112         4         650         4D4         599         5B2         184           257-D         424         32E7         182         4-20         218         4D485         273         5B2         669           26028         1097         33D.5         183         4003/C11         729         4D7/A         519         5C2E5         528           26076         1090         35         231         40H2/C7         331         4E10         676         5D9         213           268-D         474         35D10/D2         330         41-1         693         4G10         452         5F         194           28-24-10         976         36.1(ARP 329)         520         41-2         694 <td>2442</td> <td>1013</td> <td>32</td> <td>230</td> <td>3G12</td> <td>1095</td> <td>4A7C6</td> <td>284</td> <td>57H5/D7</td> <td>735</td>	2442	1013	32	230	3G12	1095	4A7C6	284	57H5/D7	735
24G3         586         32/5.8.42         4         3H6         728         4C11.D8         361         58E1/B3         336           25.3         75         322-151         359         4         234         4C9         28         59.1         502           25/03         1089         32:32K         112         4         660         4D4         599         5B2         184           257-D         424         32E7         182         4-20         218         4D4#85         273         5B2         669           25C2         587         33         244         406/01         78         4D6         209         5B3         289           26/028         1097         33DS         183         40D3/C11         729         4D7/4         519         5C2E5         528           26/76         1090         35         231         40H2/C7         331         4E10         676         5D9         213           268-D         474         35D10/D2         330         4I-1         608         4F6         211         5E2.A3k         138           28A11/B1         890         35F3/E2         892         41-1         693	2456	1014	32/1.24.89	11	3G4	266	4B3	598	58.2	485
24G3         586         32/5.8.42         4         3H6         728         4C11.D8         361         58E1/B3         336           25.3         75         322-151         359         4         234         4C9         28         59.1         502           25/03         1089         32:32K         112         4         650         4D4         599         5B2         184           257-D         424         32E7         182         4-20         218         4D4#85         273         5B2         669           25C2         587         33         244         406/01         78         4D6         209         5B3         289           26/028         1090         35         231         40H2/C7         331         4E10         676         5D9         213           268-D         474         35D10/D2         330         41-1         608         4F6         211         5E2.A3k         138           2A2         976         36.1(ARP 329)         520         41-2         694         4G2         600         5F3         58           2A2/26         604         37.1.1(ARP 327)         308         41-3         695	246-D	623	32/5.8.42	3	3H6	262	4B4C4	254	588-D	903
25/03         1089         32:32K         112         4         650         4D4         599         5B2         184           257-D         424         32E7         182         4-20         218         4D4#85         273         5B2         669           25C2         587         33         244         406/01         78         4D6         209         5B3         289           26/028         1097         33D5         183         40D3/C11         729         4D7/4         519         5C2E5         528           26/76         1090         35         231         40H2/C7         331         4E10         676         5D9         213           268-D         474         35D10/D2         330         41-1         608         4F6         211         5E2.A3k         138           28A11/B1         890         35F3/E2         892         41-1         693         4G10         452         5F         194           2A2         976         36.1(ARP 329)         520         41-2         694         4G2         600         5F3         588           2A2/26         604         37.1.1(ARP 327)         308         41-3         695	24G3	586		4	3H6	728	4C11.D8	361	58E1/B3	336
257-D         424         32E7         182         4-20         218         4D4#85         273         5B2         669           25C2         587         33         244         406/01         78         4D6         209         5B3         289           26/028         1097         33D5         183         40D3/C11         729         4D7/4         519         5C2E5         528           26/076         1090         35         231         40H2/C7         331         4E10         676         5D9         213           268-D         474         35D10/D2         330         41-1         608         4F6         211         5E2.A3k         138           28A11/B1         890         35F3/E2         892         41-1         608         4F6         211         5E2.A3k         138           28A1/B1/B1         890         35F3/E2         892         41-1         693         4G10         452         5F         194           2A2         976         36.1(ARP 329)         520         41-2         694         4G2         600         5F3         88           2A2/26         604         37.1.1(ARP 327)         308         41-3	25.3	75	322-151	359	4	234	4C9	28	59.1	502
25C2         587         33         244         406/01         78         4D6         209         5B3         289           26/028         1097         33D5         183         40D3/CI1         729         4D7/4         519         5C2E5         528           26/76         1090         35         231         40D3/CI1         729         4D7/4         519         5C2E5         528           268-D         474         35D10/D2         330         41-1         608         4F6         211         5E2.A3k         138           28A11/B1         890         35F3/E2         892         41-1         693         4G10         452         5F         194           2A2         976         36.1(ARP 329)         520         41-2         694         4G2         600         5F3         588           2A2/26         604         37.1.1(ARP 327)         308         41-3         695         4G9         259         5F4/1         559           2A3         1109         38/12b         356         41-6         651         4H2B1         29         5F7         453           2A6         137         38/60b         357         41-7 <t< td=""><td>25/03</td><td>1089</td><td>32:32K</td><td>112</td><td>4</td><td>650</td><td>4D4</td><td>599</td><td>5B2</td><td>184</td></t<>	25/03	1089	32:32K	112	4	650	4D4	599	5B2	184
26/028         1097         33D5         183         40D3/C11         729         4D7/4         519         5C2E5         528           26/76         1090         35         231         40H2/C7         331         4E10         676         5D9         213           268-D         474         35D10/D2         330         41-1         608         4F6         211         5E2.A3k         138           28A11/B1         890         35F3/E2         892         41-1         693         4G10         452         5F         194           2A2         976         36.1(ARP 329)         520         41-2         694         4G2         600         5F3         588           2A2/26         604         37.1.1(ARP 327)         308         41-3         695         4G9         259         5F4/1         559           2A3         1109         38/12b         356         41-6         651         4H2B1         29         5F7         453           2A6         137         38/60b         357         41-1         1038         5-21-3         661         5G         195           2C1         198         386-D         475         41.1 <t< td=""><td>257-D</td><td>424</td><td>32E7</td><td>182</td><td>4-20</td><td>218</td><td>4D4#85</td><td>273</td><td>5B2</td><td>669</td></t<>	257-D	424	32E7	182	4-20	218	4D4#85	273	5B2	669
26/76         1090         35         231         40H2/C7         331         4E10         676         5D9         213           268-D         474         35D10/D2         330         41-1         608         4F6         211         5E2.A3k         138           28A11/B1         890         35F3/E2         892         41-1         693         4G10         452         5F         194           2A2         976         36.1(ARP 329)         520         41-2         694         4G2         600         5F3         588           2A2/26         604         37.1.1(ARP 327)         308         41-3         695         4G9         259         5F4/1         559           2A3         1109         38/12b         356         41-6         651         4H2B1         29         5F7         453           2A6         137         38/60b         357         41-7         652         4H4         1083         5F8         202           2C11         198         386-D         475         41.1         1038         5-21-3         661         5G         195           2C4         418         38:9.6K         80         41.4         609 <td>25C2</td> <td>587</td> <td>33</td> <td>244</td> <td>406/01</td> <td>78</td> <td>4D6</td> <td>209</td> <td>5B3</td> <td>289</td>	25C2	587	33	244	406/01	78	4D6	209	5B3	289
268-D         474         35D10/D2         330         41-1         608         4F6         211         5E2.A3k         138           28A11/B1         890         35F3/E2         892         41-1         693         4G10         452         5F         194           2A2         976         36.1(ARP 329)         520         41-2         694         4G2         600         5F3         588           2A2/26         604         37.1.1(ARP 327)         308         41-3         695         4G9         259         5F41         559           2A3         1109         38/12b         356         41-6         651         4H2B1         29         5F7         453           2A6         137         38/60b         357         41-7         652         4H4         1083         5F8         202           2C11         198         386-D         475         41.1         1038         5-21-3         661         5G         195           2C4         418         38:9.6K         80         41.4         609         50-61A         898         5G11         1017           2D9E7         253         38B5/C9         725         41148D	26/028	1097	33D5	183	40D3/C11	729	4D7/4	519	5C2E5	528
28A11/B1       890       35F3/E2       892       41-1       693       4G10       452       5F       194         2A2       976       36.1(ARP 329)       520       41-2       694       4G2       600       5F3       588         2A2/26       604       37.1.1(ARP 327)       308       41-3       695       4G9       259       5F4/1       559         2A3       1109       38/12b       356       41-6       651       4H2B1       29       5F7       453         2A6       137       38/60b       357       41-7       652       4H4       1083       5F8       202         2C11       198       386-D       475       41.1       1038       5-21-3       661       5G       195         2C4       418       38:9.6K       80       41.4       609       50-61A       898       5G11       1017         2D9D5       258       38B5/C9       725       41148D       426       50-69       605       5G7D8       255         2D9E7       253       38G3/A9       893       4117C       457       50.1       436       6-19       219         2E3       199       391/95-	26/76	1090	35	231	40H2/C7	331	4E10	676	5D9	213
2A2         976         36.1(ARP 329)         520         41-2         694         4G2         600         5F3         588           2A2/26         604         37.1.1(ARP 327)         308         41-3         695         4G9         259         5F4/1         559           2A3         1109         38/12b         356         41-6         651         4H2B1         29         5F7         453           2A6         137         38/60b         357         41-7         652         4H4         1083         5F8         202           2C11         198         386-D         475         41.1         1038         5-21-3         661         5G         195           2C4         418         38:9.6K         80         41.4         609         50-61A         898         5G11         1017           2D9D5         258         38B5/C9         725         41148D         426         50-69         605         5G7D8         255           2D9E7         253         38G3/A9         893         4117C         457         50.1         436         6-19         219           2E3         199         391/95-D         427         412-D	268-D	474	35D10/D2	330	41-1	608	4F6	211	5E2.A3k	138
2A2/26       604       37.1.1(ARP 327)       308       41-3       695       4G9       259       5F4/1       559         2A3       1109       38/12b       356       41-6       651       4H2B1       29       5F7       453         2A6       137       38/60b       357       41-7       652       4H4       1083       5F8       202         2C11       198       386-D       475       41.1       1038       5-21-3       661       5G       195         2C4       418       38.9.6K       80       41.4       609       50-61A       898       5G11       1017         2D9D5       258       38B5/C9       725       41148D       426       50-69       605       5G7D8       255         2D9E7       253       38G3/A9       893       4117C       457       50.1       436       6-19       219         2E3       199       391/95-D       427       412-D       419       5020       488       6-D-12       70         2E3       1098       39A64       1079       418-D       478       5021       479       6-E-7       71         2E4       1110       39B86 <td>28A11/B1</td> <td>890</td> <td>35F3/E2</td> <td>892</td> <td>41-1</td> <td>693</td> <td>4G10</td> <td>452</td> <td>5F</td> <td>194</td>	28A11/B1	890	35F3/E2	892	41-1	693	4G10	452	5F	194
2A3         1109         38/12b         356         41-6         651         4H2B1         29         5F7         453           2A6         137         38/60b         357         41-7         652         4H4         1083         5F8         202           2C11         198         386-D         475         41.1         1038         5-21-3         661         5G         195           2C4         418         38:9.6K         80         41.4         609         50-61A         898         5G11         1017           2D9D5         258         38B5/C9         725         41148D         426         50-69         605         5G7D8         255           2D9E7         253         38G3/A9         893         4117C         457         50.1         436         6-19         219           2E3         199         391/95-D         427         412-D         419         5020         488         6-D-12         70           2E3         1098         39A64         1079         418-D         478         5021         479         6-E-7         71           2E4         1110         39B86         1080         419-D         458	2A2	976	36.1(ARP 329)	520	41-2	694	4G2	600	5F3	588
2A6       137       38/60b       357       41-7       652       4H4       1083       5F8       202         2C11       198       386-D       475       41.1       1038       5-21-3       661       5G       195         2C4       418       38:9.6K       80       41.4       609       50-61A       898       5G11       1017         2D9D5       258       38B5/C9       725       41148D       426       50-69       605       5G7D8       255         2D9E7       253       38G3/A9       893       4117C       457       50.1       436       6-19       219         2E3       199       391/95-D       427       412-D       419       5020       488       6-D-12       70         2E3       1098       39A64       1079       418-D       478       5021       479       6-E-7       71         2E4       1110       39B86       1080       419-D       458       5023A       490       6.1       1018         2F11       622       39F       1015       418-2       680       5023B       462       6.1       1119         2F2       1106       3A2 <t< td=""><td>2A2/26</td><td>604</td><td>37.1.1(ARP 327)</td><td>308</td><td>41-3</td><td>695</td><td>4G9</td><td>259</td><td>5F4/1</td><td>559</td></t<>	2A2/26	604	37.1.1(ARP 327)	308	41-3	695	4G9	259	5F4/1	559
2C11       198       386-D       475       41.1       1038       5-21-3       661       5G       195         2C4       418       38:9.6K       80       41.4       609       50-61A       898       5G11       1017         2D9D5       258       38B5/C9       725       41148D       426       50-69       605       5G7D8       255         2D9E7       253       38G3/A9       893       4117C       457       50.1       436       6-19       219         2E3       199       391/95-D       427       412-D       419       5020       488       6-D-12       70         2E3       1098       39A64       1079       418-D       478       5021       479       6-E-7       71         2E4       1110       39B86       1080       419-D       458       5023A       490       6.1       1018         2F11       622       39F       1015       41S-2       680       5023B       462       6.1       1119         2F19C       871       39H10/A11       726       428       894       5025A       507       6.7       1019         2F2       1106       3A2	2A3	1109	38/12b	356	41-6	651	4H2B1	29	5F7	453
2C4       418       38:9.6K       80       41.4       609       50-61A       898       5G11       1017         2D9D5       258       38B5/C9       725       41148D       426       50-69       605       5G7D8       255         2D9E7       253       38G3/A9       893       4117C       457       50.1       436       6-19       219         2E3       199       391/95-D       427       412-D       419       5020       488       6-D-12       70         2E3       1098       39A64       1079       418-D       478       5021       479       6-E-7       71         2E4       1110       39B86       1080       419-D       458       5023A       490       6.1       1018         2F11       622       39F       1015       41S-2       680       5023B       462       6.1       1119         2F19C       871       39H10/A11       726       428       894       5025A       507       6.7       1019         2F2       1106       3A2       1112       42F       571       5025B       480       60b       354         2F5       667       3A6	2A6	137	38/60b	357	41-7	652	4H4	1083	5F8	202
2D9D5       258       38B5/C9       725       41148D       426       50-69       605       5G7D8       255         2D9E7       253       38G3/A9       893       4117C       457       50.1       436       6-19       219         2E3       199       391/95-D       427       412-D       419       5020       488       6-D-12       70         2E3       1098       39A64       1079       418-D       478       5021       479       6-E-7       71         2E4       1110       39B86       1080       419-D       458       5023A       490       6.1       1018         2F11       622       39F       1015       41S-2       680       5023B       462       6.1       1119         2F19C       871       39H10/A11       726       428       894       5025A       507       6.7       1019         2F2       1106       3A2       1112       42F       571       5025B       480       60b       354         2F5       667       3A6       35       43A3/E4       332       504-D       460       62c       983         2G12       1045       3B10       <	2C11	198	386-D	475	41.1	1038	5-21-3	661	5G	195
2D9E7       253       38G3/A9       893       4117C       457       50.1       436       6-19       219         2E3       199       391/95-D       427       412-D       419       5020       488       6-D-12       70         2E3       1098       39A64       1079       418-D       478       5021       479       6-E-7       71         2E4       1110       39B86       1080       419-D       458       5023A       490       6.1       1018         2F11       622       39F       1015       41S-2       680       5023B       462       6.1       1119         2F19C       871       39H10/A11       726       428       894       5025A       507       6.7       1019         2F2       1106       3A2       1112       42F       571       5025B       480       60b       354         2F5       667       3A6       35       43A3/E4       332       504-D       460       62c       983         2G12       1045       3B10       12       43C7/B9       333       5042       481       63G4/E2       736         2G2       270       3D10G6 <td< td=""><td>2C4</td><td>418</td><td>38:9.6K</td><td>80</td><td>41.4</td><td>609</td><td>50-61A</td><td>898</td><td>5G11</td><td>1017</td></td<>	2C4	418	38:9.6K	80	41.4	609	50-61A	898	5G11	1017
2E3       199       391/95-D       427       412-D       419       5020       488       6-D-12       70         2E3       1098       39A64       1079       418-D       478       5021       479       6-E-7       71         2E4       1110       39B86       1080       419-D       458       5023A       490       6.1       1018         2F11       622       39F       1015       41S-2       680       5023B       462       6.1       1119         2F19C       871       39H10/A11       726       428       894       5025A       507       6.7       1019         2F2       1106       3A2       1112       42F       571       5025B       480       60b       354         2F5       667       3A6       35       43A3/E4       332       504-D       460       62c       983         2G12       1045       3B10       12       43C7/B9       333       5042       481       63G4/E2       736         2G2       270       3D10G6       94       43F       572       5042A       476       64B9/A6       337	2D9D5	258	38B5/C9	725	41148D	426	50-69	605	5G7D8	255
2E3       1098       39A64       1079       418-D       478       5021       479       6-E-7       71         2E4       1110       39B86       1080       419-D       458       5023A       490       6.1       1018         2F11       622       39F       1015       41S-2       680       5023B       462       6.1       1119         2F19C       871       39H10/A11       726       428       894       5025A       507       6.7       1019         2F2       1106       3A2       1112       42F       571       5025B       480       60b       354         2F5       667       3A6       35       43A3/E4       332       504-D       460       62c       983         2G12       1045       3B10       12       43C7/B9       333       5042       481       63G4/E2       736         2G2       270       3D10G6       94       43F       572       5042A       476       64B9/A6       337	2D9E7		38G3/A9	893		457	50.1	436	6-19	
2E4       1110       39B86       1080       419-D       458       5023A       490       6.1       1018         2F11       622       39F       1015       41S-2       680       5023B       462       6.1       1119         2F19C       871       39H10/A11       726       428       894       5025A       507       6.7       1019         2F2       1106       3A2       1112       42F       571       5025B       480       60b       354         2F5       667       3A6       35       43A3/E4       332       504-D       460       62c       983         2G12       1045       3B10       12       43C7/B9       333       5042       481       63G4/E2       736         2G2       270       3D10G6       94       43F       572       5042A       476       64B9/A6       337	2E3	199	391/95-D	427	412-D	419	5020	488	6-D-12	70
2F11       622       39F       1015       41S-2       680       5023B       462       6.1       1119         2F19C       871       39H10/A11       726       428       894       5025A       507       6.7       1019         2F2       1106       3A2       1112       42F       571       5025B       480       60b       354         2F5       667       3A6       35       43A3/E4       332       504-D       460       62c       983         2G12       1045       3B10       12       43C7/B9       333       5042       481       63G4/E2       736         2G2       270       3D10G6       94       43F       572       5042A       476       64B9/A6       337	2E3	1098	39A64	1079	418-D	478	5021	479	6-E-7	71
2F19C     871     39H10/A11     726     428     894     5025A     507     6.7     1019       2F2     1106     3A2     1112     42F     571     5025B     480     60b     354       2F5     667     3A6     35     43A3/E4     332     504-D     460     62c     983       2G12     1045     3B10     12     43C7/B9     333     5042     481     63G4/E2     736       2G2     270     3D10G6     94     43F     572     5042A     476     64B9/A6     337	2E4	1110	39B86	1080	419-D	458	5023A	490	6.1	1018
2F2     1106     3A2     1112     42F     571     5025B     480     60b     354       2F5     667     3A6     35     43A3/E4     332     504-D     460     62c     983       2G12     1045     3B10     12     43C7/B9     333     5042     481     63G4/E2     736       2G2     270     3D10G6     94     43F     572     5042A     476     64B9/A6     337	2F11		39F	1015	41S-2	680	5023B	462	6.1	1119
2F5     667     3A6     35     43A3/E4     332     504-D     460     62c     983       2G12     1045     3B10     12     43C7/B9     333     5042     481     63G4/E2     736       2G2     270     3D10G6     94     43F     572     5042A     476     64B9/A6     337	2F19C	871	39H10/A11	726	428	894	5025A	507	6.7	1019
2G12 1045 3B10 12 43C7/B9 333 5042 481 63G4/E2 736 2G2 270 3D10G6 94 43F 572 5042A 476 64B9/A6 337	2F2	1106	3A2	1112	42F	571	5025B	480	60b	354
2G2 270 3D10G6 94 43F 572 5042A 476 64B9/A6 337		667			43A3/E4	332		460		983
2G6 891 3D12 232 447-52D 681 5042B 477 654-D 904								476	64B9/A6	337
	2G6	891	3D12	232	447-52D	681	5042B	477	654-D	904

660-178         560         8.6-9         65         97B/IES         743         B26         382         C8         682           66c         994         8.41-7         66         98-4.3         141         B27         208         CA5         127           66c         995         8.22.2         349         98-4.9         142         B29         872         CD-4/1         44           670-C         978         8.27.3         1020         98-4.3         607         B2C         872         CD-4/1         41           670-C         978         8.23.8         394         98-6         663         B3         381         CD12B4         107           68.11         6.54         8.203/C3         339         9.44-C4         104         B31         683         CG-10         1072           684-238         96         8.1         461         9CL         98         B32         323         328         CG-10         1072           684-238         96         8.3         4.3         10         8.3         322         CG-25         1076           697-D         3.4         8.2         8.2         8.2         6.2 <t< th=""><th>65B12/C5</th><th>737</th><th>8-D-5</th><th>72</th><th>9305</th><th>1022</th><th>B25</th><th>380</th><th>C6</th><th>292</th></t<>	65B12/C5	737	8-D-5	72	9305	1022	B25	380	C6	292
66a         994         8-H-7         66         98-4.3         141         B27         298         CA5         127           65c         955         8.22.2         349         98-49         142         B20         38.3         CB-135.5         41           670-D         578         8.27.3         1020         98-3         607         B2C         872         CD-4/1         41           670-D         578         8.27.3         1020         98-3         607         B2C         872         CD-4/1         44           68.11         653         876-b         394         98-b         663         B3         33         CD-121.6         107           681-13         654         82D3/C3         339         94/4-4         104         B31         683         CG-10         107           684-238         996         83.1         461         9CL         90         833         38         CG-3         CG-4         B33         38         CG-4         1073           69D2/A1         338         838-D         439         965         30         834         526         CG-9         1076           69B9         193 <t< td=""><td></td><td>560</td><td></td><td>65</td><td></td><td></td><td></td><td></td><td></td><td></td></t<>		560		65						
66c         995         8.22.2         349         98.4.9         142         B90         383         CB-13/5         41           670-D         578         8.27.3         1020         98.43         607         B2C         872         CD-41         44           676-C4         905         8/38c         394         98.6         663         B3         381         CD12B4         107           68.1         653         8/64         395         989-D         584         B30         678         CD9         146           68.11         654         82D3/C3         39         9.4C+         104         B31         683         CG-10         1072           684-238         996         83.1         461         9CL         908         B32         523         CG-25         1073           694/98-D         510         830A         997         9G1         670         B33         384         CG-67         1075           697-D         341         830D         907         9G1         264         B33         684         CG-76         1075           69D2/A1         338         88-18         88-1         833         684	66a	994	8-H-7		98-4.3		B27	298		
670-D         578         x 27.3         1020         y8-43         607         B2C         872         CD-41         44           670G/C4         905         x/38c         394         y8-6         663         33         31         CD12B4         107           68.1         653         8/64b         395         y89-D         584         B30         678         CD9         146           68.11         654         x23D/C3         339         y94-C4         104         B31         683         CC1-0         1072           684-238         996         83.1         461         9C1.         908         B32         52.3         CC2-5         1073           694/98-D         310         830A         997         9C11         670         B33         32.8         CC5-6         1075           697-D         341         830D         997         9C11         670         B33         32.8         CC5-6         1075           69D/AI         338         838-D         439         905         30         B34         526         CC5-6         1076           6B9         193         847-D         368         365         468		995								
67GCGC4         995         N/3 ke         394         98-6         663         B3         381         CD12B4         107           68.1         653         8/64b         395         98-D         584         B30         678         CD P0         146           68.11         654         82D3/C3         339         9A4C4         104         B31         683         CG-10         1072           684-238         996         83.1         461         VCL         908         B32         522         CG-25         1073           697-D         311         830D         997         9G11         670         B33         684         CG-76         1075           69D2/A1         388         838-D         439         9G5         30         B34         526         CG-9         1076           689         193         847-D         368         9G5A         624         B35         300         CGP 47 439         421           668         255         858-D         583         A32         868         B36         34         CRA-3         98           6C5         206         86         616         A9         744         B48 </td <td></td>										
68.1 653 8/64b 395 899.D 584 B30 678 CD9 146 68.1 68.1 16.54 82D3/C3 339 9.4C4 104 B31 6.83 CG-10 1072 684-238 996 83.1 461 9CL 908 B32 523 CG-25 1073 694/98.D 510 830.A 997 9G11 670 B33 328 CG-4 1074 697-D 341 830D 997 9G12 264 B33 684 CG-76 1075 69D2/Δ1 338 838.D 439 905 30 B34 526 CG-9 1076 69D2/Δ1 338 838.D 439 905 30 B34 526 CG-9 1076 69D 193 847-D 386 9055 A 624 B35 300 CG-97 1076 69D 193 847-D 386 9055 A 624 B35 300 CG-97 1076 69D 193 847-D 386 9055 A 624 B35 300 CG-97 1076 69D 193 847-D 386 9055 A 624 B35 300 CG-97 4139 421 605 605 605 605 605 605 605 605 605 605										
68-11 654 82D3/C3 339 9A4C4 104 831 683 CG-10 1072 684-238 996 83.1 461 9CL 998 B32 523 CG-25 1073 694/98-D 510 830A 997 9C11 670 B33 328 CG-4 1074 697-D 341 830D 907 9C2 264 B33 684 CG-76 1075 697-D 341 830D 907 9C2 264 B33 684 CG-76 1075 69D2/A1 338 838-D 439 9C5 30 B34 526 CG-9 1076 689 193 847-D 368 9C5A 624 B35 300 CGP 47 439 421 689 235 858-D 583 A32 868 B36 3384 CH982 147 6C4/S 342 85G11/D8 741 A47/B1 468 B4 745 CRA-3 998 6C5 206 86 616 A9 A7 A7 B1 848 B4 16 CRA-4 999 6D5 332 858-L 848 B4 84 B4 145 CRA-3 999 6D5 332 858-L 848 B4 B4 848 B4 16 CRA-6 998 6D5 325 858-D 858 S8158/02 699 AC4 977 B6 747 CRA1(ARP 323) 554 6E10 738 88-158/02 699 AC4 977 B6 747 CRA1(ARP 323) 554 6E10 738 88-158/02 700 AD2 126 B8 704 Chessie 8 1069 6C5 203 88-158/02 700 AD2 126 B8 704 Chessie 8 1069 6C5 203 88-158/07 710 AD3 978 B9 299 Chim 1 567 7-1054 739 8B11 174 A103 978 B9 B9 299 Chim 1 567 7-1054 739 8B11 174 A103 979 BAT085 353 D3G5 280 7-16 210 8C10 175 A165 1116 BAT123 438 D485 301 71-31 139 8C6/1 553 A165 1116 BAT123 438 D485 301 71-31 139 8C6/1 553 A165 1116 BAT123 438 D485 301 71-31 139 8C6/1 553 A165 1116 BAT123 438 D485 301 71-31 139 8C6/1 553 A165 1116 BAT123 438 D485 301 71-31 139 8C6/1 553 A165 1116 BAT123 438 D485 301 71-31 139 8C6/1 553 A165 1116 BAT123 438 D485 301 71-31 139 8C6/1 553 A165 1116 BAT123 438 D485 301 71-31 139 8C6/1 553 A165 1116 BAT123 438 D485 301 71-31 139 8C6/1 553 A165 1112 BAT267 748 D5K111 281 729-D 906 8F5 222 A61121 1023 BAT509 750 D6A11 281 729-D 906 8F5 222 A61121 1023 BAT509 750 D6A11 281 729-D 906 8F5 202 A61121 1023 BAT509 750 D6A11 281 729-D 906 8F5 202 A61121 1023 BAT509 750 D6A11 281 729-D 906 8F5 202 A61121 1023 BAT509 750 D6A11 281 752 750-D 576 8C4 207 A15 A16 207 A16 A16 207 A16										
684-238         996         8.1.         461         OCL         908         B.32         523         CG-25         1073           694/98-D         510         830A         997         9G11         670         B.33         328         CG-4         1074           697-D         341         830D         907         9G2         264         B.33         684         CG-76         1075           69D2/AI         338         838-D         439         905         30         B.34         526         CG-9         1076           689         193         847-D         368         905A         624         B.35         300         CGF 47 439         421           689         235         88-B.D         583         A32         868         B.36         384         CH9B2         147           6C4/S         342         85G11/D8         741         A47/B1         468         B4         745         CRA-3         998           6C5         206         86         616         A9         744         B478         16         CRA-4         999           6D8         309         88-158/022         700         AC2         143										
694Ps-D 510 830A 997 9G11 670 B33 328 CG-4 1074 697-D 341 830D 907 9G2 26 B33 684 CG-76 1075 697-D 341 830D 907 9G2 26 B33 684 CG-76 1075 689 193 847-D 368 9G5A 624 B33 684 CG-76 1075 689 193 847-D 368 9G5A 624 B35 300 CGP 47 439 421 644 845 845 845 845 845 845 845 845 845 8										
697-D         341         830D         907         9G2         264         B33         684         CG-76         1075           68D         193         847-D         368         9G5A         30         B34         526         CG-9         1076           68D         193         847-D         368         9G5A         624         B35         300         CGP 47 439         421           68D         235         858-D         583         A32         868         B36         384         CH9B2         147           6C4/S         342         856 II/D8         741         A47/B1         468         B4         745         CRA-3         998           6C5         206         86         616         A9         744         B4f8         16         CRA-3         998           6DS         327         87E4/A8         742         AC2         143         B5         746         CRA-6         984           6DS         327         87E4/A8         742         AC2         143         B5         746         CRA-6         984           6DS         327         88B1         742         AC2         88         167         <										
69D2/A1         338         838 - D         439         9G5         30         B34         526         CG-9         1076           6B9         193         847-D         368         9G5A         624         B35         300         CGP 47 439         421           6B9         235         858-D         583         A32         868         B36         384         CH9B2         147           6C4/8         342         85G11/D8         741         A47/B1         468         B4         745         CRA-3         998           6C5         206         86         616         A9         744         B488         16         CRA-4         999           6D5         327         87E4/A8         742         AC2         143         B5         746         CRA-6         984           6D8         309         88-158/022         700         AD2         126         B8         704         CRA-6         984           6G5         203         88-158/029         701         AD3         978         B9         299         Chim 1         567           7-1654         739         8B11         174         AD3         99         B47 </td <td></td>										
6B9         193         847-D         368         9G5A         624         B35         300         CGP 47 439         421           6B9         235         858-D         583         A32         868         B36         384         CH9B2         147           6C4/S         342         85G11/D8         741         A47/B1         468         B4         745         CRA-3         998           6C5         206         86         616         A9         744         B4f8         16         CRA-4         999           6D5         327         8764/A8         742         AC2         143         B5         746         CRA-6         984           6D8         309         88-158/022         700         AD2         126         B8         704         Chessic 8         1069           6G5         203         88-158/022         700         AD2         126         B8         704         Chessic 8         1069           6G5         203         88-158/022         700         AD2         126         B8         704         Chessic 8         1069           6G5         203         88-158/029         701         AD3         979										
6B9         235         858-D         583         A32         868         B36         384         CH9B2         147           6C5         206         86         616         A9         744         8468         B4         745         CRA-3         998           6C5         206         86         616         A9         744         B4R8         16         CRA-4         999           6D5         327         87E4/A8         742         AC2         143         B5         746         CRA-6         984           6D8         309         38-158/022         700         AD2         126         B8         744         CRA1(ARP 323)         554           6E10         738         88-158/072         701         AD3         978         B9         299         Chim 1         Chessie 8         1069           6G5         203         88-158/079         701         AD3         978         B9         299         Chim 1         567           7-1054         739         8811         174         AD3         979         BAT085         353         D/365         280           7-14         133         8610         157         AE										
6C4/S         342         85G1I/D8         741         A47/B1         468         B4         745         CRA-3         998           6C5         206         86         616         A9         744         B4R8         16         CRA-4         999           6D5         327         87E4/A8         742         AC2         143         B5         746         CRA-6         984           6D8         309         88-158/022         609         AC4         977         B6         747         CRA1(ARP 323)         554           6E10         738         88-158/022         700         AD2         126         B8         704         Chessie 8         1069           6G5         203         88-158/079         701         AD3         979         BAT085         353         D/3G5         280           7-1054         739         8B11         174         AD3         979         BAT085         353         D/3G5         280           7-16         139         8C6/1         153         AE6         1116         BAT123         438         D/4B5         301           71-31         139         8C6/1         163         AE6         1123<										
6C5         206         86         616         A9         744         B4f8         16         CRA-4         999           6D5         327         87E4/A8         742         AC2         143         B5         746         CRA-6         984           6D8         309         88-158/022         699         AC4         977         B6         747         CRA1(ARP 323)         554           6E10         738         88-158/022         700         AD2         126         B8         704         Chessie 8         1069           6G5         203         88-158/022         700         AD3         978         BB         299         Chim 1         567           7-1054         739         8B1         174         AD3         979         BAT085         353         D/3G5         280           7-166         210         8C10         175         AE6         1116         BAT123         438         D/4B5         301           71-31         139         8C6/1         563         AE6         1112         BAT267         748         D/5A11         141         141         141         141         142         142         143         144										
6D5         327         87E4/A8         742         AC2         143         B5         746         CRA-6         984           6D8         309         88-158/02         699         AC4         977         B6         747         CRA1(ARP 323)         554           6E10         738         88-158/022         700         AD2         126         B8         704         Chessis 8         1069           6G5         203         88-158/079         701         AD3         978         B9         299         Chim 1         567           7-1054         739         8B11         174         AD3         979         BAT085         353         D/3G5         280           7-106         210         8C10         175         AE6         1116         BAT123         438         D/5A11         302           71-31         139         8C6/1         563         AE6         11123         BAT267         748         D/5A11         302           71401         53         8E11/A8         1021         AG11         1117         BAT401         749         D/5E12         222         AG1121         1023         BAT509         750         D/6A11         24 <td></td> <td></td> <td></td> <td></td> <td></td> <td>744</td> <td></td> <td>16</td> <td></td> <td></td>						744		16		
6D8         309         88-158/02         699         AC4         977         B6         747         CRA1(ARP 323)         554           6E10         738         88-158/022         700         AD2         126         B8         704         Chessie 8         1069           6G5         203         88-158/079         701         AD3         978         B9         299         Chim 1         567           7-1054         739         8B11         174         AD3         979         BAT085         353         D/3G5         280           7-16         210         8C10         175         AE6         1116         BAT123         438         D/4B5         301           71-31         139         8C6/1         563         AE6         1123         BAT267         748         D/5A11         302           714/01         53         8E11/A8         1021         AG11         1117         BAT401         749         D/5E12         282           722-D         580         8E7         263         AM5C6         1087         BC1071         144         D/6B2         303           729-D         906         8E7         263         AM5C6										
6E10         738         88-158/022         700         AD2         126         B8         704         Chessie 8         1069           6G5         203         88-158/079         701         AD3         978         B9         299         Chim 1         567           7-1054         739         8B11         174         AD3         979         BAT085         353         D/3G5         280           7-16         210         8C10         175         AE6         1116         BAT123         438         D/4B5         301           71-31         139         8C6/1         563         AE6         1123         BAT267         748         D/5A11         302           71-4/01         53         8E11/A8         1021         AG11         1117         BAT401         749         D/5E12         222         222         AG1121         1023         BAT509         750         D/6A11         281         722-D         580         8E5         222         AG1121         1023         BAT509         750         D/6A11         281         722-D         750         D/6A11         281         722-D         750         D/6A11         281         722         722-D <td< td=""><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></td<>										
6G5         203         88-158/079         701         AD3         978         B9         299         Chim 1         567           7-1054         739         8B11         174         AD3         979         BAT085         353         D/3G5         280           7-16         210         8C10         175         AE6         1116         BAT123         438         D/4B5         301           71-31         139         8C6/1         563         AE6         1123         BAT267         748         D/5A11         302           714/01         53         8E11/A8         1021         AG11         1117         BAT401         749         D/5E12         282           722-D         580         8E5         222         AG1121         1023         BAT509         750         D/6A11         281           729-D         906         8E7         263         AM5C6         1087         BC1071         144         D/6B2         303           74         355         8F102         1071         Ab2         260         BE3         108         D1         752           750-D         576         8G4         207         Ab3         269										
$ \begin{array}{cccccccccccccccccccccccccccccccccccc$								299		
$ \begin{array}{cccccccccccccccccccccccccccccccccccc$						979				
$\begin{array}{cccccccccccccccccccccccccccccccccccc$	7-16	210	8C10	175		1116		438		
$\begin{array}{cccccccccccccccccccccccccccccccccccc$						1123		748		
$\begin{array}{cccccccccccccccccccccccccccccccccccc$										
729-D         906         8E7         263         AM5C6         1087         BC1071         144         D/6B2         303           74         355         8F101         1070         AM5C6         1088         BE10         145         D/6D1         518           75         655         8F102         1071         Ab2         260         BE3         108         D1         752           750-D         576         8G4         207         Ab3         269         BM12         909         D12         753           782-D         441         8G5         176         Ab4         265         Bw         429         D16         754           7B2         740         8H10         14         Aw         428         Cβ1, 0.5β         498         D20         910           7B6         204         9-11         606         B10         290         C108G         343         D21         911           7C10         324         902         509         B12         373         C11         869         D24         912           7C3         220         907         413         B13         374         C12         51	722-D	580	8E5	222	AG1121	1023	BAT509	750	D/6A11	
$74$ $355$ $8F101$ $1070$ $AM5C6$ $1088$ $BE10$ $145$ $D/6D1$ $518$ $75$ $655$ $8F102$ $1071$ $Ab2$ $260$ $BE3$ $108$ $D1$ $752$ $750$ -D $576$ $8G4$ $207$ $Ab3$ $269$ $BM12$ $909$ $D12$ $753$ $782$ -D $441$ $8G5$ $176$ $Ab4$ $265$ $Bw$ $429$ $D16$ $754$ $782$ -D $740$ $8H10$ $14$ $Aw$ $428$ $C\beta1, 0.5\beta$ $498$ $D20$ $916$ $786$ $204$ $9-11$ $606$ $B10$ $290$ $C108G$ $343$ $D21$ $910$ $760$ $324$ $902$ $509$ $B12$ $373$ $C11$ $869$ $D24$ $912$ $7C3$ $220$ $907$ $413$ $B13$ $374$ $C12$ $521$ $D25$ $913$ $7C4$ $196$ $908$ -D $442$ $B15$ $525$ $C13$ $375$	729-D	906	8E7		AM5C6	1087		144	D/6B2	
756558F1021071Ab2260BE3108D1752750-D5768G4207Ab3269BM12909D12753782-D4418G5176Ab4265Bw429D167547B27408H1014Aw428 $Cβ1, 0.5β$ 498D209107B62049-11606B10290C108G343D219117C10324902509B12373C11869D249127C3220907413B13374C12521D259137C4196908-D442B15525C13375D2710437C623691-548B18304C2003192D289147C620591-6140B2291C31751D339667E2/42729201556B20305C311E412D359157F112219205514B21377C4325D399167F11527924414B221562C5122103D47558-222179284400B23378C512367D429178-62149301561B24379C512626D43756										
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7B6         204         9-11         606         B10         290         C108G         343         D21         911           7C10         324         902         509         B12         373         C11         869         D24         912           7C3         220         907         413         B13         374         C12         521         D25         913           7C4         196         908-D         442         B15         525         C13         375         D27         1043           7C4         236         91-5         48         B18         304         C2003         192         D28         914           7C6         205         91-6         140         B2         291         C31         751         D33         966           7E2/4         272         9201         556         B20         305         C311E         412         D35         915           7F11         221         9205         514         B21         377         C4         325         D39         916           7F11         527         924         414         B221         562         C5122         103         D4 </td <td></td> <td>441</td> <td></td> <td></td> <td></td> <td></td> <td></td> <td>429</td> <td></td> <td></td>		441						429		
7B6         204         9-11         606         B10         290         C108G         343         D21         911           7C10         324         902         509         B12         373         C11         869         D24         912           7C3         220         907         413         B13         374         C12         521         D25         913           7C4         196         908-D         442         B15         525         C13         375         D27         1043           7C4         236         91-5         48         B18         304         C2003         192         D28         914           7C6         205         91-6         140         B2         291         C31         751         D33         966           7E2/4         272         9201         556         B20         305         C311E         412         D35         915           7F11         221         9205         514         B21         377         C4         325         D39         916           7F11         527         924         414         B221         562         C5122         103         D4 </td <td>7B2</td> <td>740</td> <td>8H10</td> <td>14</td> <td>Aw</td> <td>428</td> <td><math>C\beta 1, 0.5\beta</math></td> <td>498</td> <td>D20</td> <td>910</td>	7B2	740	8H10	14	Aw	428	$C\beta 1, 0.5\beta$	498	D20	910
7C10         324         902         509         B12         373         C11         869         D24         912           7C3         220         907         413         B13         374         C12         521         D25         913           7C4         196         908-D         442         B15         525         C13         375         D27         1043           7C4         236         91-5         48         B18         304         C2003         192         D28         914           7C6         205         91-6         140         B2         291         C31         751         D33         966           7E2/4         272         9201         556         B20         305         C311E         412         D35         915           7F11         221         9205         514         B21         377         C4         325         D39         916           7F21         527         924         414         B221         562         C5122         103         D4         755           8-22         217         9284         400         B23         378         C5123         67         D42 </td <td>7B6</td> <td>204</td> <td>9-11</td> <td>606</td> <td>B10</td> <td>290</td> <td></td> <td>343</td> <td>D21</td> <td></td>	7B6	204	9-11	606	B10	290		343	D21	
7C4         196         908-D         442         B15         525         C13         375         D27         1043           7C4         236         91-5         48         B18         304         C2003         192         D28         914           7C6         205         91-6         140         B2         291         C31         751         D33         966           7E2/4         272         9201         556         B20         305         C311E         412         D35         915           7F11         221         9205         514         B21         377         C4         325         D39         916           7F11         527         924         414         B221         562         C5122         103         D4         755           8-22         217         9284         400         B23         378         C5123         67         D42         917           8-6         214         9301         561         B24         379         C5126         26         D43         756	7C10	324	902	509	B12	373		869	D24	
7C4       236       91-5       48       B18       304       C2003       192       D28       914         7C6       205       91-6       140       B2       291       C31       751       D33       966         7E2/4       272       9201       556       B20       305       C311E       412       D35       915         7F11       221       9205       514       B21       377       C4       325       D39       916         7F11       527       924       414       B221       562       C5122       103       D4       755         8-22       217       9284       400       B23       378       C5123       67       D42       917         8-6       214       9301       561       B24       379       C5126       26       D43       756	7C3	220	907	413	B13	374	C12	521	D25	913
7C4       236       91-5       48       B18       304       C2003       192       D28       914         7C6       205       91-6       140       B2       291       C31       751       D33       966         7E2/4       272       9201       556       B20       305       C311E       412       D35       915         7F11       221       9205       514       B21       377       C4       325       D39       916         7F11       527       924       414       B221       562       C5122       103       D4       755         8-22       217       9284       400       B23       378       C5123       67       D42       917         8-6       214       9301       561       B24       379       C5126       26       D43       756	7C4	196	908-D	442	B15	525	C13	375	D27	1043
7E2/4         272         9201         556         B20         305         C311E         412         D35         915           7F11         221         9205         514         B21         377         C4         325         D39         916           7F11         527         924         414         B221         562         C5122         103         D4         755           8-22         217         9284         400         B23         378         C5123         67         D42         917           8-6         214         9301         561         B24         379         C5126         26         D43         756	7C4	236	91-5	48	B18	304	C2003	192	D28	914
7F11     221     9205     514     B21     377     C4     325     D39     916       7F11     527     924     414     B221     562     C5122     103     D4     755       8-22     217     9284     400     B23     378     C5123     67     D42     917       8-6     214     9301     561     B24     379     C5126     26     D43     756			91-6							
7F11     527     924     414     B221     562     C5122     103     D4     755       8-22     217     9284     400     B23     378     C5123     67     D42     917       8-6     214     9301     561     B24     379     C5126     26     D43     756	7E2/4	272	9201	556	B20	305	C311E	412	D35	915
8-22 217 9284 400 B23 378 C5123 67 D42 917 8-6 214 9301 561 B24 379 C5126 26 D43 756	7F11	221	9205	514	B21	377	C4	325	D39	916
8-6 214 9301 561 B24 379 C5126 26 D43 756	7F11	527	924	414	B221	562	C5122	103	D4	755
8-6 214 9301 561 B24 379 C5126 26 D43 756	8-22									
	8-6	214	9301			379		26	D43	
		64								

D49	629	F91	924	G3-523	454	IIIB-13 V3	466	M-11	635
D50	660	FC12	130	G3-536	538	IIIB-34 V3	467	M-13	636
D52	918	FF1	73	G3-537	530	IIIB-V3-01	517	M-2	637
D53	919	FH2	114	G44/H7	470	IIIB-V3-21	388	M-22	638
D56	1044	Fab A1	610	G45-60	542	IIIB-V3-26	387	M-24	639
D59/A2	469	Fab A12	760	GE4	131	IVI-4G6	769	M-25	640
D60	920	Fab A2	761	GP13	925	IgG1b12	934	M-28	641
D61	630	Fab A4	611	GP44	926	IgGCD4	935	M-29	642
D7324	876	Fab A9	1063	GP68	927	J1	365	M-36	643
DA48	921	Fab D11	1050	GV1A8	320	J3	366	M-4	644
DF3	128	Fab D5	1051	GV1G2	575	J4	247	M-6	645
DG8	123	Fab G1	1052	GV4D3	297	JB7	132	M096/V3	471
DO142-10	430	Fab G15	1064	GV4H3	364	JF11	133	M12	122
DO8i	922	Fab G5	1065	Gv	433	K14	770	M12	942
DZ	707	Fab L1	1066	H11	564	K24	1027	M13	943
Dv	431	Fab L11	1067	H2	765	L-anti-Tat	257	M25	771
E7	1115	Fab L2	1068	Н8	766	L100	866	M38	566
E9	1107	Fab L9	762	HBW4	767	L14	109	M6	944
EB1A9	81	Fab M10	1053	HF1.7	928	L14.17	1	M77	447
EB5	124	Fab M12	1054	HH3	125	L15	985	M85	271
EC3	129	Fab M12B	612	HIVIG	768	L17	1000	M86	275
EC6	121	Fab M15	1055	HT5	929	L19	858	M89	376
ED6	696	Fab M26B	613	HT6	930	L25	1002	M90	859
ED8	148	Fab M8B	614	HT7	931	L28	936	M91	555
EF7	84	Fab S10	1056	Hv	434	L33	937	M92	274
EH1	1118	Fab S6	1057	HyHIV-1	5	L39	1003	M96	310
EH12E1	149	Fab S8	1058	HyHIV-15	34	L40	1004	MAG 104	860
F1	1105	Fab S9	1059	HyHIV-19	152	L41	938	MAG 109	405
F105	923	Fab T2	615	HyHIV-2	6	L42	939	MAG 116	945
F11.2.32	172	Fab T3	1060	HyHIV-21	15	L5.1	283	MAG 12B	946
F14.11	1100	Fv	432	HyHIV-22	17	L52	940	MAG 29B	947
F172-D8	659	G11G1	150	HyHIV-3	7	L72	941	MAG 3B	948
F19.26-4	444	G11H3	151	HyHIV-4	8	L78	1005	MAG 45	861
F19.48-3	445	G12	763	HyHIV-5	9	L81	870	MAG 49	406
F19.57-11	446	G2	764	HyHIV-6	10	LA9 (121-134)	697	MAG 53	407
F223	757	G3-136	351	ICR 39.13g	932	LH-104-A	88	MAG 55	949
F240	628	G3-1472	1026	ICR 39.3b	933	LH-104-B	117	MAG 56	408
F285	758	G3-211	529	ICR38.1a	533	LH-104-C	101	MAG 6B	772
F5-2	40	G3-299	534	ICR38.8f	539	LH-104-E	85	MAG 72	950
F5-4	96	G3-4	352	ID6	980	LH-104-G	119	MAG 86	951
F5.5	1025	G3-42	535	ID6	981	LH-104-I	118	MAG 95	862
F58/D1	463	G3-508	536	ID8F6	39	LH-104-K	87	MAG 96	952
F7	759	G3-519	537	IE8G2	153	M-1	634	MAG 97	863

MAb 35	223	P5-3	779	V7-8	154	polyclonal	167	polyclonal	592
MF119.1	311	PC5009	590	W1	318	polyclonal	168	polyclonal	601
MF169.1	369	RC25	489	W2	565	polyclonal	185	polyclonal	602
MF170.1	370	RL4.72.1	77	X5	973	polyclonal	191	polyclonal	603
MF39.1	306	RSD-33	347	Z13	677	polyclonal	241	polyclonal	617
MF4.1	312	RT-4	237	anti-CD4BS summary	959	polyclonal	242	polyclonal	619
MF46.1	326	RT6H	189	anti-HIV-1 RT	240	polyclonal	243	polyclonal	620
MF49.1	293	RT7O	238	anti-HIV-2 polyclonal	516	polyclonal	248	polyclonal	621
MF53.1	313	RT7U	239	anti-K159	212	polyclonal	276	polyclonal	626
MF58.1	314	RTMAb8	187	anti-gp120/V3	1029	polyclonal	329	polyclonal	648
MF77.1	315	RV110026	573	anti-p24	155	polyclonal	358	polyclonal	656
MF87.1	371	S1-1	954	b11	960	polyclonal	389	polyclonal	668
MN215	455	SC258	1001	b13	961	polyclonal	390	polyclonal	672
MO101/V3,C4	511	SP.BAL114	448	b14	962	polyclonal	392	polyclonal	673
MO101/V3,C4	512	SP.SF2:104	449	b3	963	polyclonal	396	polyclonal	674
MO101/V3,C4	513	T1.1	294	b6	964	polyclonal	397	polyclonal	675
MO28	773	T11	319	clone 3	649	polyclonal	398	polyclonal	679
MO30	774	T13	955	human sera	156	polyclonal	399	polyclonal	702
MO43	775	T15G1	780	i5B11	120	polyclonal	401	polyclonal	703
MO86/C3	540	T2.1	316	loop 2	473	polyclonal	402	polyclonal	706
MO9.42.2	97	T20	781	multiple Fabs	786	polyclonal	403	polyclonal	790
MO9.50.2	98	T22	974	multiple MAbs	787	polyclonal	404	polyclonal	791
MO97/V3	391	T27	782	multiple MAbs	788	polyclonal	410	polyclonal	792
MO99/V3	411	T3	783	multiple MAbs	789	polyclonal	415	polyclonal	793
MTW61D	953	T30	784	p7	865	polyclonal	416	polyclonal	794
Md-1	1061	T32	631	polyclonal	2	polyclonal	420	polyclonal	795
N11-20	506	T34	632	polyclonal	23	polyclonal	422	polyclonal	796
N2-4	776	T4	785	polyclonal	42	polyclonal	435	polyclonal	797
N70-1.9b	508	T49	956	polyclonal	47	polyclonal	437	polyclonal	798
N70-2.3a	777	T52	986	polyclonal	54	polyclonal	450	polyclonal	799
NC-1	1082	T54	987	polyclonal	79	polyclonal	486	polyclonal	800
ND-15G1	665	T56	957	polyclonal	82	polyclonal	492	polyclonal	801
NF1A1	1113	T7.1	295	polyclonal	95	polyclonal	496	polyclonal	802
NF2B2	1120	T9	296	polyclonal	157	polyclonal	503	polyclonal	803
NF3A3	1121	T9	864	polyclonal	158	polyclonal	505	polyclonal	804
NF8B4	1122	TG001	246	polyclonal	159	polyclonal	524	polyclonal	805
NM-01	499	TG002	245	polyclonal	160	polyclonal	531	polyclonal	806
NT2/4D5.24	256	TH-Ab1	671	polyclonal	161	polyclonal	543	polyclonal	807
NT3/2D1.1	249	TH1	1028	polyclonal	162	polyclonal	552	polyclonal	808
Nea 9301	456	TH9	958	polyclonal	163	polyclonal	553	polyclonal	809
P1/D12	464	V10	99	polyclonal	164	polyclonal	568	polyclonal	810
P4/D10	465	V10-9	618	polyclonal	165	polyclonal	579	polyclonal	811
P43110	778	V107	100	polyclonal	166	polyclonal	581	polyclonal	812

polyclonal	813	polyclonal	988
polyclonal	814	polyclonal	1030
polyclonal	815	polyclonal	1031
polyclonal	816	polyclonal	1032
polyclonal	817	polyclonal	1033
polyclonal	818	polyclonal	1034
polyclonal	819	polyclonal	1035
polyclonal	820	polyclonal	1036
polyclonal	821	polyclonal	1041
polyclonal	822	polyclonal	1042
polyclonal	823	polyclonal	1084
polyclonal	824	polyclonal	1093
polyclonal	825	polyclonal	1094
polyclonal	826	polyclonal	1099
polyclonal	827	polyclonal	1102
polyclonal	828	polyclonal	1103
polyclonal	829	polyclonal	1104
polyclonal	830	polyclonal	1114
polyclonal	831	polyclonal	1124
polyclonal	832	polyclonal	1125
polyclonal	833	polyclonal	1126
polyclonal	834	polyclonal	1127
polyclonal	835	polyclonal	1128
polyclonal	836	polyclonal	1129
polyclonal	837	polyclonal	1130
polyclonal	838	polyclonal	1131
polyclonal	839	polyclonal α577-596	591
polyclonal	840	polyclonal α598-609	646
polyclonal	841	polyclonal HIVIG	169
polyclonal	842	sc-FV p17	33
polyclonal	843		
polyclonal	844		
polyclonal	845		
polyclonal	846		
polyclonal	847		
polyclonal	848		
polyclonal	849		
polyclonal	850		
polyclonal	851		
polyclonal	852		
polyclonal	873		
polyclonal	965		
polyclonal	975		

IV-B-3 MAbs by order of appearance in tables

No.	MAb ID	39	ID8F6	80	38:9.6K	<b>p2p7</b>	p1p6	159	polyclonal
p17		40	F5-2	81	EB1A9	120	i5B11	160	polyclonal
1	L14.17	41	CB-13/5	82	polyclonal	121	EC6	161	polyclonal
2	polyclonal	42	polyclonal	83	30:3E5	122	M12	162	polyclonal
3	32/5.8.42	43	3D3	84	EF7	123	DG8	163	polyclonal
4	32/5.8.42	44	CD-4/1	85	LH-104-E	124	EB5	164	polyclonal
5	HyHIV-1	45	15F8C7	86	1B2C12	125	HH3	165	polyclonal
6	HyHIV-2	46	111/052	87	LH-104-K	126	AD2	166	polyclonal
7	HyHIV-3	47	polyclonal	88	LH-104-A	127	CA5	167	polyclonal
8	HyHIV-4	48	91-5	89	1.17.3	128	DF3	168	polyclonal
9	HyHIV-5	49	1109/01	90	1A7	129	EC3	169	polyclonal HIVIG
10	HyHIV-6	50	14D4E11	91	1F6	130	FC12	Prote	ease
11	32/1.24.89	51	1G5C8	92	23A5G4	131	GE4	170	1696
12	3B10	52	47-2	93	23A5G5	132	JB7	171	10E7
13	3E11	53	714/01	94	3D10G6	133	JF11	172	F11.2.32
14	8H10	54	polyclonal	95	polyclonal	Gag		173	13E1
15	HyHIV-21	55	111/073	96	F5-4	134	16/4/2	174	8B11
16	B4f8	56	113/038	97	MO9.42.2	135	183-H12-5C	175	8C10
17	HyHIV-22	57	1-E-4	98	MO9.50.2	136	241-D	176	8G5
18	12H-D3b3	58	1-E-9	99	V10	137	2A6	RT	
19	12G-A8g2	59	10-E-7	100	V107	138	5E2.A3k	177	1E8
20	12G-D7h11	60	10-G-9	101	LH-104-C	139	71-31	178	1.152 B3
21	12G-H1c7	61	11-C-5	102	12-B-4	140	91-6	179	1.158 E2
22	12I-D12g2	62	2-E-4	103	C5122	141	98-4.3	180	31D6
23	polyclonal	63	2-H-4	104	9A4C4	142	98-4.9	181	31G8
24	11H9	64	8-D-2	105	11C10B10	143	AC2	182	32E7
25	3-H-7	65	8-G-9	106	11D11F2	144	BC1071	183	33D5
26	C5126	66	8-H-7	107	CD12B4	145	BE10	184	5B2
27	1D9	67	C5123	108	BE3	146	CD9	185	polyclonal
28	4C9	68	1-B-7	109	L14	147	CH9B2	186	1.153 G10
29	4H2B1	69	3-B-7	110	108/03	148	ED8	187	RTMAb8
30	9G5	70	6-D-12	111	110/015	149	EH12E1	188	1D4A3
31	15-21	71	6-E-7	112	32:32K	150	G11G1	189	RT6H
32	31-11	72	8-D-5	113	C5200	151	G11H3	190	1.160 B3
33	sc-FV p17	73	FF1	114	FH2	152	HyHIV-19	191	polyclonal
34	HyHIV-15	74	113/072	115	13B5	153	IE8G2	192	C2003
p24		75	25.3	116	106/01	154	V7-8	193	6B9
35	3A6	76	13-102-100	117	LH-104-B	155	anti-p24	194	5F
36	111/182	77	RL4.72.1	118	LH-104-I	156	human sera	195	5G
37	112/021	78	406/01	ր24-լ	p2p7p1p6	157	polyclonal	196	7C4
38	112/047	79	polyclonal	119	LH-104-G	158	polyclonal	Integ	rase

197	1C4	239	RT7U	278	133/290	321	11	364	GV4H3
198	2C11	240	anti-HIV-1 RT	279	133/11	322	12G10	365	J1
199	2E3	241	polyclonal	280	D/3G5	323	135/9	366	J3
200	3E11	242	polyclonal	281	D/6A11	324	7C10	367	1006-30-D
201	3F9	243	polyclonal	282	D/5E12	325	C4	368	847-D
202	5F8	244	33	283	L5.1	326	MF46.1	369	MF169.1
203	6G5	Vif		284	4A7C6	327	6D5	370	MF170.1
204	7B6	245	TG002	285	1D10	328	B33	371	MF87.1
205	7C6	246	TG001	286	B242	329	polyclonal	372	213.1
206	6C5	247	J4	287	133/192	330	35D10/D2	373	B12
207	8G4	248	polyclonal	288	489.1(961)	331	40H2/C7	374	B13
208	17	Tat		289	5B3	332	43A3/E4	375	C13
209	4D6	249	NT3/2D1.1	290	B10	333	43C7/B9	376	M89
210	7-16	250	1.2	291	B2	334	45D1/B7	377	B21
211	4F6	251	1D9D5	292	C6	335	46E3/E6	378	B23
212	anti-K159	252	1D2F11	293	MF49.1	336	58E1/B3	379	B24
213	5D9	253	2D9E7	294	T1.1	337	64B9/A6	380	B25
214	8-6	254	4B4C4	295	T7.1	338	69D2/A1	381	B3
215	19	255	5G7D8	296	T9	339	82D3/C3	382	B26
216	2-19	256	NT2/4D5.24	297	GV4D3	340	2H1B	383	B29
217	8-22	257	L-anti-Tat	298	B27	341	697-D	384	B36
218	4-20	258	2D9D5	299	B9	342	6C4/S	385	110.E
219	6-19	Rev		300	B35	343	C108G	386	110.C
220	7C3	259	4G9	301	D/4B5	344	10/76b	387	IIIB-V3-26
221	7F11	260	Ab2	302	D/5A11	345	11/41e	388	IIIB-V3-21
222	8E5	261	10.1	303	D/6B2	346	11/4b	389	polyclonal
223	MAb 35	262	3H6	304	B18	347	RSD-33	390	polyclonal
Pol		263	8E7	305	B20	348	11/4c	391	MO97/V3
224	12	264	9G2	306	MF39.1	349	8.22.2	392	polyclonal
225	13	265	Ab4	307	187.2.1	350	12b	393	55/11
226	14	266	3G4	308	37.1.1(ARP 327)	351	G3-136	394	8/38c
227	16	267	1G10	309	6D8	352	G3-4	395	8/64b
228	1C12B1	268	1G7	310	M96	353	BAT085	396	polyclonal
229	21	269	Ab3	311	MF119.1	354	60b	397	polyclonal
230	32	270	2G2	312	MF4.1	355	74	398	polyclonal
231	35	gp16		313	MF53.1	356	38/12b	399	polyclonal
232	3D12	271	M85	314	MF58.1	357	38/60b	400	9284
233	3F10	272	7E2/4	315	MF77.1	358	polyclonal	401	polyclonal
234	4	273	4D4#85	316	T2.1	359	322-151	402	polyclonal
235	6B9	274	M92	317	11/65	360	3D3.B8	403	polyclonal
236	7C4	275	M86	318	W1	361	4C11.D8	404	polyclonal
237	RT-4	276	polyclonal	319	T11	362	493-156	405	MAG 109
238	RT7O	277	133/237	320	GV1A8	363	110.1	406	MAG 49

407	MAG 53	450	polyclonal	493	10/36e	536	G3-508	579	polyclonal
408	MAG 56	451	19b	494	10/54	537	G3-519	580	722-D
409	1324-E	452	4G10	495	11/85b	538	G3-536	581	polyclonal
410	polyclonal	453	5F7	496	polyclonal	539	ICR38.8f	582	1131-A
411	MO99/V3	454	G3-523	497	$0.5\beta$	540	MO86/C3	583	858-D
412	C311E	455	MN215	498	$C\beta 1, 0.5\beta$	541	13H8	584	989-D
413	907	456	Nea 9301	499	NM-01	542	G45-60	585	1A1
414	924	457	4117C	500	1026	543	polyclonal	586	24G3
415	polyclonal	458	419-D	501	1034	544	1662	587	25C2
416	polyclonal	459	453-D	502	59.1	545	1663	588	5F3
417	10F10	460	504-D	503	polyclonal	546	1664	589	$\alpha(566-586)$
418	2C4	461	83.1	504	10E3	547	1697	590	PC5009
419	412-D	462	5023B	505	polyclonal	548	1794	591	polyclonal α577-596
420	polyclonal	463	F58/D1	506	N11-20	549	1804	592	polyclonal
421	CGP 47 439	464	P1/D12	507	5025A	550	1807	593	
422	polyclonal	465	P4/D10	508	N70-1.9b	551	1808	594	
423	178.1	466	IIIB-13 V3	509	902	552	polyclonal	595	1F11
424	257-D	467	IIIB-34 V3	510	694/98-D	553	polyclonal	596	1H5
425	311-11-D	468	A47/B1	511	MO101/V3,C4	554	CRA1(ARP 323)	597	3D9
426	41148D	469	D59/A2	512	MO101/V3,C4	555	M91	598	4B3
427	391/95-D	470	G44/H7	513	MO101/V3,C4	556	9201	599	4D4
428	Aw	471	M096/V3	514	9205	557	1C1	600	4G2
429	Bw	472	μ5.5	515	110.I	558	3F5	601	polyclonal
430	DO142-10	473	loop 2	516	anti-HIV-2 polyclonal	559	5F4/1	602	polyclonal
431	Dv	474	268-D	517	IIIB-V3-01	560	660-178	603	polyclonal
432	Fv	475	386-D	518	D/6D1	561	9301	604	2A2/26
433	Gv	476	5042A	519	4D7/4	562	B221	605	50-69
434	Hv	477	5042B	520	36.1(ARP 329)	563	8C6/1	606	9-11
435	polyclonal	478	418-D	521	C12	564	H11	607	98-43
436	50.1	479	5021	522	110.D	565	W2	608	41-1
437	polyclonal	480	5025B	523	B32	566	M38	609	41.4
438	BAT123	481	5042	524	polyclonal	567	Chim 1	610	Fab A1
439	838-D	482	110.3	525	B15	568	polyclonal	611	Fab A4
440	1006-15D	483	110.4	526	B34	569	1331A	612	Fab M12B
441	782-D	484	110.5	527	7F11	570	110.1	613	Fab M26B
442	908-D	485	58.2	528	5C2E5	571	42F	614	Fab M8B
443	1027-15D	486	polyclonal	529	G3-211	572	43F	615	Fab T2
444	F19.26-4	487	537-D	530	G3-537	573	RV110026	616	86
445	F19.48-3	488	5020	531	polyclonal	574	105-306	617	polyclonal
446	F19.57-11	489	RC25	532	1795	575	GV1G2	618	V10-9
447	M77	490	5023A	533	ICR38.1a	576	750-D	619	polyclonal
448	SP.BAL114	491	110.6	534	G3-299	577	450-D	620	polyclonal
449	SP.SF2:104	492	polyclonal	535	G3-42	578	670-D	621	polyclonal
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622	2F11	665	ND-15G1	Env		750	BAT509	793	polyclonal
623	246-D	666	167-D	708		751	C31	794	polyclonal
624	9G5A	667	2F5	709		752	D1	795	polyclonal
625	181-D	668	polyclonal	710		753	D12	796	polyclonal
626	polyclonal	669	5B2	711		754	D16	797	polyclonal
627	240-D	670	9G11	712		755	D4	798	polyclonal
628	F240	671	TH-Ab1	713	102-135	756	D43	799	polyclonal
629	D49	672	polyclonal	714	1025	757	F223	800	polyclonal
630	D61	673	polyclonal	715	105-134	758	F285	801	polyclonal
631	T32	674	polyclonal	716	10E9	759	F7	802	polyclonal
632	T34	675	polyclonal	717	126-50	760	Fab A12	803	polyclonal
633	115.8	676	4E10	718	12H2	761	Fab A2	804	polyclonal
634	M-1	677	Z13	719	13.10	762	Fab L9	805	polyclonal
635	M-11	678	B30	720	1B1	763	G12	806	polyclonal
636	M-13	679	polyclonal	721	1F7	764	G2	807	polyclonal
637	M-2	680	41S-2	722	2.2B	765	H2	808	polyclonal
638	M-22	681	447-52D	723	30D	766	Н8	809	polyclonal
639	M-24	682	C8	724	31710B	767	HBW4	810	polyclonal
640	M-25	683	B31	725	38B5/C9	768	HIVIG	811	polyclonal
641	M-28	684	B33	726	39H10/A11	769	IVI-4G6	812	polyclonal
642	M-29	685	1576	727	3D5	770	K14	813	polyclonal
643	M-36	686	1578	728	3H6	771	M25	814	polyclonal
644	M-4	687	1579	729	40D3/C11	772	MAG 6B	815	polyclonal
645	M-6	688	1583	730	49B11/A1	773	MO28	816	polyclonal
646	polyclonal α598-609	689	1899	731	52G5/B9	774	MO30	817	polyclonal
647	1B8.env	690	1907	732	55E4/H1	775	MO43	818	polyclonal
648	polyclonal	691	1908	733	56C4/C8	776	N2-4	819	polyclonal
649	clone 3	692	1909	734	57B6/F1	777	N70-2.3a	820	polyclonal
650	4	693	41-1	735	57H5/D7	778	P43110	821	polyclonal
651	41-6	694	41-2	736	63G4/E2	779	P5-3	822	polyclonal
652	41-7	695	41-3	737	65B12/C5	780	T15G1	823	polyclonal
653	68.1	696	ED6	738	6E10	781	T20	824	polyclonal
654	68.11	697	LA9 (121-134)	739	7-1054	782	T27	825	polyclonal
655	75	698	1575	740	7B2	783	T3	826	polyclonal
656	polyclonal	699	88-158/02	741	85G11/D8	784	T30	827	polyclonal
657	105-732	700	88-158/022	742	87E4/A8	785	T4	828	polyclonal
658	3D6	701	88-158/079	743	97B1/E8	786	multiple Fabs	829	polyclonal
659	F172-D8	702	polyclonal	744	A9	787	multiple MAbs	830	polyclonal
660	D50	703	polyclonal	745	B4	788	multiple MAbs	831	polyclonal
661	5-21-3	704	B8	746	B5	789	multiple MAbs	832	polyclonal
662	120-16	705	1577	747	B6	790	polyclonal	833	polyclonal
663	98-6	706	polyclonal	748	BAT267	791	polyclonal	834	polyclonal
664	167-7	707	DZ	749	BAT401	792	polyclonal	835	polyclonal
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836	polyclonal	879	1125H	922	DO8i	965	polyclonal	1008	1334-D
837	polyclonal	880	120-1B1	923	F105	966	D33	1009	2182
838	polyclonal	881	1202-D	924	F91	967		1010	2191
839	polyclonal	882	1331E	925	GP13	968	17b	1011	2219
840	polyclonal	883	1570	926	GP44	969	21c	1012	2412
841	polyclonal	884	1595	927	GP68	970	23e	1013	2442
842	polyclonal	885	1599	928	HF1.7	971	48d	1014	2456
843	polyclonal	886	15e	929	HT5	972	49e	1015	39F
844	polyclonal	887	205-43-1	930	HT6	973	X5	1016	55/68b
845	polyclonal	888	205-46-9	931	HT7	974	T22		5G11
846	polyclonal	889	21h	932	ICR 39.13g	975	polyclonal	1018	6.1
847	polyclonal	890	28A11/B1	933	ICR 39.3b	976	2A2	1019	6.7
848	polyclonal	891	2G6	934	IgG1b12	977	AC4	1020	8.27.3
849	polyclonal	892	35F3/E2	935	IgGCD4	978	AD3		8E11/A8
850	polyclonal	893	38G3/A9	936	L28	979	AD3	1022	9305
851	polyclonal	894	428	937	L33	980	ID6	1023	AG1121
852	polyclonal	895	448-D	938	L41	981	ID6	1024	
853	101-342	896	44D2/D5	939	L42	982	11/68b	1025	F5.5
854	101-451	897	48-16	940	L52	983	62c	1026	G3-1472
855	120-1	898	50-61A	941	L72	984	CRA-6	1027	K24
856	212A	899	5145A	942	M12	985	L15	1028	TH1
857	522-149	900	558-D	943	M13	986	T52	1029	anti-gp120/V3
858	L19	901	559/64-D	944	M6	987	T54	1030	polyclonal
859	M90	902	55D5/F9	945	MAG 116	988	polyclonal	1031	
860	MAG 104	903	588-D	946	MAG 12B	989	1088	1032	polyclonal
861	MAG 45	904	654-D	947	MAG 29B	990	110-B	1033	polyclonal
862	MAG 95	905	67G6/C4	948	MAG 3B	991	1357		polyclonal
863	MAG 97	906	729-D	949	MAG 55	992	1361	1035	polyclonal
864	T9	907	830D	950	MAG 72	993	1393A		polyclonal
865	p7	908	9CL	951	MAG 86	994	66a		11/75a/21/41
866	L100	909	BM12	952	MAG 96	995	66c	1038	41.1
867	2/11c	910	D20	953	MTW61D	996	684-238	1039	55/45a/11
868	A32	911	D21	954	S1-1	997	830A	1040	1108
869	C11	912	D24	955	T13	998	CRA-3	1041	polyclonal
870	L81	913	D25	956	T49	999	CRA-4	1042	polyclonal
871	2F19C	914	D28	957	T56	1000	L17	1043	D27
872	B2C	915	D35	958	TH9	1001	SC258	1044	D56
873	polyclonal	916	D39	959	anti-CD4BS summary	1002	L25	1045	2G12
874	1024	917	D42	960	b11	1003	L39	1046	1367
875	23A	918	D52	961	b13	1004	L40	1047	126-6
876	D7324	919	D53	962	b14	1005	L78	1048	1342
877	10/46c	920	D60	963	b3	1006		1049	1379
878	1027-30-D	921	DA48	964	b6	1007	110.J	1050	Fab D11

1051	Fab D5	1093	polyclonal
1052	Fab G1	1094	polyclonal
1053	Fab M10	1095	3G12
1054	Fab M12	1096	13/058
1055	Fab M15	1097	26/028
1056	Fab S10	1098	2E3
1057	Fab S6	1099	polyclonal
1058	Fab S8	1100	F14.11
1059	Fab S9	1101	31/03
1060	Fab T3	1102	polyclonal
1061	Md-1	1103	polyclonal
1062	1281	1104	polyclonal
1063	Fab A9	1105	F1
1064	Fab G15	1106	2F2
1065	Fab G5	1107	E9
1066	Fab L1	1108	3E6
1067	Fab L11	1109	2A3
1068	Fab L2	1110	2E4
1069	Chessie 8	1111	2H12
1070	8F101	1112	3A2
1071	8F102	1113	NF1A1
1072	CG-10	1114	polyclonal
1073	CG-25	1115	E7
1074	CG-4	1116	AE6
1075	CG-76	1117	AG11
1076	CG-9	1118	EH1
1077	105-518	1119	6.1
1078	31A1	1120	NF2B2
1079	39A64	1121	NF3A3
1080	39B86	1122	NF8B4
1081	9303	1123	AE6
1082	NC-1	HIV-	1
Nef		1124	polyclonal
1083	4H4	1125	polyclonal
1084	polyclonal	1126	polyclonal
1085	13/042	1127	polyclonal
1086	13/035	1128	polyclonal
1087	AM5C6	1129	polyclonal
1088	AM5C6	1130	polyclonal
1089	25/03	1131	polyclonal
1090	26/76		
1091	3F2		
1092	3D12		

# **IV-C HIV Antibodies Tables**

All HIV MAbs and polyclonal Abs that bind to linear epitopes 30 amino acids or less in length arranged by protein position. The table entries are sorted in a nested way—first by protein, then by HXB2 start location, then by antibody type and finally by antibody name. Abs that bind to conformational epitopes or with unknown epitopes are listed at the end of each protein section.

### IV-C-1 p17 Antibodies

No.	MAb ID	<b>HXB2</b> Location	<b>Author's Location</b>	Sequence	Neutralizing	Immunogen	Species(Isotype)
1	L14.17	* 1	p17 (11–25 BRU) e: viral lysate <i>Strain:</i> BR 1990, Robert-Hebmann19	GELDRWEKIRLRPGG LU <i>HIV component:</i> virus 92b, Robert-Hebmann1992a	no	Vaccine	murine (IgG)
2	polyclonal	References Truongl  An ELISA assay wa recognized by antibodies raised again	1997 Is used to study a panel of odies elicited by rp24CA – ainst anti-p55 virus-like pa	GELDRWEKIRLRPGG us-like particle Strain: LAI HIV Gag peptides – mature p24 CA epito one p17MA epitope, residues 11-25 urticles, suggesting a differentantigen rotein or the immature assembled for	pes mapped to residue, and one p24CA epitoic properties for p24C.	s 176-192, 201-218, ppe, residues 176-192 A and p17MA antibo	233-253, 285-304, and were 2, were recognized by
3	32/5.8.42	p17 (12–19 + 100–105)  Vaccine Vector/Type References Papside: • 32/5.8.42: Binds to [Papsidero1989]	ro1989	ELDRWEKI+ALDKIE , positions 12-19 and 100-105, peptic	no les ELDRWEKI and A	Vaccine LDKIE – inhibited i	murine (IgG) nfectivity of cell free virus
4	32/5.8.42	References Papside		ELDRWEKI+ALDKIE  onent: virus  us – bound to two peptides, ELDRWI	no EKI and ALDKIE, at p	Vaccine  positions 12-19 + 100	murine (IgG) 0-105 [Papsidero1989]
5	HyHIV-1	<ul><li>References Liu1995</li><li>HyHIV-1: This paper isotope-free BIAcor</li></ul>	er compares the results of a	affinity constant (Ka) measurements of found to be similar for HyHIV-(1-6)			

p17 Antibodies

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizing	Immunogen	Species(Isotype)
6	HyHIV-2	References Liu199			no	Vaccine	murine (IgG1)
		isotope-free BIAco		of affinity constant (Ka) measurements ere found to be similar for HyHIV-(1-6 alization [Ota1998b]			
7	HyHIV-3	p17 (12–29) <b>Vaccine</b> <i>Vector/Typ</i> <b>References</b> Liu199	p17 (12–29 JMH1) e: recombinant protein 5, Ota1998b	ELDKWEKIRLRPGGKTLY  HIV component: p17	no	Vaccine	murine (IgG1)
		isotope-free BIAco		of affinity constant (Ka) measurements ere found to be similar for HyHIV-(1-6 alization [Ota1998b]			
8	HyHIV-4		p17 (12–29 JMH1) e: recombinant protein 5, Ota1998a, Ota1998b	ELDKWEKIRLRPGGKTLY?  HIV component: p17	no	Vaccine	murine (IgG1)
		<ul> <li>HyHIV-4: epitope to indicating the antig</li> <li>HyHIV-4: This pap isotope-free BIAco</li> </ul>	uncertain, based on the b en is exposed at the cell er compares the results of	of affinity constant (Ka) measurements ere found to be similar for HyHIV-(1-6	of anti-p17 MAbs usin	g double Ab metho	ods versus the faster,
9	HyHIV-5	<ul><li>References Liu199</li><li>HyHIV-5: This pap isotope-free BIAco</li></ul>	er compares the results	of affinity constant (Ka) measurements ere found to be similar for HyHIV-(1-6			
10	HyHIV-6	References Liu199 • HyHIV-6: This pap	er compares the results	of affinity constant (Ka) measurements			
			re system, and results we binding and nuclear loc	ere found to be similar for HyHIV-(1-6 alization [Ota1998b]	o) – six MAds all bind to	o the first alpha hei	ix of p17, a functional domain
11	32/1.24.89	p17 (17–22) Vaccine Vector/Typ References Papside  32/1.24.89: Inhibite		EKIRLR virus [Papsidero1989]	L	Vaccine	murine (IgG)
12	3B10	p17 (19–38) <b>Vaccine</b> Vector/Typ	p17 (19–38 SIVmac	) IRLPGGKKKYMLKHVVWAA rain: AGM TYO-7 HIV component:	no virus	Vaccine	murine (IgG1)

No.	MAb ID	<b>HXB2</b> Location	Author's Location	Sequence	Neutralizing	Immunogen	Species(Isotype)
		•	n epitope present on HIV-	2/SIVmac (MAC251/32H), SIVagm, HIVesses at least one conserved immunogenic		•	•
13	3E11	References Otteken • 3E11: There is anotl • 3E11: Recognized a	1992, Nilsen1996 ner MAb with this ID that n epitope present on HIV-2	IRLPGGKKKYMLKHVVWAA  n: AGM TYO-7 HIV component: virus  recognizes integrase [Nilsen1996] 2/SIVmac (MAC251/32H), SIVagm, HIV- esses at least one highly conserved immun		•	murine (IgG1) e matrix protein of all nine
14	8H10	<ul><li>References Ota1999</li><li>8H10: The p17 MAI</li><li>8H10: Inhibits viral</li></ul>	Da, Ota1999b  In also can bind to the V3 lost replication of the HIV-1 in	KLKHIVWASRELERFAVNPGLLE  HIV component: p17 Adjuvant: BSA  coop [Ota1999a]  affected MT-4 cells by decreasing p17 DNA  MT-4 cells was studied [Ota1999b]		Vaccine fected cells, and the e	murine (IgM)  ffect of growing the 8H10
5	HyHIV-21	References Liu1995 • HyHIV-21: epitope	uncertain, based on the bes	KLKHIIWASRELERFAVNPGLLE IIV component: p17 st estimate from JMH1 sequence – Ka is 3 face –inhibited growth of HIV-1 JMH1 in		•	
6	B4f8	References Shang19	991	LETSEGCRQILGQLQ  cain: IIIB HIV component: virus  alls that had been made permeable with according to the component of the co	no etone [Shang199	Vaccine	rat (IgG2a)
17	HyHIV-22	References Liu1995 • HyHIV-22: epitope		st estimate from JMH1 sequence – stains t		Vaccine  ected cells indicating	murine (IgG1) the antigen is exposed at the
18	12H-D3b3	References Shang19	991	GQLQPSLQTGSEELRSL  ain: IIIB HIV component: virus  ally cells that had been made permeable wi	no th acetone [Shan	Vaccine g1991]	rat (IgG2a)
19	12G-A8g2	p17 (86–115)  Vaccine Vector/Type References Shang 19		YCVHQRIEIKDTKEALDKIEEEQNK- SKKKA  ain: IIIB HIV component: virus	- no	Vaccine	rat (IgG2a)

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizing	Immunogen	Species(Isotype)
		• 12G-A8g2: This epi	itope is similar to a fragme	al peptides – did not bind live ent of the human protein CD40 is-epithelium-derived growth f	ligand TNF-related activation	n protein(T-cell ant	
20	12G-D7h11		p17 (86–115)  e: infected-cell lysate Sti 991, Maksiutov2002	YCVHQRIEIKDTKEALDI SKKKA rain: IIIB HIV component: v		Vaccine	rat (IgG2a)
		• 12G-D7h11: This ep	pitope is similar to a fragm	rnal peptides – did not bind liv nent of the human protein CD4 is-epithelium-derived growth f	0 ligand TNF-related activati	on protein (T-cell a	
21	12G-H1c7	p17 (86–115)	p17 (86–115)	YCVHQRIEIKDTKEALDH SKKKA		Vaccine	rat (IgG)
		References Shang 1  12G-H1c7: Bound t  12G-H1c7: This epi	991, Maksiutov2002 to 30-mer, but not to intern tope is similar to a fragme	rain: IIIB HIV component: val peptides – did not bind live ent of the human protein CD40 as-epithelium-derived growth f	infected cells – antigenic dor ligand TNF-related activatio	n protein (T-cell an	
22	12I-D12g2	References Shang1  12I-D12g2: Bound  12I-D12g2: This ep	991, Maksiutov2002 to 30-mer, but not to interritope is similar to a fragmo	YCVHQRIEIKDTKEALDE SKKKA  rain: IIIB HIV component: value peptides – did not bind live ent of the human protein CD40 us-epithelium-derived growth f	irus infected cells – antigenic do ligand TNF-related activatio	on protein (T-cell ar	
23	polyclonal	p17 (86–115)  Vaccine Vector/Type References Bukawa  • Polyclonal secretory	p17 (86–115) e: peptide HIV compone. 11995 v IgA antibody raised by o	YSVHQRIDVKDTKEALER SKKKA  nt: p17 Adjuvant: cholera to ral mucosal immunization is a mponent peptide immunogen	XIEEEQNK – L  xin adjuvant  ble to neutralize IIIB, SF2, ar	Vaccine	murine (IgA)
24	11H9	Donor R. B. Ferns a References Ferns 19 11H9: Reactive aga 11H9: This epitope	and R. S. Tedder 187, Ferns1989, Maksiutov inst p18 and p55 [Ferns19	87] Lens-epithelium-derived grov		Vaccine  GQ [Maksiutov200	murine (IgG1)
25	3-H-7 (3H7)	p17 (113–122) Vaccine Strain: IIII	p17 (113–122 BH10)	KKAQQAAADT	L	Vaccine	murine (IgG)

No.	MAb ID	HXB2 Location	<b>Author's Location</b>	Sequence	Neutralizing	Immunogen	Species(Isotype)
		<ul><li>3-H-7: No cross-read</li><li>3-H-7: Called 3H7 – CD4+ T cells – HXE</li></ul>	ctivity with HIV-2 ROD or using a bicistronic vector,	2b, Robert-Hebmann1992a, Le SIV MAC by immunoblot [Nie an intracellular Fab intrabody, e virions from 3H7 expressing of	edrig1989] 3H7, can inhibit HIV-1 inf		
26	C5126	References Hinkula		KKAQQAAADT  nent: virus  binding to native protein – WE	no  3 reactive with p53 and p1	Vaccine 7 [Hinkula1990]	murine (IgG1κ)
27	1D9	Donor R. B. Ferns a References Ferns 19 1D9: Reactive again	nd R. S. Tedder		us	Vaccine	murine (IgG2a)
28	4C9	Donor R. B. Ferns a References Ferns 196  • 4C9: Reactive against	nd R. S. Tedder		us	Vaccine	murine (IgG2a)
29	4H2B1						murine (IgG1)
30	9G5	Donor R. B. Ferns a References Ferns 19 • 9G5: Reactive again	nd R. S. Tedder		us	Vaccine	murine (IgM)
31	15-21	p17 (121–132) <b>Vaccine</b> <i>Strain:</i> BRU <b>References</b> Robert-F	p17 (121–132 BRU) J Hebmann1992b, Robert-He	DTGHSSQVSQNY bmann1992a	no	Vaccine	murine (IgG)
32	31-11	p17 (121–132) <b>Vaccine</b> <i>Strain:</i> BRU <b>References</b> Robert-F	p17 (121–132 BRU) J Hebmann1992b, Robert-He	DTGHSSQVSQNY bmann1992a	no	Vaccine	murine (IgG)

HIV Antibodies Tables p17 Antibodies

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizing	Immunogen	Species(Isotype)
33	sc-FV p17	p17 (121–132)	p17 (121–132 BRU)	DTGHSSQVSQNY	L	Vaccine	murine (IgG1 $\kappa$ )
		Vaccine Strain: BRI	U				
		Ab type C-term D	onor Paul Zhou, NIH, Betl	hesda, MD, USA			
		References Robert-1	Hebmann1992a, Tewari199	98			
				nti-p17 MAb, and intracellular binding of the cytoplasm instead of the nucleus [Tewar		n inhibition of vira	l replication that was more
34	HyHIV-15	p17 (122–115)	p17 (87–115 JMH1)	SVHQRIDVKDTKEALEKIEEEQNKS- KKKA?	L	Vaccine	murine (IgG1)
		Vaccine Vector/Type	e: recombinant protein H	IV component: p17			
		References Liu1995	5, Ota1998a	-			
			,	t estimate from JMH1 sequence – Ka is 1.4 ace – inhibited growth of HIV-1 JMH1 in M			

## IV-C-2 p24 Antibodies

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizing	Immunogen	Species(Isotype)
35	3A6	p24 (1–17)	p24 (122–149 BH10)	TGHSSQVSQNYPIVQNIQGQMVHQA- ISP	no	HIV-1 infection	human (IgG1 $\kappa$ )
			her1992, Buchacher1994				
				order of gag [Buchacher1994] electrofusion of PBL from HIV-1 positive v	volunteers with	CB-F7 cells [Buchach	er1994]
66	111/182	p24 (1–20)	p24 (134–153 IIIB)	PIVQNIQGQMVHQAISPRTL		Vaccine	murine (IgG1)
U	111/162	Vaccine Vector/Typ References Niedrig	e: beta-galactosidase fusion 1991	protein Strain: IIIB HIV component: p		vaccine	murme (1gO1)
		• 111/182: Test speci	fic evidence of cross-reactive	rity between HIV-1, HIV-2 and SIV MAC [	Niedrig1991]		
7	112/021	References Niedrig	1991	PIVQNIQGQMVHQAISPRTL  a protein Strain: IIIB HIV component: privity between HIV-1, HIV-2 and SIV MAC		Vaccine	murine (IgG1)
3	112/047	p24 (1–20)	p24 (134–153 IIIB)	PIVQNIQGQMVHQAISPRTL	no	Vaccine	murine (IgG1)
•	112/04/	Vaccine Vector/Typ References Niedrig	e: beta-galactosidase fusion 1991	a protein <i>Strain:</i> IIIB <i>HIV component:</i> prity between HIV-1, HIV-2 and SIV MAC	p24	vaccine	murme (igG1)
)	ID8F6	Donor R. B. Ferns References Ferns 19 ID8F6: Reacted with	and R. S. Tedder 987, Ferns1989	VHQAISPRTLNAWVK  CBL-1 HIV component: virus  ed less than 75% homologous inhibition [Feagent: ARP348	no Gerns1987]	Vaccine	murine (IgG1)
)	F5-2	p24 (14–23) <b>References</b> Kusk19 • F5-2: In HIV-1+ inc		AISPRTLNAW RTLNAW is associated with CD4 T-cell de	no ecline [Kusk198	8, Kusk1992]	murine
	CB-13/5 (CB-mab-	p24 (21–25) <b>References</b> Grunov	p24 (152–156) v1990, Franke1992, Kuttner	NAWVK 1992, Glaser1996	no		murine (IgG1 $\kappa$ )
	p24/13-15)	<ul><li>to be (database note</li><li>CB-13/5: Called CI</li><li>CB-13/5: Inhibits specified</li></ul>	e) 3-mab-p24/13-15 – the VD pread of HIV-1 in cell cultu	-13/5 and CB-mab-p24/13-15 are the same, J H and VJ L regions of CB-mab-p24/13-15 res [Franke1992] NAWVK – binding not affected by bound I	5 were sequence	ed [Kuttner1992]	primary articles they see
<u> </u>	nolvolonol					Vaccine	murina (IaC)
	polyclonal	p24 (44–60) <b>Vaccine</b> <i>Vector/Typ</i>	p24 (176–192 LAI) e: recombinant protein, viru	SEGATPQDLNTMLNTVG  as-like particle Strain: LAI HIV composition	no <i>nent:</i> p24, p17,		murine (IgG) nd's adiuvant

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutral	lizing Immunogen	Species(Isotype)
	,	recognized by ant antibodies raised	was used to study a panel of ibodies elicited by rp24CA	one p17MA epitope, resi articles, suggesting a diffe	idues 11-25, and one p24CA rent antigenic properties for	esidues 176-192, 201-218, 2 A epitope, residues 176-192, p p 24CA and p 17MA antiboo oteins [Truong 1997]	were recognized by
43		Donor R. B. Fern References Ferns 3D3: Most broadl	p24 (177–182 LAI)  pe: inactivated virus Strats s and R. S. Tedder 1987, Ferns 1989 y reactive of all the antibodi l Research Council AIDS re	es in this study[Ferns1987		Vaccine	murine (IgG2b)
14	•	References Grund CD-4/1: Inhibits s CD-4/1: Affinity o CD-4/1: Unusual [Glaser1996]	p24-MAb binding kinetics, ation of p24 lysine residues b	e1993, Glaser1996, Ehrhanes [Franke1992] wer than to peptide or den with biphasic association	rd1996 atured p24 – proposed that – probably due to conforma	Vaccine the peptide binds in a loop c tional changes in p24, not to resumably due to conformat	p24 dimerization
5	15F8C7	References Janvie	p24 (183–197) epe: purified HIV-1 er1990, Janvier1992 to aa209-217 through Pepso	ATPQDLNTML can method – cross-reacts	no with HIV-2 [Janvier1990] –	Vaccine maps to aa203-217 through	murine (IgG1)  EIA pentadecapeptide
16	111/052	References Niedr	p24 (183–192 IIIB)  pe: beta-galactosidase fusionig1991  oss-reaction with HIV-2 on	-		Vaccine  MAC [Niedrig1991]	murine (IgG1)
<b>1</b> 7	polyclonal	References Pialon  28 subjects were v adjuvant QS21 – 1	vaccinated with six HIV-1 pe	EAAEWDR AI HIV component: p24 eptides that were selected were detected in 25/28 (89)	to be particularly rich in CT %), proliferative in 19/28 (7	Vaccine L epitopes, presented in lipo 9%), and CTL in 13/24 (549 FL response [Pialoux2001]	
48	91-5	p24 (64–75) <b>References</b> Gorny	p24 (196–207) y1989, Tyler1990, Robinson I by immortalization of perij	AAMQMLKETINE 1990b, Gorny1998	no	HIV-1 infection	human (IgG1λ)

No.	MAb ID	<b>HXB2</b> Location	<b>Author's Location</b>	Sequence	Neutralizing	Immunogen	Species(Isotype)
			ce HIV-1 IIIB infection [Ro search and Reference Reago	-			
49	1109/01		p24 (201–218 BRU) HIV component: virus Hebmann1992b, Robert-Hel	LKETINEEAAEWDRVHP	V no	Vaccine	murine (IgG)
50	14D4E11	• 14D4E11: Mapped t	990, Robert-Hebmann1992		V no  AAEWDRVHP) – cross-reacts	Vaccine s with HIV-2 [Janvie	murine (IgG1) er1990] and to aa203-217
51	1G5C8	References Janvier1	p24 (201–218 BRU) e: protein HIV component. 990, Robert-Hebmann1992 aa209-217 through Pepscan	b, Robert-Hebmann1992a	V no LEWDRVHP) [Janvier1990] a	Vaccine nd to aa203-217 thre	murine (IgG2b) ough EIA pentadecapeptide
2	47-2	p24 (69–86) <b>Vaccine</b> <i>Strain:</i> BRI <b>References</b> Robert-	p24 (201–218 BRU) U Hebmann1992b, Robert-Hel	LKETINEEAAEWDRVHP	V no	Vaccine	murine (IgG)
3	714/01		p24 (201–218 BRU) HIV component: virus Hebmann1992b, Robert-Hel	LKETINEEAAEWDRVHP	V no	Vaccine	murine (IgG)
54	polyclonal	<ul> <li>References Truong I</li> <li>An ELISA assay wa recognized by antibodies raised aga</li> </ul>	997 s used to study a panel of G odies elicited by rp24CA – c ainst anti-p55 virus-like part	ag peptides – mature p24 C. one p17MA epitope, residue cicles, suggesting a different	N no HIV component: p24, p17, A epitopes mapped to residue s 11-25, and one p24CA epito antigenic properties for p24C bled form of the gag proteins	s 176-192, 201-218, ope, residues 176-19 'A and p17MA antib	, 233-253, 285-304, and were 2, were recognized by
55	111/073	References Niedrig	1991	ETINEEAAEWD protein Strain: IIIB HIV and SIV MAC by multiple a	• •	Vaccine	murine (IgG1)
56	113/038	References Niedrig	1991	ETINEEAAEWD protein Strain: IIIB HIV and SIV MAC by multiple a		Vaccine	murine (IgG1)

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizing	Immunogen	Species(Isotype)
57	1-E-4	References Niedrig	p24 (203–217)  8 HIV component: virus 1989  MAbs that bind to this pepti	ETINEEAAEWDRVHP	no	Vaccine	murine (IgG)
	1 E 0					V:	i (I-C)
58	1-E-9	References Niedrig	p24 (203–217)  HIV component: virus 1989  MAbs that bind to this pepti	ETINEEAAEWDRVHP  de [Niedrig1989]	no	Vaccine	murine (IgG)
59	10-E-7	p24 (71–85)  Vaccine Strain: IIIB  References Niedrig  10-E-7: Cross reacti	p24 (203–217) 8 HIV component: virus 1988, Niedrig1989 ve between HIV-1, HIV-2 a	ETINEEAAEWDRVHP	no DD and SIV MAC [Nie	Vaccine drig1989]	murine (IgG1)
60	10-G-9	References Niedrig	_	ETINEEAAEWDRVHP tide [Niedrig1989]	no	Vaccine	murine (IgG1)
51	11-C-5	References Niedrig		ETINEEAAEWDRVHP tide [Niedrig1989]	no	Vaccine	murine (IgG1)
62	2-E-4	References Niedrig	e between HIV-1, HIV-2 an	ETINEEAAEWDRVHP  d SIV by ELISA, HIV-1 and HIV-2 de – cross-reactive with HIV-2 ROI		Vaccine	murine (IgG2a)
63	2-H-4	References Niedrig: • 2-H-4: Cross reactiv	e between HIV-1, HIV-2 ar	ETINEEAAEWDRVHP  d SIV by ELISA, HIV-1 and HIV-2 ide – cross-reactive with HIV-2 ROI	•	Vaccine	murine (IgG1)
64	8-D-2		p24 (203–217) 8 HIV component: virus 1989, Robert-Hebmann199 ic [Niedrig1988]	ETINEEAAEWDRVHP  2b, Robert-Hebmann1992a	no	Vaccine	murine (IgG2a)

No.	MAb ID	<b>HXB2</b> Location	<b>Author's Location</b>	Sequence	Neutralizing	Immunogen	Species(Isotype)
		• 8-D-2: One of nine	MAbs that bind to this pept	ide [Niedrig1989]			
65	8-G-9	References Niedrig	p24 (203–217) 3 HIV component: virus 1989 MAbs that bind to this pept	ETINEEAAEWDRVHP ide [Niedrig1989]	no	Vaccine	murine (IgG)
56	8-H-7	References Niedrig	p24 (203–217) 3 HIV component: virus 1988, Niedrig1989, Robert MAbs that bind to this pept	ETINEEAAEWDRVHP -Hebmann1992b, Robert-Hebmanide [Niedrig1989]	no n1992a	Vaccine	murine (IgG3)
7	C5123	References Hinkula		ETINEEAAEWDRVHP  nent: virus  binding to native protein – WB re	no eactive with p53 and p24	Vaccine - [Hinkula1990]	murine (IgG1 $\kappa$ )
8	1-B-7	p24 (76–85)  Vaccine Strain: IIII  References Niedrig  1-B-7: Reacts with	1988, Niedrig1989	EAAEWDRVHP egion of overlap is given – reacted	no with HIV-2 and SIV M	Vaccine AC [Niedrig1989]	murine (IgG1)
9	3-B-7	p24 (76–85)  Vaccine Strain: IIII  References Niedrig  • 3-B-7: Reacts with	1988, Niedrig1989	EAAEWDRVHP egion of overlap is given – reacted	no with HIV-2 [Niedrig19	Vaccine 89]	murine (IgG1)
0	6-D-12	p24 (76–85)  Vaccine Strain: IIII  References Niedrig  6-D-12: Reacts with	1988, Niedrig1989	EAAEWDRVHP region of overlap is given – reacte	no ed with HIV-2 [Niedrig1	Vaccine 989]	murine (IgG1)
1	6-E-7	p24 (76–85)  Vaccine Strain: IIII  References Niedrig  6-E-7: Reacts with the	1988, Niedrig1989	EAAEWDRVHP egion of overlap is given – reacted	no with HIV-2 and SIV M	Vaccine AC [Niedrig1989]	murine (IgG1)
2	8-D-5	p24 (76–85)  Vaccine Strain: IIII  References Niedrig  8-D-5: Reacts with	1988, Niedrig1989	EAAEWDRVHP egion of overlap is given – bound	no only HIV-1 [Niedrig198	Vaccine	murine (IgG)
3	FF1	p24 (76–90)  Vaccine Vector/Type References Hinkula • FF1: Epitope define	11990	EAAEWDRVHPVHAGP  nding to native protein – WB reac	no tive with p53 and p24 [F	Vaccine Hinkula 1990]	murine (IgG1κ)

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizing	Immunogen	Species(Isotype)
74	113/072	References Niedrig		•	no HIV component: p24 eactive with HIV-2 or SIV MAC	Vaccine [Niedrig1991]	murine (IgG1)
75	25.3	-	ire of the CA protein boun		monomers form 7 alpha-helices CA 82 R, and interactions as far a	•	
76	13-102-100	References Parker1  13-102-100: Bindin cleave unprotected r  13-102-100: Affinit	g site (HPVHAGPIAPG) of residues, then performing ray capillary electrophoresis	defined by epitope footprin mass spectrometry to ident was used to fine map this	ting – first binding p24 to MAb, ify protected residues of epitope epitope, and the optimal peptide by binds to the cyclophilin A binds	[Parker1996] was defined as VH	AGPIAPGIAP – this method
77	RL4.72.1	References Tatsumi	p24 (219–233 BRU) e: inactivated virus Strain 1990, Robert-Hebmann19 ed with inactivated HIV N	92b, Robert-Hebmann199	•	Vaccine	murine (IgG)
78	406/01	p24 (101–121)  Vaccine Strain: IIIE  References Robert-	p24 (233–253 BRU) 3 Hebmann1992b, Robert-H	GSDIAGTTSTLQEQI	GWMTNN no	Vaccine	murine (IgG)
79	polyclonal	<ul> <li>References Truong</li> <li>An ELISA assay wa recognized by antibodies raised ag</li> </ul>	1997  Is used to study a panel of odies elicited by rp24CA – ainst anti-p55 virus-like pa	Gag peptides – mature p24 one p17MA epitope, residuality one p17MA epitope, residuality of the period of the perio	GWMTNL no AI HIV component: p24, p17, CA epitopes mapped to residue dues 11-25, and one p24CA epito ent antigenic properties for p24C embled form of the gag proteins	s 176-192, 201-218 ope, residues 176-19 CA and p17MA anti	, 233-253, 285-304, and were 92, were recognized by
80	38:9.6K (38:96K)	References Hinkula • 38:9.6K: Called 38:		peptide blocking of binding	no g to native protein – WB reactive	Vaccine with p53 and p24 [	murine (IgG1κ) Hinkula1990]
81	EB1A9	p24 (121–135) Vaccine Vector/Type Donor R. B. Ferns a References Ferns 19		NPPIPVGEIYKRWII n: CBL-1 HIV componer	at: virus	Vaccine	murine (IgG1)

No.	MAb ID	HXB2 Location	<b>Author's Location</b>	Sequence	Neutralizing	Immunogen	Species(Isotype)
			ith both p55 and p24 – show al Research Council AIDS re	ed less than 75% homologous inhibition [eagent: ARP345	Ferns1987]		
82	polyclonal	p24 (121–152)	Gag (253–284 LAI)	NPPIPVGEIYKRWIILGLNKIVRMY- SPTSILD	no	Vaccine	human (IgG)
		References Pialoux	2001	HIV component: p24 Adjuvant: QS2			
		adjuvant QS21 – Hl	V-specific Ab responses wer	tides that were selected to be particularly are detected in 25/28 (89%), proliferative in d proliferative responses, and CTL responses.	n 19/28 (79%), a	and CTL in 13/24 (54	
33	30:3E5	p24 (141–170)	p24 (273–302 HXB2)	IVRMYSPTSILDIRQGPKEPFRDYV- DRFYK		Vaccine	murine (IgG1λ)
		Donor B. Wahren References Hinkula  30:3E5: Epitope de		binding to native protein – WB reactive w	vith p53 and p24	l [Hinkula1990]	
34	EF7	p24 (141–170)	p24 (273–302 HXB2)	IVRMYSPTSILDIRQGPKEPFRDYV- DRFYK		Vaccine	murine (IgG1 $\kappa$ )
		<ul><li>References Hinkula</li><li>EF7: Epitope define</li><li>EF7: Included as a</li></ul>	ed by peptide blocking of bir	nding to native protein – WB reactive with	n p53 [Hinkula19	990]	
35	LH-104-E	References Haahein • LH-104-E: Reacts v	p24 (275–280 BRU) e: peptide Strain: BRU m1991 with both p24 and p55 [Haah dical Research Council AIDS		no	Vaccine	murine (IgG1 $\kappa$ )
36	1B2C12	p24 (149–154)  Vaccine Vector/Type References Janvier  • 1B2C12: Reacts wi method [Janvier199	1990 th HIV-1 and HIV-2 – mappe	SILDIR ed to aa281-286 through Pepscan method	no [Janvier1990], a	Vaccine and to aa273-292 thro	murine (IgG1)
37	LH-104-K	References Haahein • LH-104-K: Binds expression of the second sec	p24 (281–286 BRU) e: peptide Strain: BRU m1991 xclusively with p24 (not p55 dical Research Council AID		no	Vaccine	murine (IgG1 $\kappa$ )

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizing	Immunogen	Species(Isotype)
88	LH-104-A	p24 (152–157 + 219–224) <b>Vaccine</b> Vector/Type	p24 (BRU)  e: peptide HIV componen	DIRQGP+QGVGGP	no	Vaccine	murine (IgG1 $\kappa$ )
		References Haahein		ш. р2 і			
		indicated the region	nino acid peptide was used 270-286 [Haaheim1991] lical Research Council AII	to immunize mice – hexapeptide scans re OS reagent: ARP307	vealed two react	ive p24 peptides – ci	ross-competition studies
89	1.17.3	References Otteken	e: inactivated virus Strain 1992	CVKQGPKEPFQSYVDRFYKSL  n: AGM TYO-7 HIV component: virus  2/SIVmac (MAC251/32H) and HIV-2smr	no nH4, but not SIV	Vaccine	murine (IgG1) IIIB or SIVmnd [Otteken1992
90	1A7	p24 (152–172) Vaccine Vector/Type References Otteken	p24 (152–172 SIVmac) e: inactivated virus Strain 1992	CVKQGPKEPFQSYVDRFYKSL  n: AGM TYO-7 HIV component: virus  //SIVmac (MAC251/32H) and HIV-2smml	no	Vaccine	murine (IgG1)
91	1F6	References Otteken	e: inactivated virus Strain 1992	CVKQGPKEPFQSYVDRFYKSL  n: AGM TYO-7 HIV component: virus  SIVmac (MAC251/32H) and HIV-2smmF	no I4, but not SIVag	Vaccine mTYO-1, HIV-1 III	murine (IgG1)  B or SIVmnd [Otteken1992]
92	23A5G4	References Janvier  • 23A5G4: Mapped to	a aa209-217 through Pepsc a which were able to bind t	IRQGPKEPFRDYVDRFYKTL  at: p24  an method [Janvier1990] and to aa285-30  the linear sequence 178-192, but not sequence			
93	23A5G5		p24 (285–304 BRU) 2: protein <i>Strain</i> : IIIB <i>I</i> Hebmann1992b, Robert-He		no	Vaccine	murine (IgG)
94	3D10G6	p24 (153–172)  Vaccine Vector/Type References Janvier  • 3D10G6: Epitope compentadecapeptide m	990 coss-reacts with HIV-1 and	IRQGPKEPFRDYVDRFYKTL  HIV-2 – mapped to aa260-267 through Pe	no epscan method [J	Vaccine anvier1990] and to a	murine (IgG1) aa285-304 through EIA
95	polyclonal	p24 (153–172) Vaccine Vector/Type References Truong	•	IRQGPKEPFRDYVDRFYKTL us-like particle <i>Strain:</i> LAI <i>HIV comp</i>	no onent: p24, p17,	Vaccine p55 <i>Adjuvant:</i> Fre	murine eund's adjuvant

No.	MAb ID	HXB2 Location	<b>Author's Location</b>	Sequence	Neutralizing	Immunogen	Species(Isotype)
		recognized by antibo antibodies raised aga	odies elicited by rp24CA – c ninst anti-p55 virus-like part	ag peptides – mature p24 CA epitopes ma one p17MA epitope, residues 11-25, and o icles, suggesting a different antigenic pro- otein or the immature assembled form of t	one p24CA epito perties for p24C	ope, residues 176-192, we CA and p17MA antibodie	ere recognized by
96	F5-4	p24 (153–175) <b>References</b> Kusk198  • F5-4: Binds to a loca		IRQGPKEPFRDYVDRFYKTLRAE c region of p24 [Kusk1988, Kusk1992]	no		murine
97	MO9.42.2	References Robert-l	p24 (285–310 BRU) : virus Strain: HIV2 ROI Hebmann1992b, Robert-Hel rith HIV-1s, HIV-2s, and SI	<u>*</u>	no n1992b]	Vaccine	murine (IgG)
98	MO9.50.2		Hebmann1992b, Robert-Hel	IRQGPKEPFRDYVDRFYKTLRAEQAS bmann1992a Vs in rec protein ELISA [Robert-Hebman		Vaccine	murine (IgG)
99	V10	p24 (155–169) References Matsuol • V10: Reacts with H1	p24 (289–303 IIIB) 992 V-1 and SIV AGM analogo	QGPKEPFRDYVDRFY  us peptides [Matsuo1992]	no	virus	murine
100	V107	p24 (155–177) <b>References</b> Matsuol  • V107: Reacts with F		QGPKEPFRDYVDRFYKTLRAEQA nalogous peptides [Matsuo1992]	no	virus	murine
101	LH-104-C	References Haahein • LF-104-C: A 104 an indicated the region		o immunize mice – hexapeptide scans rev	no ealed two react	Vaccine ive p24 peptides – cross-o	murine ( $IgG3\kappa$ )
102	12-B-4	References Niedrig		FRDYVDRFYK en two HIV-1 reactive peptides – cross-rea	no acts with HIV-2	Vaccine  ROD and SIV MAC [Nic	murine (IgG1) edrig1988, Niedrig1989]
103	C5122	References Hinkula		FRDYVDRFYK  nent: virus  to native protein – WB reactive with p53	no and p24 [Hinku	Vaccine	murine (IgG1 $\kappa$ )

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizing	Immunogen	Species(Isotype)
104	9A4C4	References Janvier	990, Robert-Hebmann199	KTLRAEQASQEVKNWMTET HIV component: p24 p2b, Robert-Hebmann1992a n method [Janvier1990] – and to		Vaccine entadecapeptide m	murine (IgG1) nethod [Janvier1992]
105	11C10B10	References Janvier		TLRAEQASQEVKNWM  at: p24  bscan method [Janvier1990] and	no to aa303-317 through EIA	Vaccine pentadecapeptide	murine (IgG1) method [Janvier1992]
106	11D11F2	References Janvier		TLRAEQASQEVKNWM  nt: p24  scan method [Janvier1990] and t	no o aa303-317 through EIA p	Vaccine entadecapeptide n	murine (IgG1) nethod [Janvier1992]
107	CD12B4	Donor R. B. Ferns a References Ferns 19 CD12B4: Reacted v	nd R. S. Tedder 87, Ferns1989	TLRAEQASQEVKNWM  n: CBL-1 HIV component: vir  rain-specific binding [Ferns1987  S reagent: ARP346		Vaccine	murine (IgG1)
108	BE3	Donor B. Wahren References Hinkula  BE3: Defined by pe		to native protein – WB reactive	no with p53 and p24 [Hinkula1	Vaccine 990]	murine (IgG1κ)
109	L14	<ul><li>Donor B. Wahren</li><li>References Hinkula</li><li>L14: Defined by per</li></ul>		o native protein – WB reactive v	no vith p53 and p24 [Hinkula1	Vaccine 990]	murine (IgG1κ)
110	108/03	References Niedrig	1991	VKNWMTETLL  n protein Strain: IIIB HIV co  and SIV MAC by multiple tests		Vaccine	murine (IgG1)
111	110/015	p24 (181–190) <b>Vaccine</b> <i>Vector/Type</i> <b>References</b> Niedrig	_	VKNWMTETLL n protein Strain: IIIB HIV co	no omponent: p24	Vaccine	murine (IgG1)

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizing	Immunogen	Species(Isotype)
		• 110/015: Cross-read	tive between HIV-1, HIV-2	and SIV MAC by multiple tests [Niedri	g1991]		
112	32:32K	References Hinkula • 32:32K: Epitope def		binding to native protein – WB reactive	with p53 and p2-	Vaccine [Hinkula1990]	murine (IgG1λ)
113	C5200	p24 (199–222) Vaccine Vector/Type References Hinkula • C5200: Epitope defi	1990	KTILKALGPAATLEEMMTACQGVG binding to native protein [Hinkula1990]		Vaccine	murine (IgG1κ)
114	FH2	References Hinkula		ILKALGPAATLEEMM  V component: p24-p15  p native protein – WB reactive with p53 a	no and p24 [Hinkula	Vaccine	murine (IgG1κ)
115	13B5	Ab type C-term D References Berthet-	Colominas 1999	LGPAATLEEM  V component: p24  crystallization and study of p24's structu	re [Berthet-Colon	Vaccine ninas1999]	murine
116	106/01	References Niedrig	1991	LEEMMTACQGVGGPGHKARV protein Strain: IIIB HIV component and SIV MAC by multiple tests [Niedrig		Vaccine	murine (IgG1)
117	LH-104-B	References Haahein • LH-104-B: Binds ex		GHKARV 4), in contrast to LH-104-I [Haaheim199 S reagent: ARP308	no 1]	Vaccine	murine (IgG1 $\kappa$ )
118	LH-104-I	References Haahein • LH-104-I: Binds exc		HKARVL ), in contrast to LH-104-B [Haaheim199 S reagent: ARP321	no 1]	Vaccine	murine (IgG1κ)

# IV-C-3 p24-p2p7p1p6 Antibodies

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizing	Immunogen	Species(Isotype)
119	LH-104-G	p24-p2p7p1p6 (231–5)	p24 (363–368 BRU)	LAEAMS	no	Vaccine	murine (IgG1 $\kappa$ )
		Vaccine Vector/Type:	peptide Strain: BRU				
		References Haaheim	1991				
	•	LH-104-G: Reacts wi	th both p24 and p55, in co	ntrast to LH-104-I [Haaheim1991]			
		LH-104-G: This epito	ppe overlaps the p24-p2 cle	avage site, database note			
	•	LH-104-G: UK Medi	cal Research Council AID	S reagent: ARP320			

# IV-C-4 p2p7p1p6 Antibodies

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizing	Immunogen	Species(Isotype)
120	i5B11	References Otake 19 • i5B11: i5B11 and 1 • i5B11: Epitope map		ou1995		Vaccine	rat (IgG2a)
121	EC6	References Hinkula		PRKKGCWKCG HIV component: p24-p15 binding to native protein – WB r	no reactive with p53 [Hinkula1	Vaccine 990]	murine (IgG2aκ)
122	M12	References Hinkula • M12: There is a p15	and a gp120 MAb both c		no reactive with p53 [Hinkula1	Vaccine 990]	murine (IgG1κ)
123	DG8	References Tanchor		RQANFLGKIWPSYKGR  nt: NCp7  er, inhibits NCp7-tRNA interacti	on [Tanchou1995]	Vaccine	murine
124	EB5	References Tanchor		RQANFLGKIWPSYKGR  nt: NCp7  r – mutation at position 59 (Lys	to Ser) results in 10-fold rec	Vaccine duction in reactivity	murine [Tanchou1995]
125	НН3	References Tanchou  HH3: Epitopes map	p7 (52–67) e: protein HIV compone 11994, Tanchou1995 ped by ELISA and BIAco al to the second zinc-finge	ore – does not inhibit NCp7 prim	no er tRNA binding [Tanchou1	Vaccine	murine (IgG2b)
126	AD2	References Tanchor	p7 (64–72) e: protein HIV compone 11995 m of NCp7 [Tanchou1995		no	Vaccine	murine (IgG)
127	CA5	p2p7p1p6 (78–86) <b>Vaccine</b> <i>Vector/Type</i> <b>References</b> Tanchor	p7 (64–72) e: protein HIV compone 11995	YKGRPGNFL  nt: NCp7	no	Vaccine	murine (IgG)

No.	MAb ID	<b>HXB2</b> Location	<b>Author's Location</b>	Sequence	Neutralizing	Immunogen	Species(Isotype)
		CA5: Binds at C ter	m of NCp7 [Tanchou199	95]			
128	DF3	References Tancho	p7 (64–72) e: protein HIV compon u1995 m of NCp7 [Tanchou199		no	Vaccine	murine (IgG)
29	EC3	References Tancho	p7 (64–72) e: protein HIV compon u1995 m of NCp7 [Tanchou199		no	Vaccine	murine (IgG)
30	FC12	References Tancho		YKGRPGNFL nent: NCp7  NCp15, inhibits NCp7-tRNA ir	no nteraction [Tanchou1995]	Vaccine	murine (IgG)
31	GE4	References Tancho	p7 (64–72) e: protein HIV comport u1995 m of NCp7 [Tanchou199		no	Vaccine	murine (IgG)
32	JB7	References Tancho	p7 (64–72) e: protein HIV comport u1995 n of NCp7 [Tanchou199	•	no	Vaccine	murine (IgG)
.33	JF11	References Tancho • JF11: Epitopes map	p7 (64–72) e: protein HIV compore u1994, Tanchou1995 pped by ELISA and BIAG rm of NCp7 [Tanchou19	core – does not inhibit NCp7 pri	no mer tRNA binding [Tanchou	Vaccine	murine (IgG1)

Gag Antibodies Tables

HIV Antibodies Tables

## IV-C-5 Gag Antibodies

No.	MAb ID	HXB2 Location	<b>Author's Location</b>	Sequence	Neutralizing	Immunogen	Species(Isotype)
134	16/4/2	References Bojak2  • 16/4/2: The ability which allows constit differentiated, mult promoter in combin	002 of three different promoter tutive expression in differe inucleated myofibers and s ation with a codon optimis	ent cells of host tissue, the to safer, and a hybrid MCK, zed gag gene generated hur	no motors  mune responses was compared. This sue specific muscle creatine king/CMV promoter – intramuscular in moral (IgG1 (Th1) and IgG2a (Ths) compared to CMV promotor-dri	nase (MCK) promoto immunization of BA 2)) and CTL immun	er, which may be restricted to ALB/c mice utilizing the MCK ne responses against HIV-1
135	183-H12-5C	Donor Bruce Chese References Cheseb • 183-H12-5C: Used • 183-H12-5C: Cross	ro1992, Toohey1995, Weh as antigen capture reagent -reacts with HIV1 and HIV	ocky Mountain Laboratories rly1997 for p24 ELISA [Chesebro] V-2 p24, and SIV p27 [Web ence Reagent Program: 353	1992, Toohey1995] rly1997]		murine (IgG1)
136	241-D	References Gorny1 • 241-D: An antibody [Gorny1989, Tyler1	989, Tyler1990, Robinson by this name is available	in the NIH AIDS Research no p24 MAb by this name i	and Reference Reagent Program	, and they refer to th	human (IgG1λ) ne papers
137	2A6	References Pincus	1998	rch and Development Center	er, Frederick, MD	p17 and mycoplasm	a [Pincus1998]
138	5E2.A3k	References Hochle • 5E2.A3k: The Ab be proteolytic enzyment	oinding site was studied wi s) and extraction (protein i uous, but involves the high	th epitope excision (proteins digested then allowed to a	no  a is bound in native conformation react with Ab), followed by mass are, and the antibody recognizes Si	spectroscopy, as we	ell as lysine modification – the
139	71-31	<ul><li>71-31: Did not enhancin</li><li>71-31: No enhancin</li></ul>	ance HIV-1 IIIB infection   ag or neutralizing activity [	[Robinson1990b] Robinson1991]	no rny1997, Gorny1998, Bandres199 / infected cells [Spear1993]	98	human (IgG1λ)

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizing	Immunogen	Species(Isotype)
		binding can be enha	a negative control in studie inced by Env deglycosylati Research and Reference Re	ion [Bandres1998]	R4 can bind to gp120 in the ab	sence of CD4-gp120 ir	nteractions, and that this
140	91-6	• 91-6: No enhancing	p24 (121–240 IIIB) 989, Robinson1990b activity for HIV-1 IIIB [Research and Reference Rea		no	HIV-1 infection	human (IgG1λ)
141	98-4.3	Gag References Robinso 98-4.3: No enhancin	p24 on1991 ng or neutralizing activity	[Robinson1991]	no	HIV-1 infection	human (IgG1λ)
142	98-4.9	Gag <b>References</b> Gorny1	p24 989		no	HIV-1 infection	murine (IgG3λ)
143	AC2	References Tanchor		nt: NCp7 does not react with NCp15 [	no Tanchou1995]	Vaccine	murine (IgG)
144	BC1071	Gag  Donor Aalto BioRe  References Schonn  BC1071: The stoich	ing1999	ation was tested and MAb B	no C1071 was used in this study f	HIV-1 infection or virion quantification	murine [Schonning1999]
145	BE10	References Tanchor		-	no bits NCp7-tRNA interaction [7]	Vaccine [anchou1995]	murine (IgG)
146	CD9	References Tanchor		nt: NCp7  does not react with NCp15 [	no Tanchou1995]	Vaccine	murine (IgG)
147	CH9B2	Donor R. B. Ferns a References Ferns 19 • CH9B2: Reactive as	and R. S. Tedder		virus	Vaccine	murine (IgG1)
148	ED8	Gag Vaccine Vector/Type References Tanchor	p7 e: protein HIV componer u1995	nt: NCp7	no	Vaccine	murine (IgG)

No. MAb II	HXB2 Location Author's Location Sequence	Neutralizing Immuno	gen Species(Isotype)
	• ED8: Binds NCp7 independent of Zn fingers, does not react with NCp15 [Tancho	u1995]	
149 EH12E	Gag p24 Vaccine Vector/Type: inactivated virus Strain: CBL-1 HIV component: virus Donor R. B. Ferns and R. S. Tedder References Ferns1987, Ferns1989  • EH12E1: Reacted with p55 and p24 in WB [Ferns1987]  • EH12E1: UK Medical Research Council AIDS reagent: ARP313	Vaccine	murine (IgG1)
150 G11G1	Gag p17 References Shang1991, Pincus1996  • G11G1: Immunotoxins were generated by linking Env MAbs to ricin A – immunocell surface – ricin-G11G1 did not mediate cell killing [Pincus1996]	otoxins mediated cell killing, but o	rat
151 G11H3	Gag p17 References Shang1991, Pincus1998  • G11H3: This MAb is cross-reactive between p17 and mycoplasma – this antibody hyorhinis, in the region of the carboxy-terminal repeat CGGSTPTPEQGNNQGG F share the tetrapeptide SQVS [Pincus1998]		
152 НуНІV-	9 Gag p17 (JMH1)  Vaccine Vector/Type: recombinant protein HIV component: p17  References Liu1995, Ota1998a  • HyHIV-19: Does not react with p17 peptides – Ka is 3.7 x 106 M-1 for rec p17 – the initial culture [Ota1998a]	no Vaccine inhibited growth of HIV-1 JMH1	murine (IgG1) n MT-4 cells when added 24 hours afte
153 IE8G2	Gag p24 Vaccine Vector/Type: inactivated virus Strain: CBL-1 HIV component: virus Donor R. B. Ferns and R. S. Tedder References Ferns1987, Ferns1989  • IE8G2: Reacted with both p55 and p24 – broadly reactive – showed less than 75%  • IE8G2: UK Medical Research Council AIDS reagent: ARP347	Vaccine  homologous inhibition [Ferns198]	murine (IgG1)
154 V7-8	Gag p24 References Robinson1990b, Montefiori1991  • V7-8: Did not enhance HIV-1 IIIB infection [Robinson1990b]  • V7-8: Reacted with HIV-1IIIB, RF, and MN [Montefiori1991]  • V7-8: NIH AIDS Research and Reference Reagent Program: 381	no HIV-1 in	fection murine (IgG3 $\kappa$ )
155 anti-p24	Gag p24  Vaccine Vector/Type: recombinant protein, virus-like particle HIV component: O  Donor Intracel Co  References Buonaguro2001	Vaccine Gag, Pol, Nef, gp120	murine (IgG)

No.	MAb ID	HXB2 Location	<b>Author's Location</b>	Sequence	Neutralizing	Immunogen	Species(Isotype)
		were created using a	a Baculovirus expression s	ystem to package addition	and Pol open reading frames, as all ORFS into the VLP – anti-V3 comparable levels on the VLP [F	and anti-p24 Abs wer	
156	human sera		nv antibodies and loss of a		progression was studied, and suggining CD4 cells, because of the ab		
157	polyclonal	References Billaut-  • DNA vaccinated BA	Mulot2001 ALB/c mice primed and bo	osted with a multiepitopic	ain: LAI HIV component: Gag, c vaccine with IL18 showed lympl cHIV Ab levels [Billaut-Mulot200	hoproliferative and C	
158	polyclonal	Freund's adjuvant References Moss20 • Lewis rats co-immu	000	in Freund's and with imm	no 21 (subtype A env, subtype G gag) unostimulatory sequences CpG st hout CpG [Moss2000]	-	
159	polyclonal	References O'Haga • Microparticles were	n2000 used as an adjuvant for en	ntrapped HIV-1 gp120 and	ent: gp120, p24 Adjuvant: PLG l induced strong serum IgG response and also induced p24 spec	nses in mice – polyla	ctide co-glycolide polymer
160	polyclonal	References O'Haga  • DNA vaccines of co	n2001 don-optimized Env and G	ag genes driven by CMV	omponent: p55 Adjuvant: PLG promotors absorbed on to PLG motomparable to gp120 in MF-59 [O	icroparticles were mo	
161	polyclonal	• Gag p24 is the most regions: 70% of the	ly widely used HIV proteiclones that were identified	n for serological based dia dusing immunized rabbit	no  component: p24  agnostic kits — phage display librate had DNA fragments from the 10–360 — subtype B and C comp	N-terminal region sp	panning 150–240 of Gag, and
162	polyclonal	Gag	p55		no LAI <i>HIV component:</i> V3, CD4F	Vaccine	murine

No.	MAb ID	HXB2 Location Author's Location	Sequence	Neutralizi	ng Immunogen	Species(Isotype)
		References Truong1996  • Antibodies raised against recombinant anti-ps regions of gp120 were studied – no neutralizi proximal sequences was found to be required	ng responses, weak Env and st	ong Gag responses were e		
163	polyclonal	Gag p24 (LAI)  Vaccine Vector/Type: virion, baculovirus and and incomplete adjuvant,  References Devito2000c  To compare vaccine strategies, rabbits were in peptides – the rabbit immunized with peptide shown to capture isolates from HIV-1 subtype IgG that was capable of efficiently capturing	mmunized with virion HIV-1/L s had the broadest linear epitop es or clades A to G – only imm	ai, baculovirus recombina e responses – the capture l unization with virion HIV-	nt p24, E. coli recomb ELISA method using 1/Lai and baculovirus	oinant p24-15, and p24-derived anti-p24 IgG preparations was s recombinant p24 developed
164	polyclonal	Gag Vaccine Vector/Type: DNA Adjuvant: CpG References Deml2001  Immunization mice with a codon-optimized C levels and Rev independent with the codon-optimized C intradermal immunization with either Gag DN	Gag was compared with a non-optimized Gag, and i.m. immun	optimized Rev dependent C zation gave a stronger Th		
165	polyclonal	Gag References Montefiori2001  In 7/9 patients in whom HAART was initiated interuption after 1-3 years, and Env and Gag to HIV-1, presumably by limiting the concent rapidly appeared and correlated with spontant absence of detectable NAbs, suggesting that contion that virus-specific B-cell priming, comabsence of complete protection to prevent dis	Abs were low or undetected by ration of viral antigens needed cous down-regulation of virem rellular immune responses alon bined with CD8+ CTL induction	ELISA indicating, that ea to drive B-cell maturation a – prolonged control of v e can control viremia unde on, may be beneficial for I	rly HAART suppress – in 3 patients with a iremia after stopping er certain circumstanc HIV-1 vaccines that ai	es the normal antibody response viral rebound autologous NAb treatment persisted in the es – these results support the
166	polyclonal	Gag Vaccine Vector/Type: virus-like particle HI References Lebedev2000  • Virus-like particles (VLPs) in the form of sph fragments of HIV Env and Gag, were used to [Lebedev2000]	erical particles with yeast dsRl	NA enveloped in a polysac		
167	polyclonal	Gag  Vaccine Vector/Type: DNA with CMV, MCK References Bojak2002	, or CMV/MCK hybrid promo	no	Vaccine	murine (IgG1, IgG2a)

HIV Antibodies Tables Gag Antibodies

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizir	ng Immunogen	Species(Isotype)
		allows constitutive differentiated, me promoter in com	we expression in different cell ultinucleated myofibers and s bination with a codon optimize	s of host tissue, the tissue so safer, and a hybrid MCK zed gag gene generated hur	esponses was compared. The copecific muscle creatine kinase /CMV promoter – intramuscul moral (IgG1 (Th1) and IgG2a (so compared to CMV promotor-	(MCK) promoter, which ar immunization of BAL Th2)) and CTL immune	may be restricted to B/c mice utilizing the MCK responses against HIV-1
168	polyclonal	gave equivocal re	B in Ethiopians: of 12,124 spesults, most often due to p24	reactivity – subsequent test	no from Ethiopia, 1,437 (11.9%) ing confirmed many of the ind yould have given some false po	eterminants were HIV-ne	gative – the American Red
169	polyclonal HIVIG	Gag	p24		P	HIV-1 infection	human
		References Nich	nols2002				
		neutralizing assa	y against a panel of six prima	ry isolates—both could ne	VIG derived from patients with utralize all isolates tested but the utralize the effective concentration.	he NYBC-HIVIG dose re	equired for 50%

### **IV-C-6** Protease Antibodies

	MAb ID	HXB2 Location Author's Location Sequence	Neutralizing	Immunogen	Species(Isotype)
170	1696	Protease (1–7) Protease (1–7 BH10) PQIYLWQ  Vaccine Vector/Type: protein HIV component: Protease  Ab type N-term  References Lescar1999  1696: MAb binds to HIV-1 and HIV-2, putative epitopes are PQIYLWQ and PQ compete - MAb disrupts catalytic activity – crystal structure of Fab at 3 A resolution binding region is located within the region required for dimerization and the Fab [Lescar1999]	tion reveals a deep cavity	lined by acidic and l	hydrophobic residues – the
171	10E7	Protease (36–46) Protease (38–45 HXB2) MSLPGRWKPKM  Vaccine Vector/Type: recombinant protein HIV component: Protease  References Croix1993, Bjorling1992  • 10E7: Immunodominant region of protease in Armenian hamster (but only weak protease binding [Croix1993]	no ly reactive in people, see	Vaccine : [Bjorling1992]) – p	hamster (IgG) eptide MSLPGRWKP block
172	F11.2.32	Protease (36–46) Protease (36–46 BH10) MSLPGRWKPKM  Vaccine Vector/Type: recombinant protein Strain: BH10 HIV component: Pr Ab type flap region  References Lescar1996, Lescar1997, Lescar1999  • F11.2.32: Binding leads to significant inhibition in proteolytic activity – crystal s shows no structural similarity to the corresponding segment in native protease su	structure of Fab-peptide w		
		• F11.2.32: Distortion may occur in the flap region of the protein, important for re			
173	13E1				
173 174	13E1 8B11	• F11.2.32: Distortion may occur in the flap region of the protein, important for re  Protease (38–45) Protease (38–45 HXB2) LPGRWKPK  Vaccine Vector/Type: recombinant protein HIV component: Protease  References Croix1993	gulating access of substra	ate to the catalytic site	e [Lescar1999]
		<ul> <li>F11.2.32: Distortion may occur in the flap region of the protein, important for reprotease (38–45)</li> <li>Protease (38–45 HXB2)</li> <li>LPGRWKPK</li> <li>Vaccine Vector/Type: recombinant protein HIV component: Protease References Croix1993</li> <li>13E1: Binds to MSLPGRWKPKM with sightly higher affinity [Croix1993]</li> <li>Protease (38–45)</li> <li>Protease (38–45 HXB2)</li> <li>LPGRWKPK</li> <li>Vaccine Vector/Type: recombinant protein HIV component: Protease References Croix1993</li> </ul>	gulating access of substra	te to the catalytic site	hamster (IgG)

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No. I	MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizing Immunogen	Species(Isotype)

### **IV-C-7** RT Antibodies

No.	MAb ID	HXB2 Location	<b>Author's Location</b>	Sequence		Neutralizing	Immunogen	Species(Isotype)
77	1E8	References Wu1993 • 1E8: Inhibits RT act	ivity, binding site overlap hibits DNA polymerase a	s with two AZT res	istance mutations [Wu199	93]	Vaccine ynergistic RT inhibit	murine (IgG1)
78	1.152 B3	References Orvell1	RT (294–302) e: recombinant protein <i>B</i> 991 ositive by immunofluores	-		no ty [Orvell1991]	Vaccine	murine (IgG1)
179	1.158 E2	References Orvell1	RT (294–302) e: recombinant protein <i>B</i> 991 by immunofluorescence –	-		no ell1991]	Vaccine	murine (IgG1)
80	31D6	References Szilvay	RT (294–319) e: E. coli Trp fusion prote 1992 tor of RT, > 50% inhibition	in HIV component	AENREILKEPVHGVY :: RT	no	Vaccine	murine (IgG1)
81	31G8	References Szilvay	RT (294–319) 2: E. coli Trp fusion prote 1992 or of RT, reactive by imm	in HIV component		no	Vaccine	murine (IgG1)
182	32E7	References Szilvay	RT (294–319) 2: E. coli Trp fusion prote 1992 Dr of RT, reactive by immu	in HIV component		no	Vaccine	murine (IgG1)
183	33D5	References Szilvay	RT (294–319) 2: E. coli Trp fusion prote 1992 or of RT, reactive by imm	in HIV component		no	Vaccine	murine (IgG1)
184	5B2	<ul><li>References Szilvay</li><li>5B2: There is an RT</li></ul>	RT (294–319) 2: E. coli Trp fusion prote 1992 3 specific Ab [Szilvay1992 5 of RT, reactive by immure	in HIV component  2] and a gp41 specifi	ic Ab [Tian2001] both ca	no lled 5B2	Vaccine	murine (IgG1)

No.	MAb ID	<b>HXB2</b> Location	<b>Author's Location</b>	Sequence	Neutralizing	Immunogen	Species(Isotype)
		• 5B2: UK Medical R	Research Council AIDS rea	agent: ARP3018			
185	polyclonal	RT (295–304) <b>References</b> Grimiso	RT (295–304 PV22) on1995	LTEEAELELA	no	HIV-1 infection	human (IgG)
186	1.153 G10	RT (350–354)  Vaccine Vector/Type References Orvell1	RT (350–354) e: recombinant protein F 991	KTGKY HIV component: RT	no	Vaccine	murine (IgG1)
187	RTMAb8	RT (376–383)  Vaccine Vector/Type References Tisdale	RT (532–539)  e: recombinant protein F 1988, Ferns1991	TTESIVIW HIV component: RT	no	Vaccine	murine (IgG)
188	1D4A3	RT (384–387)  Vaccine Vector/Type References Ferns 19	RT (540–543) e: recombinant protein F	GKIP HIV component: RT	no	Vaccine	murine (IgG)
189	RT6H	RT (384–387) Vaccine Vector/Type References Ferns 19	RT (540–543) e: recombinant protein F	GKIP HIV component: RT	no	Vaccine	murine (IgG)
190	1.160 B3	RT (442–450) <b>Vaccine</b> <i>Vector/Type</i> <b>References</b> Orvell1	RT (442–450) e: recombinant protein F 991	VDGAANRET HIV component: RT	no	Vaccine	murine (IgG1)
191	polyclonal	RT (521–531) References Grimiso	RT (521–531 PV22) on1995	IIEQLIKKEKV	no	HIV-1 infection	human (IgG)
192	C2003	References DeVico		VPAHKGIGGNEQVD  uriety of retroviruses – RT protect	no	Vaccine	rabbit (IgG) e primer [DeVico1991]
193	6B9	Ab type palm doma References Chiba19	996, Chiba1997, Ohba200		yes nds to the palm subdomain a	Vaccine  and does not inhibit RT	murine (IgG)  Cactivity [Chiba1996]
194	5F	Ab type thumb don References Ohba20 • 5F: BALB/c mice w both recognizing an	001 vere vaccinated with vaccion immunodominant neutral	2 HIV component: RT  nia carrying RT and a phage dispizing RT epitope in the region one in an and light chains of 7C4, 5C	f the template primer-bindir	ng site in the thumb do	

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No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizing	Immunogen	Species(Isotype)			
195	5G	Ab type thumb dom		HIV component: RT	yes	Vaccine	murine			
		<ul> <li>References Ohba2001</li> <li>5G: BALB/c mice were vaccinated with vaccinia carrying RT and a phage display library was produced and panned with RT – Fabs 5F and 5G were cloned, both recognizing an immunodominant neutralizing RT epitope in the region of the template primer-binding site in the thumb domain also recognized by MAb 7C4 – sequencing revealed the heavy chains and light chains of 7C4, 5G and 7C4 are related [Ohba2001]</li> </ul>								
196	7C4	RT (252–335) yes Vaccine murine (IgG2a)  Vaccine Vector/Type: vaccinia Strain: HXB2 HIV component: RT  Ab type thumb domain  References Chiba1996, Chiba1997, Ohba2001  • 7C4: 7C4 was produced from a hybridoma cell line derived from a BALB/c mouse repeatedly immunized with RT in a vaccinia construct, and was foun inhibit RT through binding to the template primer-binding site, a possible target for RT inhibitors [Chiba1996]  • 7C4: 7C4 inhibits RT from HIV-1 strains IIIB, Bru, and IMS-1 but not HIV-2 strains GH-1 and LAV-2, SIV MAC, nor SIV MND [Chiba1997]  • 7C4: Fabs 5F and 5G both recognize the same immunodominant neutralizing RT epitope in the region of the template primer-binding site in the thumb domain recognized by MAb 7C4 – sequencing revealed the heavy chains and light chains of 7C4, 5G and 7C4 are related [Ohba2001]								

## **IV-C-8** Integrase Antibodies

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizing	Immunogen	Species(Isotype)
197	1C4	Ab type N-term References Haugan  1C4: MAb interfere 1C4: One of a large	1995, Nilsen1996 s with integrase binding to set of MAbs that interact v	rain: HXB2 HIV component: In	se: 1C4, 2C11, 2E3, 3E1	Vaccine 1, 3F9, 5F8, 6G5, 7	murine (IgG1 $\kappa$ ) B6, 7C6 – these MAbs inhibit
198	2C11	Ab type N-term References Nilsen1 • 2C11: One of a larg	e: recombinant protein St 996 e set of MAbs that interact	FLDGIDKAQDEHEKYH train: HXB2 HIV component: In with the N-terminal part of integration activities [N	ase: 1C4, 2C11, 2E3, 3E	Vaccine 11, 3F9, 5F8, 6G5,	murine (IgG1κ) 7B6, 7C6 – these MAbs inhibit
199	2E3	Ab type N-term References Nilsen1 • 2E3: There are two • 2E3: One of a large	e: recombinant protein St 996, Ovod1992 MAbs called 2E3 – the oth set of MAbs that interact w	FLDGIDKAQDEHEKYH train: HXB2 HIV component: In the ser one binds to Nef [Ovod1992] with the N-terminal part of integra effect on integration activities [N	se: 1C4, 2C11, 2E3, 3E1	Vaccine 1, 3F9, 5F8, 6G5, 7	murine (IgG1 $\kappa$ ) B6, 7C6 – these MAbs inhibit
200	3E11	Ab type N-term References Otteken  3E11: There is anott  3E11: Recognized a  3E11: One of a large	2: recombinant protein St 1992, Nilsen1996 ther MAb with this ID that in an epitope present on HIV-2 e set of MAbs that interact	FLDGIDKAQDEHEKYH train: HXB2 HIV component: In trecognizes p17 [Otteken1992] 2/SIVmac, SIVagm, HIV-1, and S with the N-terminal part of integration activities [N	[Vmnd [Otteken1992] ase: 1C4, 2C11, 2E3, 3E	Vaccine 11, 3F9, 5F8, 6G5, 7	murine (IgG1κ) 7B6, 7C6 – these MAbs inhibit
201	3F9	Integrase (1–16) Vaccine Vector/Type Ab type N-term References Nilsen1 • 3F9: One of a large	Integrase (1–16 HXB2)  recombinant protein St  996  set of MAbs that interact w	FLDGIDKAQDEHEKYH  train: HXB2 HIV component: In  with the N-terminal part of integra  effect on integration activities [N	no ntegrase se: 1C4, 2C11, 2E3, 3E1	Vaccine 1, 3F9, 5F8, 6G5, 71	murine (IgG1 $\kappa$ ) 36, 7C6 – these MAbs inhibit
202	5F8	Integrase (1–16) <b>Vaccine</b> Vector/Type		FLDGIDKAQDEHEKYH train: HXB2 HIV component: In	no ntegrase	Vaccine	murine (IgG1κ)

No. MAb ID	HXB2 Location	Author's Location	Sequence	Neutrali	zing Immunogen	Species(Isotype)
	<ul><li>5F8: MAb interferes</li><li>5F8: One of a large</li></ul>	er MAb with this ID that r s with integrase binding to set of MAbs that interact		integrase: 1C4, 2C11, 2E3,	3E11, 3F9, 5F8, 6G5, 7B	6, 7C6 – these MAbs inhibit
203 6G5	Ab type N-term References Nilsen1  • 6G5: One of a large	e: recombinant protein S 996 set of MAbs that interact	) FLDGIDKAQDEHEKY train: HXB2 HIV composition that the N-terminal part of the effect on integration activ	onent: Integrase  integrase: 1C4, 2C11, 2E3,	Vaccine , 3E11, 3F9, 5F8, 6G5, 7E	murine (IgG1 $\kappa$ )  36, 7C6 – these MAbs inhibit
204 7B6	Integrase (1–16) Vaccine Vector/Type Ab type N-term References Nilsen1 • 7B6: One of a large	Integrase (1–16 HXB2 : recombinant protein S	) FLDGIDKAQDEHEKY train: HXB2 HIV compo	no no noent: Integrase  integrase: 1C4, 2C11, 2E3,	Vaccine 3E11, 3F9, 5F8, 6G5, 7E	murine (IgG1 $\kappa$ ) 36, 7C6 – these MAbs inhibit
205 7C6	Ab type N-term References Nilsen1 • 7C6: One of a large	e: recombinant protein S 996 set of MAbs that interact	) FLDGIDKAQDEHEKY train: HXB2 HIV composition the N-terminal part of the effect on integration active	integrase: 1C4, 2C11, 2E3,	Vaccine 3E11, 3F9, 5F8, 6G5, 7E	murine (IgG1 $\kappa$ ) 36, 7C6 – these MAbs inhibit
206 6C5	Ab type N-term References Haugan  6C5: MAb interfere	e: recombinant protein S 1995, Nilsen1996 s with integrase binding to			Vaccine es [Nilsen1996]	murine (IgG1κ)
207 8G4	References Haugan  • 8G4: This MAb read of positions 17-38 —	e: recombinant protein S 1995, Nilsen1996 cted strongly with peptide	ocessing and DNA joining,	onent: Integrase		murine ( $IgG1\kappa$ ) of react with a deletion mutant
208 17 (mAb17)	Integrase (25–35) <b>Vaccine</b> Vector/Type	Integrase (25–35)	DFNLPPVVAKE  HIV component: Integrase	no	Vaccine	murine (IgG1)

No.	MAb ID	HXB2 Location Author's Location	Sequence	Neutralizing	Immunogen	Species(Isotype)
		<ul> <li>References Bizub-Bender1994, Levy-Mintz1996</li> <li>17: BALBc mice were immunized with rec integration motif is in the binding region – MAbs 14 at 17: Used for the creation of single chain variable integration, whether the Ab is expressed in the nute 17: Epitope mapped to helix-turn-helix motif in the both MAb and Fab form of mAb17 inhibit Integration.</li> </ul>	ase, hybridomas expressing anti-integras nd 17 form a competition group [Bizub-l antibody fragments (SFvs) for internal c cleolus or the cytoplasm – relative bindin ne N-term domain of Integrase, positions	Bender1994] ellular expression ng affinity to IN s 25-35 – Zn bir	on – neutralization of IN act 12 > 17 = 33 > 21 > 4 [Le ding stabilizes the Integrason	tivity prior to vy-Mintz1996] mAb17complex –
209	4D6	Integrase (42–55) Integrase (42–55 HXB2)  Vaccine Vector/Type: recombinant protein Strate Ab type N-term  References Haugan1995, Nilsen1996  4D6: MAb interferes with integrase binding to DI  4D6: This MAb inhibits end processing and DNA	n: HXB2 HIV component: Integrase  NA [Haugan1995]	no ity [Nilsen1996	Vaccine	murine (IgG1 $\kappa$ )
210	7-16 (7-19)	Integrase (50–159) Integrase (50–159 HXB2)  Vaccine Vector/Type: chimeric maltose binding p Ab type Integrase catalytic core Donor Yoshihi References Ishikawa1999  • 7-16: Binds to the central catalytic domain – the p	ro Kitamura, Div of Mol Genetics, Nat I	Inst of Infectiou	s Diseases, Musashimuraya	-
211	4F6	Integrase (56–102) Integrase (56–102 HXB2)  Vaccine Vector/Type: recombinant protein Strate Ab type Integrase catalytic core References Haugan1995, Nilsen1996  4F6: MAb binding had minimal effects on IN in value 4F6: MAb interferes with integrase binding to DN	vitro activities [Nilsen1996]	no	Vaccine	murine (IgG1 $\kappa$ )
212	anti-K159	Integrase (151–163) Integrase (163–175)  Vaccine Vector/Type: peptide HIV component:  References Maroun1999, Maksiutov2002  • anti-K159: Both the peptide K159, SQGVVESM was found to fulfill condition of minimal number function as a dimer interacting in this region [Material of the condition of	NKELKKIIGQVRDQAEHLKTA, and the of helical heptads to achieve the formation of helical heptads to achieve the formation of the constant of the	on of a stable co	oiled-coil structure – Integra	ase is proposed to
213	5D9	Integrase (186–250) Integrase (186–250 HXB2)  Vaccine Vector/Type: recombinant protein Strate Ab type Integrase DNA binding domain References Nilsen1996  • 5D9: MAb binding had minimal effects on IN in		no	Vaccine	murine (IgG1 $\kappa$ )

Integrase Antibodies Tables

HIV Antibodies Tables

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizing	Immunogen	Species(Isotype)
		• 5D9: While C-term a	nd N-term anti-Integrase	MAbs interfere with Integrase-D	NA binding, 5D9 which b	inds more centrally	, does not [Haugan1995]
214	8-6	Integrase (211–227)	Integrase (211–227 HXB2)	KELQKQITKIQNFRVYY	no	Vaccine	murine (IgG1)
		<b>Donor</b> Yoshihiro Kita <b>References</b> Ishikawa	chimeric maltose bindin amura, Div of Mol Genet 1999	g protein (MBP) Strain: IIIB ics, Nat Inst of Infectious Diseaseding region [Ishikawa1999]	-		
215	19 (2-19, scAb2-19)	Vaccine Vector/Type: References Bizub-Be • 19: BALBc mice wer	ender1994, Levy-Mintz19 re immunized with rec int	IV component: Integrase	no nti-integrase Abs were ger	Vaccine nerated, and the anti	murine (IgG1) bodies characterized – 19 has
		interfered with the fo	o2-19 is a single-chain Ab lding of Gag-Pol polypro	o made from MAb 2-19 –acts int tein, the Ab did not affect viral p formational [Kitamura1999]		-	
216	2-19	Integrase (228–236)	Integrase (228–236 HXB2)	RDSRNPLWK	no	Vaccine	murine (IgG2b)
		<b>Ab type</b> Integrase DN <b>References</b> Ishikawa	NA binding domain <b>Doi</b> 1999	g protein (MBP) Strain: IIIB nor Yoshihiro Kitamura, Div of I nd the terminal cleavage and stra	Mol Genetics, Nat Inst of l	Infectious Diseases,	
217	8-22	Integrase (237–252)	Integrase (237–252 HXB2)	GPAKLLWKGEGAVVIQ	no	Vaccine	murine (IgG1)
		<b>Ab type</b> Integrase DN <b>References</b> Ishikawa	NA binding domain <b>Do</b> 1999	g protein (MBP) Strain: IIIB nor Yoshihiro Kitamura, Div of I strand transfer functions of Integ	Mol Genetics, Nat Inst of l	Infectious Diseases,	
218	4-20	Integrase (253–261)	Integrase (253–261 HXB2)	DNSDIKVVP	no	Vaccine	murine (IgG1)
		<b>Ab type</b> Integrase DN <b>References</b> Ishikawa	NA binding domain <b>Do</b> 1999	g protein (MBP) <i>Strain:</i> IIIB <b>nor</b> Yoshihiro Kitamura, Div of I transfer functions of Integrase, b	Mol Genetics, Nat Inst of l	Infectious Diseases,	
219	6-19	Integrase (262–270)	Integrase (261–270 HXB2)	RRKAKIIRD	no	Vaccine	murine (IgG2b)
			chimeric maltose bindin NA binding domain <b>Dom</b>	g protein (MBP) <i>Strain:</i> IIIB <b>nor</b> Yoshihiro Kitamura, Div of I			Musashimurayama, Japan

	MAb ID	HXB2 Location	<b>Author's Location</b>	Sequence	Neutralizing	Immunogen	Species(Isotype)
		• 6-19: Inhibits the ter	minal cleavage and strar	d transfer functions of Integrase,	, but not the disintegration a	ctivity [Ishikawa1999	]
220	7C3	Integrase (262–271)	Integrase (262–271 HXB2)	RRKAKIIRDY	no	Vaccine	murine (IgG1κ)
		**	•	Strain: HXB2 HIV component.	: Integrase		
		References Haugan		DNA (III. 1007)			
			s with integrase binding t	o DNA [Haugan1995] pe in this region, 7C3, 7F11, and	PE5 all three UIV 1 MAI	or areas react with UI	V 2 IN those MAbs inhibit
				on, and had little effect on disinte		os cioss-leact with fil	v-2 IIv – tilese MAUS lilliloit
221	7F11	Integrase (262–271)	Integrase (262–271 HXB2)	RRKAKIIRDY	no	Vaccine	murine (IgG1 $\kappa$ )
		Vaccine Vector/Type References Nilsen19	•	Strain: HXB2 HIV component.	: Integrase		
			•	ope in this region, 7C3, 7F11, and	d 8E5 – all three HIV-1 MA	hs cross-react with H	IV-2 IN – these MAbs inhibi
				on, and had little effect on disinte		os cross react with H	i v 2 ii v   uiese ivii tos iiiiioi
				that binds to gp120 [Lasky1987]			
222	8E5	Integrase (262–271)	Integrase (262–271 HXB2)	RRKAKIIRDY	no	Vaccine	murine (IgG1κ)
			1:	Ctuain, HVD2 HIV samman and	<b>.</b>		
		Vaccine Vector/Type		Strain: fixb2 fiv component.	: Integrase		
		References Haugan	1995, Nilsen1996		: Integrase		
		References Haugan  • 8E5: MAb interferes	1995, Nilsen1996 s with integrase binding t	o DNA [Haugan1995]		os cross-react with HT	V-2 IN – these MAbs inhibit
		References Haugan  • 8E5: MAb interferes  • 8E5: A set of three M	1995, Nilsen1996 s with integrase binding t MAbs recognize an epito		8E5 – all three HIV-1 MA	os cross-react with HI	V-2 IN – these MAbs inhibit
223	MAb 35	References Haugan  • 8E5: MAb interferes  • 8E5: A set of three Nend-processing, DNA	1995, Nilsen1996 s with integrase binding t MAbs recognize an epito	o DNA [Haugan1995] pe in this region, 7C3, 7F11, and	8E5 – all three HIV-1 MA	os cross-react with HI	V-2 IN – these MAbs inhibit murine (IgGκ)
223	MAb 35	References Haugan  8E5: MAb interferes  8E5: A set of three Nend-processing, DNA  Integrase (264–273)	1995, Nilsen1996 s with integrase binding to MAbs recognize an epito A joining and reintegration Integrase (264–273) recombinant protein	o DNA [Haugan1995] pe in this region, 7C3, 7F11, and on, and had little effect on disinte	8E5 – all three HIV-1 MAb gration [Nilsen1996]		
223	MAb 35	References Haugan  • 8E5: MAb interferes  • 8E5: A set of three Mend-processing, DNA  Integrase (264–273)  Vaccine Vector/Type References Barsov1  • MAb 35: There appears	1995, Nilsen1996 s with integrase binding to MAbs recognize an epito A joining and reintegration Integrase (264–273) r: recombinant protein 1996, Acel 1998 ears to be two different II	o DNA [Haugan1995] pe in this region, 7C3, 7F11, and on, and had little effect on disinte KAKIIRDYGK HIV component: Integrase N Abs with similar names: MAb	8E5 – all three HIV-1 MAE gration [Nilsen1996] no 35 and 35 [Barsov1996, Bir	Vaccine zub-Bender1994]	murine (IgG $\kappa$ )
223	MAb 35	References Haugan  8E5: MAb interferes  8E5: A set of three Mend-processing, DNA  Integrase (264–273)  Vaccine Vector/Type References Barsov1  MAb 35: There appo  MAb 35: Although Mab 35: Although Mab 35: Although Mab 35: Although Mab 35: Market M	1995, Nilsen1996 s with integrase binding to MAbs recognize an epito A joining and reintegration Integrase (264–273) recombinant protein 1996, Acel1998 ears to be two different II MAb 35 does not inhibit	o DNA [Haugan1995] pe in this region, 7C3, 7F11, and on, and had little effect on disinte  KAKIIRDYGK  HIV component: Integrase	8E5 – all three HIV-1 MAb gration [Nilsen1996] no 35 and 35 [Barsov1996, Bid I processing, strand transfer	Vaccine zub-Bender1994] and disintegration [B	murine ( $\operatorname{IgG}\kappa$ ) arsov1996]

Pol Antibodies Tables
HIV Antibodies Tables

## **IV-C-9** Pol Antibodies

No. MAb ID	HXB2 Location	<b>Author's Location</b>	Sequence	Neutralizing	Immunogen	Species(Isotype)
224 12	<ul> <li>References Bizul</li> <li>12: BALBc mice finger motif is in the control of the control</li></ul>	b-Bender 1994, Levy-Mintz were immunized with rec i the binding region – MAbs creation of single-chain var	ntegrase, hybridomas express 12, 13 and 35 form a compet iable antibody fragments (SFv	no ing anti-integrase Abs were ger ition group [Bizub-Bender1994 vs) for internal cellular expressi  – relative binding affinity to IN	·] on – neutralization	of IN activity prior to
225 13	References Bizult • 13: BALBc mice	o-Bender1994 were immunized with rec i		no ing anti-integrase Abs were ger ition group [Bizub-Bender1994		murine (IgG1) ibodies characterized – the Zn
226 14	References Bizult • 14: BALBc mice	o-Bender1994 were immunized with rec i	HIV component: Integrase ntegrase, hybridomas express 14 and 17 form a competition	no ing anti-integrase Abs were ger 1 group [Bizub-Bender1994]	Vaccine nerated, and the anti	murine (IgG1) ibodies characterized – the Zn
227 16	References Bizul	o-Bender1994 were immunized with rec i	HIV component: Integrase ntegrase, hybridomas express	no ing anti-integrase Abs were ger	Vaccine nerated, and the anti-	murine (IgG2a)
228 1C12B1	References Ferns • 1C12B1: Recogn		Vestern blot, binds to C termin	us [Ferns1991]	Vaccine	murine
229 21	• 21: BALBc mice [Bizub-Bender19] • 21: Used for the company of th	o-Bender 1994, Levy-Mintz were immunized with rec i 94] creation of single chain var	ntegrase, hybridomas express iable antibody fragments (SFv	no ing anti-integrase Abs were ger vs) for internal cellular expression—relative binding affinity to IN	on – neutralization	of IN activity prior to
230 32 (mAb Fab32)	32, Pol	Integrase (223–266)	HIV component: Integrase	no	Vaccine	murine (IgG2b)

HIV Antibodies Tables

Pol Antibodies

No. MAb ID	<b>HXB2</b> Location	<b>Author's Location</b>	Sequence	Neutralizing	Immunogen	Species(Isotype)
	<ul> <li>32: BALBc mice w</li> <li>32 and 33 form a co</li> <li>32: Limited proteol</li> <li>228R and beta5 264</li> <li>32: Called mAb32</li> </ul>	ompetition group [Bizub- ysis combined with mass kK and 266K [Yi2000a] – mAb33 and mAb32 cor	ntegrase, hybridomas expresender 1994] spectrometric analysis indicates an appeter for binding to the C-to-	essing anti-integrase Abs were generates Fab32 binds to two strands erm domain of Integrase – while es not inhibit at all while Fab33 is	of the beta sheet, be mAb32 only weakly	eta1 223F, 224R, 226Y, and y inhibits IN activity, mAb33
231 35	<ul><li>References Bizub-l</li><li>35: There appears t</li><li>35: BALBc mice w</li></ul>	Bender1994 o be two IN Abs with sin ere immunized with rec i	ntegrase, hybridomas expre	no [Barsov1996, Bizub-Bender199 ssing anti-integrase Abs were ger etition group [Bizub-Bender1994	nerated, and the anti	murine (IgG2b) bodies characterized – the Zn
232 3D12	References Chiba1		nent: RT as this name (see [Chiba199	7])	Vaccine	murine (IgG2a)
233 3F10	Pol Vaccine Vector/Typ References Chibal	RT e: vaccinia HIV compo. 997	nent: RT		Vaccine	murine (IgG2a)
234 4	<ul> <li>References Bizub-1</li> <li>4: There is another</li> <li>4: BALBc mice we low binding affinity</li> <li>4: Used for the crea</li> </ul>	Bender1994, Levy-Mintz MAb with this ID that re- re immunized with rec in [Bizub-Bender1994] ttion of single chain varia	acts with gp41 [Oldstone199] tegrase, hybridomas express ble antibody fragments (SF	no  1, Bizub-Bender1994]  1, Bizub-Bender1994]  1, Bizub-Bender1994  2, Bizub-Bender1994  2, Bizub-Bender1994  2, Bizub-Bender1994  3, Bizub-Bender1994  4, Bizub-Bender1994  5, Bizub-Bender1994  6,	n – neutralization of	f IN activity prior to
235 6B9	Pol Vaccine Vector/Typ References Chibal	RT e: vaccinia HIV compo. 997	nent: RT		Vaccine	murine (IgG2a)
236 7C4	References Chiba1			IIIB, Bru and IMS-1, but not HIV	Vaccine  V-2 strains GH-1 or	murine (IgG1)  LAV-2 or SIV strains MAC or
237 RT-4	Pol <b>References</b> Li1993	RT , Gu1996		no		murine (IgG2b)

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizing	Immunogen	Species(Isotype)
		• RT-4: Increased ne	virapine and delavirdine	inhibition, no effect on AZT i	nhibition [Gu1996]		
238	RT7O	Donor B. Ferns an References Ferns 1 • RT7O: Conformati [Ferns 1991]	991	rally in the protein – inhibited	IRT enzyme activity and thus m	Vaccine hay bind close to the	murine (IgG1) active site of the enzyme
239	RT7U	Donor B. Ferns and References Ferns 1  RT7U: Has a confo	991	ts with p66 and p51 in WB [F	erns1991]	Vaccine	murine
240	anti-HIV-1 I	References diMarz  • anti-HIV-1 RT: Clo clinical strains and		ki1995]	ly, preventing HIV infection in	vitro – this MAb wa	murine (IgG) as broadly cross-reactive with
241	polyclonal	References Wagne  A VLP is a non-inf linear domains – ga neutralizing respon	r1998b ectious virus-like particle ag and env CTL specific se occurred only with wl	e self-assembled from HIV Pr CTL were stimulated in each	no nored gp120, V3+CD4 linear do 55 gag – macaques were immun case, and Ab response to gag an spite the CTL and Ab response, b]	ized with VLPs bou d gp120 and was eli	cited, but the gp120
242	polyclonal	<ul><li>References Kim19</li><li>A gag/pol, vif or C</li></ul>	97b MN160 DNA vaccine, w		want: B7, IL-12 with the plasmid encoding the coe, as well as Ab response detectors		
243	polyclonal	References Burnet  • A live attenuated by	acterial vaccine, Salmone		inserted HIV RT gene fragment ice [Burnett2000]	Vaccine in the Lpp-OmpA-F	murine (IgA) HIV fusion protein, induced a

HIV Antibodies Tables

Pol Antibodies

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizing	Immunogen	Species(Isotype)	
244	33 (mAb33,	Pol	Integrase (223–268		no	Vaccine	murine (IgG2b)	
	Fab33, 33D5,		HXB2)					
	mab 33)	Vaccine Vector/Type	e: recombinant protein	HIV component: Integrase				
References Bizub-Bender1994, Levy-Mintz1996, Yi2000a, Yi2002								
	•	33: BALBc mice we	ere immunized with rec i	ntegrase, hybridomas expressing anti-integra	ase Abs were gei	nerated, and the antil	oodies characterized – MAbs	
		32 and 33 form a co	mpetition group [Bizub-	Bender1994]				
	•	• 33: Used for the cre	ation of single chain vari	able antibody fragments (SFvs) for internal	cellular expressi	on – neutralization o	f IN activity prior to	
		integration, whether	the Ab is expressed in the	ne nucleolus or the cytoplasm - relative bind	ling affinity to IN	V: 12 > 17 = 33 > 21	> 4 [Levy-Mintz1996]	
		<ul> <li>33: Limited proteoly</li> </ul>	ysis combined with mass	spectrometric analysis were used to define	the binding site f	for Fab32, but Fab33	binding to the Intergrase	
		C-term domain left	it resistant to proteolytic	digestion [Yi2000a]				
	•	<ul> <li>33: Called mAb33 -</li> </ul>	- mAb33 and mAb32 cor	npete for binding to the C-term domain of I	ntegrase – while	mAb32 only weakly	inhibits IN activity, mAb33	
		inhibits strongly, ma	Ab32 has a lower affinity	than mAb33, and Fab32 does not inhibit at	all while Fab33	inhibits catalytic acti	vity and DNA binding –	
		heteronuclear NMR	indicated eight residues	of Integrase are immobilized upon Fab33 bi	nding, two in the	e core of the protein,	and 6 on the outer face that	
		form a contiguous p	atch likely to contain the	epitope – 223F, 224R, 226Y, 244K, 267I, a	nd 268I, which n	nay be a useful targe	t for drug design – the	
		Fab33-IN complex i	s far more soluble than I	N alone and may be useful for crystallizatio	n [Yi2002]			

Vif Antibodies Tables

HIV Antibodies Tables

## **IV-C-10** Vif Antibodies

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizing	Immunogen	Species(Isotype)
245	TG002	Donor Transgene	Vif (34–47) e: recombinant protein	KARGWFYRHHYESP?  HIV component: Vif  a rec Vif protein derived from E. coli	no	Vaccine	murine
			_	Reagent Program: 2746			
246	TG001	Ab type C-term Γ	<b>Donor</b> Transgene	KPQKTKGHRGSHTMNGH?  HIV component: Vif  e to a rec Vif protein derived from E. co	no oli	Vaccine	murine
		• TG001: NIH AIDS	Research and Reference	Reagent Program: 2745			
247	J4	Vif	(HXB2)				chimeric rabbit/human FAb
		intrabody efficiently	eloped a Vif-specific into bound Vif protein and a	rabody single-chain FAb fragment of J4 neutralized its infectivity enhancing fun train NL43 and with primary isolates st	ction – intrabody-exp	ressing transduced co	
248	polyclonal	References Kim199	97b	nt: Gag, Pol, Vif, Env Adjuvant: B7, hen delivered in conjunction with the pl		Vaccine	murine
				proliferative responses in mice, as well		•	

HIV Antibodies Tables Tat Antibodies

## **IV-C-11 Tat Antibodies**

No.	MAb ID	<b>HXB2</b> Location	<b>Author's Location</b>	Sequence	Neutralizing	Immunogen	Species(Isotype)
249	NT3/2D1.1	Ab type N-term References Dingwa  • NT3/2D1.1: Immur		blots HIV-1 tat protein [Dingwall198	9]	Vaccine	murine (IgG1a)
250	1.2	Tat (2–17) <b>References</b> Ovod19 • 1.2: Weak expression		EPVDPRLEWKHPGSQ  + brain tissue sample, in contrast to N	ef [Ranki1995]		
251	1D9D5	Ab type N-term References Mhashi  1D9D5: Single chai N-term intrabody ca activity [Mhashilka  1D9D5: Exogenous	an inhibit transactivation o r1995] sly delivered Tat can efficie	EPVDPRLEWKHPGSQPKTA  HIV component: Tat  were engineered that can be stably ex f an HIV LTR-CAT construct and blo ently transactivate an HIV-LTR-CAT of [5], that free Tat and not Ab bound is the stable of the sta	ck import into nucleus	s, but intrabody speci	fic for exon 2 did not inhibit
252	1D2F11	Ab type C-term References Valvatn • 1D2F11: MAb did to		this MAb inhibited exogenously deli		Vaccine  on of an HIV-LTR-C	murine (IgG1)  AT construct in HeLa cells b
253	2D9E7	Ab type C-term References Valvatn • 2D9E7: MAb did no	ot bind shorter peptides –	RKKRRQRRRPPQGSQTHQVSLS: TSQSRGDPTGPKE HIV component: Tat this MAb inhibited exogenously delive ficiently than MAbs 1D2F11 or 4B4C	ered Tat transactivatio	Vaccine on of an HIV-LTR-CA	murine (IgG1)  AT construct in HeLa cells by
254	4B4C4 (4B4)	Tat (49–86)	Tat  e: recombinant protein I	RKKRRQRRRPPQGSQTHQVSLS TSQSRGDPTGPKE		Vaccine	murine (IgG1)

Tat Antibodies Tables

HIV Antibodies Tables

No.	MAb ID	HXB2 Location	<b>Author's Location</b>	Sequence	Neutralizing	Immunogen	Species(Isotype)
			not bind shorter peptides ar uptake of Tat [Valvatne	this MAb inhibited exogenously delivered	d Tat transactivation	on of an HIV-LTR-CA	AT construct in HeLa cells by
255	5G7D8	Tat (49–86)	Tat	RKKRRQRRRPPQGSQTHQVSLSKQF TSQSRGDPTGPKE	)_	Vaccine	murine (IgG1)
		Vaccine Vector/Typ Ab type C-term References Valvati	pe: recombinant protein ne1996	HIV component: Tat			
				<ul> <li>this MAb inhibited exogenously delivere efficiently than 1D2F11 or 4B4C4 [Valvatn</li> </ul>		on of an HIV-LTR-CA	AT construct in HeLa cells by
256	NT2/4D5.24	Ab type C-term References Dingw		PTSQPRGDPTGPKE  nent: Tat  unoblots HIV-1 tat protein [Dingwall1989]		Vaccine	murine
257	L-anti-Tat	Tat	Tat	, , ,	L P (when lipidated)	Vaccine	murine (IgG1)
		Donor AGMED, In References Cruiks		HIV component: Tat  up by cells and effectively block IIIB and I	orimary virus HIV	-1 replication in activ	ely and latently infected cells
258	2D9D5	Tat	Tat pe: recombinant protein	HIV component: Tat		Vaccine	murine (IgG)
			ain antibodies, intrabodies	s, were engineered that can be stably expres n HIV LTR-CAT construct, in contrast to N			lls – co-expression of C-term

HIV Antibodies Tables Rev Antibodies

## **IV-C-12** Rev Antibodies

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizing	Immunogen	Species(Isotype)
259	4G9	References Jensen1	Rev (5–15) 2: recombinant protein 1997 ng location by protein foo	-		Vaccine	murine
260	Ab2	Donor Tony Lowe a References Hender  • Ab2: The Ab2 binds	ing site overlaps the nucle				
261	10.1	• 10.1: Binds to the R using 10.1, suggesti	ng most Rev was bound to	nal anti-Rev Ab detected Rev in	•		•
262	3Н6	References Orsini I      3H6: There is anoth     3H6: Directed agair [Orsini1995]	nst nucleolar localization/l	RRNRRR HIV component: Rev recognizes gp41 [Pinter1995] RRE binding domain – antigeni the human protein Complement			
263	8E7	References Kalland  References Kalland  References Kalland  References Kalland  References Kalland  References Kalland  Rev shuttles continu  References Kalland  Rev shuttles continu  References Kalland  Rev shuttles continu  References Kalland  Rev shuttles continue  References Kalland  Rev shuttles continue  References Kalland  Rev shuttles continue  References Kalland  Rev shuttles co	indirect immunofluorescioli, nucleoplasm, perinucleously between cytoplasm etion mapped to aa 70-84, and Rev localize to the samulatining beta-globin was blicing [Boe1998] similar fragments of the	PVPLQLPPLERLTLD HIV component: Rev ilvay1995, Jensen1997, Boe 199 ence and also detected Rev in Vear zone, and cytoplasm – Rev o ic and nucleoplasmic compartm 75-88 – protein footprint to 65- e region in the nucleoplasm, bu distributed similarly to HIV-1, s human protein Epidermal grow cursor, QPPGLERLWLEGNPV	B assays – used to detect lo o-localized with host cell fa ents [Kalland1994a, Kalland 88 [Jensen1997] the splicing factor SC-35 k uggesting Rev and HIV-1 R	ctors known to assen d1994b, Szilvay1995 ocalizes in different s NAs interact at putat	nble on nascent transcripts – ] peckles with the nucleoplasm ive sites of mRNA
<del></del> 264	9G2 (9G2G4D6	Rev (70–84)	Rev (70–84)  e: recombinant protein	PVPLQLPPLERLTLD	Ded [Mansiate (2002]	Vaccine	murine (IgG2aκ)

No. MAb l	ID HXB2	Location	Author's Location	Sequence	Neutralizing	Immunogen	Species(Isotype)
	• 9G2: 1 • 9G2: 1 • 9G2: 1 • 9G3: 1	Worked in ind Peptide interac This epitope is g protein com	1994a, Jensen1997, Maks frect immunofluorescence ction mapped to aa 70-84, s similar fragments of the plex acid labile chain pred	and also detected Rev in V 75-88 – protein footprint to human protein Epidermal g	growth factor receptor substrate 1 NPWDCG [Maksiutov2002]	_	
265 Ab4	Dono Refer • Ab4: ' [Hend • Ab4: '	ne Vector/Type Tony Lowe a ences Henders The binding si erson1997] This epitope is	similar fragments of the	Center, Cambridge port signal – binding was n human protein Epidermal §	ot blocked by bound HIV RNA a	•	•
266 3G4	Rev (9	00–116)	Rev (90–116)  :: recombinant protein	GTSGTQGVGSPQILV KE?	NPWDCG [Maksiutov2002] ESPTVLESGT-	Vaccine	murine (IgG1κ)
	• 3G4:		on that can be dispensed	with and still retain Rev fu	nction [Orsini1995]		
267 1G10 (IG10F	F4) Vaccii Dono Refer • 1G10: • 1G10:	Anne Marie ences Kalland Bound Rev in Peptide intera	1994a n indirect immunofluoresc action mapped to aa 91-10	ence and also detected Rev	v in WB – used to detect localization to an 10-20, and 95-105 [JenseRP3060		murine (IgG2b $\kappa$ ) out the cell [Kalland1994a]
268 1G7	Vacci Refer • 1G7:	ences Kalland Worked in ind		and also detected Rev in V	VB – used to detect localization of t to aa 95-105 [Jensen1997]	Vaccine  of Rev throughout th	murine (IgG2bκ) e cell [Kalland1994a]
269 Ab3	Vacci Dono Refer	Tony Lowe a		Cambridge	ot blocked by bound HIV RNA [	Vaccine Henderson1997]	(IgG1)
270 2G2	Rev <b>Vacci</b>	ne Vector/Type	Rev : recombinant protein I	HIV component: Rev		Vaccine	murine (IgG1κ)

No. I	MAb ID	HXB2 Location	<b>Author's Location</b>	Sequence	Neutralizing Immunogen	Species(Isotype)
		References Orsini19 • 2G2: Does not bind t [Orsini1995]		one S-transferase (GSZ	') Rev fusion proteins, or to Rev in a RIPA buffer, suggesting	a conformational epitope

# IV-C-13 gp160 Antibodies

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizing	Immunogen	Species(Isotype)
271	M85	Ab type C1 Dono References diMarzo M85: Immunoblot a M85: C1 domain – [Moore1994c] M85: Binding inhib	and RIP reactive for strains mutation 40 Y/D impairs b ited by MAb 4D4#85, enh		el1997, Wyatt1997 nds deglycosylated gp1 atured/native gp120 is anti-V3 MAb 5G11, a	< .01, suggesting co	nformational component Abs [Moore1996]
272	7E2/4	Ab type C1 Dono References Moore 1  • 7E2/4: C1 domain -  • 7E2/4: This epitope PLYKEATSTF [Ma	has a high degree of simil	enatured/native gp120 is .07, suggest arity with the platelet membrane gly			
273	4D4#85	Ab type C1 Dono References Moore1  4D4#85: C1 domain  4D4#85: Inhibits bi  4D4#85: Binds efficif the 19 C-term am  4D4#85: A panel of core gp120 protein (	994c, Moore1994d, Mooren – the relative affinity, derending of C1 MAb M85, Contently to sgp120 but not so into acids, in conjunction with MAbs were shown to bing Delta V1, V2, and V3), the has a high degree of single-	GVPVWKEATT  NCI, Frederick, MD USA e1996, Wyatt1997, Binley1998, Mak natured/native gp120 is 0.1 – mutatio 1-C5 discontinuous epitope MAbs 13 oluble gp120+gp41, suggesting its gp vith C1 positions 31-50, are deleted [ d with similar or greater affinity and nus such a core protein produces a st nilarity with the platelet membrane g	on 45 W/S impairs bind 81 and 212A, and CD4 p120 epitope is blocked Wyatt1997] similar competition producture closely approxi	binding induced M l by gp41 binding – ofiles to a deglycosy mating full length f	does not bind to HXBc2 gp120 rlated or variable loop deleted olded monomer [Binley1998]
274	M92	Ab type C1 Dono References diMarzo • M92: Immunoblot r [diMarzo Veronese I	eactive, RIP negative, but 992]		no reacts with strains IIIB	Vaccine , 451, MN, RF, and	rat (IgG1) RUTZ

gp160 Antibodies

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizing	Immunogen	Species(Isotype)
		• M92: This epitope h PLYKEATSTF [Ma		rity with the platelet membrane gly	coprotein IIIA precurso	r (GLIIIA) (integrin l	peta- 3) (CD61):
275	M86	Ab type C1 Dono References diMarzo  M86: Immunoblot a  M86: C1 domain – to	the relative affinity for den has a high degree of similar	se	94c]	_	-
276	polyclonal	Ab type C1 References Collado Vaccinia p14 can eli noted when p14 or p domain, depending of	cit NAbs and p39 tends to 39 was placed in the N-tentric to the construct – all chim	LFCASDAKAYDTEVHNVWAT  ent: Env  be immunodominant, so these two rm region of the fusion protein – ch eric Env proteins: 14kEnv, 39kEnv 9k mounted a strong response to th	nimeric proteins shifted to y, and Env39k elicited a s	the Env Ab response strong Ab response to	from V3 to either a C1 or C4 the C1 region of gp120
277	133/237	Ab type C1 References Niedrig • 133/237: Region of					murine (IgG1)
278	133/290	Ab type C1 References Niedrig  133/290: Region of  133/290: The relativ  133/290: Used for a  133/290: Reciprocal site antibodies [Moc  133/290: Binds effic  133/290: A panel of	overlap for reactive peptid re affinity for denatured/na ntigen capture assay, eithe binding inhibition with the ore 1996] ciently to sgp120 but not so MAbs were shown to bind	YDTEVHNVWA HIV component: gp120  1994c, Moore1994d, Wyatt1995, B les is WATHA – weak neutralization tive gp120 is 2.2 – mutation in poser to bind gp120 to the ELISA plate he antibody 522-149, that binds to a collable gp120+gp41, suggesting its d with similar or greater affinity an hus such a core protein produces a second	on of lab strains [Niedrig ition 69 W/L impairs bit e, or to quantify bound gradiscontinuous epitope - gp120 epitope is blocked d similar competition pr	1992b] nding [Moore1994c] p120 [Wyatt1995] – binding is enhanced d by gp41 binding [Wofiles to a deglycosyl	/yatt1997] lated or variable loop deleted

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutraliz	ing Immunogen	Species(Isotype)
		trimers (gp140-GN0 F91) and CD4i (17t gp140-GNC4 glyco	C4) that preserve and expo and 48d) recognized gp1	compared to gp120 – MAbs of	s while occluding some nor r gp140 – non-neutralizing	n-neutralizing epitopes - MAbs C11, A32, 522-1	
279	133/11	Ab type C1 References Niedrig		EVHNVWATHACVPTD  HIV component: gp120  es is WATHA – weak neutral	L ization of lab strains [Niedr	Vaccine ig1992b]	murine (IgG1)
280	D/3G5	<b>Ab type</b> C1 <b>References</b> Bristow	1994	ACVPTDPNPQ  Strain: LAI HIV componen  numoral immune response to		Vaccine  -folded rgp120 and rgp1	murine (IgG1)  60 [Bristow1994]
281	D/6A11	<b>Ab type</b> C1 <b>References</b> Bristow	1994	ACVPTDPNPQ  Strain: LAI HIV componen  humoral immune response to		Vaccine s-folded rgp120 and rgp	murine p160 [Bristow1994]
282	D/5E12	<b>Ab type</b> C1 <b>References</b> Bristow	1994	ACVPTDPNPQEVVLVN  Strain: LAI HIV componen  humoral immune response to	t: gp120	Vaccine s-folded rgp120 and rgp	murine v160 [Bristow1994]
283	L5.1	gp160 (79–93) <b>Vaccine</b> <i>Vector/Type</i> <b>Ab type</b> C1 <b>References</b> Akerble		PNPQEVVLVNVTENF HIV component: gp160		Vaccine	murine (IgG)
284	4A7C6	Ab type C1 Donc References Thiriart • 4A7C6: Bound pref • 4A7C6: The relativ • 4A7C6: C1 region of • 4A7C6: Reciprocal	1989, Thali1993, Moore I ferentially to denatured III e affinity for denatured/na epitope (88 N/P substitution	993a, Moore1994c, Moore19 B gp120 [Moore1993a] tive gp120 is 7.9 – mutation ons abrogates binding), but so he antibody 133/192 – enhance	88 N/P impairs binding [Molbstitutions 380 G/F and 420	0 I/R also impaired bind	

HIV Antibodies Tables gp160 Antibodies

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizing	Immunogen	Species(Isotype)
285	1D10	Vaccine Vector/Type: r Ab type C1 References Dowbenko 1D10: Cross-blocks 5E	1988, Berman1991, N 33 in IIIB-rsgp160 EL	PQEVVLVNVTENFDMWKNDM Strain: IIIB HIV component: gp12 [akamura1992, Moore1994c ISA – type specific in rgp120 ELISA ve gp120 is 13 – mutation 88 N/P in	A binding [Nakamura199		rat
286	B242	Vaccine Vector/Type: r Ab type C1 References Bristow199	94	EVVLVNVTEN  Strain: NL43 HIV component: gp  umoral immune response to Baculov		Vaccine ed rgp160 IIIB:NL43	murine (IgG1)  MicroGenSys [Bristow1994
287	133/192	Vaccine Vector/Type: p Ab type C1 Donor M References Niedrig 199  133/192: Epitope seem 133/192: The relative a 133/192: Reciprocal bi 133/192: Does not neut 133/192: A panel of M	Matthias Niedrig 92b, Moore1993c, Moore199	ENFDMWKNDM  HIV component: gp120  ore1994c, Moore1996, Trkola1996a iple peptides – weak neutralization lative gp120 is 1.8 [Moore1994c] 3 D/A or R, 117 K/W, 420 I/R, 427 the antibody 4A7C6 – enhanced by k gp120 interaction with CCR-5 in and with similar or greater affinity and thus such a core protein produces a	of lab strain [Niedrig199 W/S impair binding, oth some anti-C5 and-C1 and a MIP-1beta-CCR-5 comd d similar competition pro	2b] er substitutions enha tibodies [Moore1996 upetition study [Trkol ofiles to a deglycosyl	] a1996a] ated or variable loop deleted
288	489.1(961)	gp160 (91–100) Vaccine Strain: LAI Ab type C1 Donor C References Moore1994  489.1(961): The relativ	gp120 (91–100 LAI) HIV component: Env C. Bruck, SKB, Belgiu 4c ve affinity for denature	ENFDMWKNDM	7 11	Vaccine	murine (IgG)
289	5B3	Vaccine Vector/Type: r Ab type C1 References Berman199 • 5B3: Blocks gp120 -Cl • 5B3: Cross-blocks 1D1 [Nakamura1992]	91, Nakamura1992, Bo D4 binding [Berman19 10 in competitive IIIB-	ENFDMWKNDM  Strain: IIIB HIV component: gp10 eretta1994, Moore1994c ersgp160 ELISA – no neutralization ersgp120 is 8.3 [Moore1994c]		Vaccine  O4 binding – localize	murine (IgG) d binding to residues 72-106
290	B10	gp160 (91–100)	gp120 (91–100 LAI)	ENFDMWKNDM  Strain: LAI HIV component: gp10	50	Vaccine	murine (IgG1)

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizing	Immunogen	Species(Isotype)
		<ul><li>B10: C1 region – e</li><li>B10: The relative a</li></ul>	glu1994, Moore1994c pitope boundaries mapped ffinity for denatured/native I/FDM polymorphism in L	gp120 is 0.4 [Moore1994c		m.)	
291	B2	Ab type C1 References Thali19 B2: C1 region – ep B2: The relative aff	gp120 (91–100 LAI)  e: recombinant protein S  993, Abacioglu1994, Mooritope boundaries mapped b finity for denatured/native g  FDM polymorphism in LA	e1994c, Moore1994d, Binl y peptide scanning, FNMV pp120 is 1.4 [Moore1994c]	ey1997a	Vaccine	murine (IgG2b)
292	C6 (Ch6)	Ab type C1 References Pincus C6: C1 region – ep C6: The relative aff C6: There is FNM/ C6: Called Ch6 – b [Pincus1993a, Pinc	inds to gp120 but not to inf	oore1994c, Pincus1996 y peptide scanning, FNMV p120 is 0.9 [Moore1994c] I-based peptides – N is ess fected cells – when linked t		Vaccine  not mediate cell killin	murine (IgG1) g – sCD4 has no effect
293	MF49.1	<b>Ab type</b> C1 <b>References</b> Thiriar	gp120 (91–100 LAI) AI HIV component: Env t1989, Moore1994c we affinity of denatured/nat	ENFDMWKNDM ive gp120 is 3.8 [Moore19	94c]	Vaccine	murine (IgG)
294	T1.1	Ab type C1 References Akerble T1.1: Also reacted T1.1: No ADCC ac	gp120 (91–100 LAI)  ne: vaccinia HIV compone  om1990, Broliden1990, Mo  in solid phase with gp120(2  tivity – reactive peptide: N  he relative affinity for dena	oore1994c 234-248) NGTGPCTNVST VTENFNMWKNDMVEQ	, IIIB [Broliden1990]	Vaccine	murine (IgG)
295	T7.1	<b>Ab type</b> C1 <b>References</b> Akerble	gp120 (91–100 LAI) AI HIV component: Env om1990, Bolmstedt1990, Maffinity of denatured/native		ı	Vaccine	murine (IgG)

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizing	Immunogen	Species(Isotype)
296	Т9	Ab type C1 Dono References Akerblo T9: There are two H T9: The relative affi	om1990, Bolmstedt1990, M IIV-Abs with the name T9, nity of denatured/native gp region – 45 W/S, 88 N/P, 2		nley1997a	Vaccine d binding, no substit	murine (IgG) ution tested significantly
297	GV4D3	Ab type C1 Dono References Denisov  • GV4D3: When anti-	<b>r</b> Patricia Earl and Christo <sub>l</sub> va1996 ·V3 MAb M77 was bound		nunogen, it stimulated many N	Vaccine IAbs to linear epitop	murine res – MAbs GV4H4 and
298	B27	Ab type C1 References Abacios B27: C1 region – ep	glu1994, Bristow1994 oitope boundaries mapped b	FNMW train: NL43 HIV componer by peptide scanning [Abaciogoral immune response to Bac	O.	Vaccine d rgp160 IIIB:NL43,	murine (IgG1)  MicroGenSys [Bristow1994
299	В9	<b>Ab type</b> C1 <b>References</b> Abaciog	glu1994	FNMW train: LAI HIV component.  pped by peptide scanning [Ab	-	Vaccine	murine (IgG1)
00	B35	Ab type C1 References Abacios	şlu1994	FNMWKN train: LAI HIV component.  by peptide scanning [Abacios		Vaccine	murine (IgG1)
801	D/4B5	<b>Ab type</b> C1 <b>References</b> Bristow	1994	FNMWKNDMV train: LAI HIV component.	no gp120 Baculovirus-expressed mis-fol	Vaccine  ded rgp120 and rgp1	murine 60 [Bristow1994]
302	D/5A11	gp160 (93–101) <b>Vaccine</b> <i>Vector/Type</i> <b>Ab type</b> C1	gp120 (93–101 LAI)	FNMWKNDMV train: LAI HIV component.	no gp120	Vaccine	murine

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizing	Immunogen	Species(Isotype)
		References Bristow • D/5A11: C1 MAb g		numoral immune response to Bac	ulovirus-expressed mis-fo	lded rgp120 and rgp	160 [Bristow1994]
303	D/6B2	<b>Ab type</b> C1 <b>References</b> Bristow	1994	FNMWKNDMV  train: LAI HIV component: gpl  umoral immune response to Bacul		Vaccine  led rgp120 and rgp10	murine (IgG1)  50 [Bristow1994]
304	B18	Ab type C1 References Abacios B18: C1 region – ep	glu1994, Moore1994c	VEQMHEDIIS train: LAI HIV component: gpl by peptide scanning, HEDII core gp120 is 1 [Moore1994c]		Vaccine	murine (IgG2a)
305	B20	Ab type C1 References Abacios • B20: C1 region – ep	glu1994, Moore1994c	VEQMHEDIIS  train: LAI HIV component: gpt  by peptide scanning – HEDII core gp120 is 1 [Moore1994c]		Vaccine	murine (IgG2a)
306	MF39.1 (39.	Ab type C1 References Thiriart  • MF39.1: Called 39. negative cells from a does not inhibit MA	the brain and colon – MAb b binding [Cook1994]	VEQMHEDIIS  194c e as MF39.1 – MAbs against the gs against the N-terminal half of g  ve gp120 is 30 [Moore1994c]			
307	187.2.1 (187.1)	Ab type C1 Dono References Thiriart • 187.2.1: Called 187 • 187.2.1: Called 187 negative cells from a does not inhibit MA • 187.2.1: The relative	.1, and is probably the sam. .1, and is probably the sam: the brain and colon – MAb: b binding [Cook1994]	hilde Thiriart 994, Moore1994c, Moore1994d e as 187.2.1 – bound preferential e as 187.2.1 – MAbs against the s s against the N-terminal half of g ive gp120 is 7 – mutations 113 D	lycosphingolipid GalCer 120 do not inhibit gp120	block HIV infection binding to GalCer –	binding of GalCer to gp120
308	37.1.1(ARP	gp160 (101–120)	gp120 (101–120 LAI)	VEQMHEDIISLWDQSLKPCV		Vaccine	murine (IgG)

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizing	Immunogen	Species(Isotype)
		<ul><li>37.1.1: Called 37.1 -</li><li>37.1.1: The relative at the second second</li></ul>	1989, Moore1993a, Moore bound preferentially to c	denatured IIIB gp120 [Moore199 ve gp120 is 8.6 – mutations 113		W impair binding [M	oore1994c]
309	6D8	<ul><li>Ab type C1</li><li>References Dowben</li><li>6D8: Highly cross re</li></ul>	ako1988, Nakamura1992, eactive with multiple stain	Strain: IIIB HIV component: gj	992]	Vaccine  ling [Moore1994c]	rat
310	M96	Ab type C1 Donor References diMarzo • M96: Immunoblot re		nt: Env se	Veronese1992]	Vaccine	rat (IgG2a)
311	MF119.1	<b>Ab type</b> C1 <b>References</b> Thiriart		VEQMHEDIISLWDQSLKPC		Vaccine  K/W impair binding [	murine (IgG)  Moore1994c]
312	MF4.1	<b>Ab type</b> C1 <b>References</b> Thiriart		VEQMHEDIISLWDQSLKPC	V	Vaccine	murine (IgG)
313	MF53.1	<b>Ab type</b> C1 <b>References</b> Thiriart	<i>'</i>	VEQMHEDIISLWDQSLKPC	V	Vaccine	murine (IgG)
314	MF58.1	gp160 (101–120) Vaccine Strain: LAI Ab type C1 References Thiriant	gp120 (101–120 LAI) I HIV component: Env	VEQMHEDIISLWDQSLKPC	V	Vaccine	murine (IgG)
	MF77.1	gp160 (101–120)	gp120 (101–120 LAI)	VEQMHEDIISLWDQSLKPC		Vaccine	

No.	MAb ID	<b>HXB2</b> Location	Author's Location	Sequence	Neutralizing Immunogen	Species(Isotype)
		Ab type C1 References Thiriart19 • MF77.1: The relative		ve gp120 is 11 [Moore1994c]		
316	T2.1	<b>Ab type</b> C1 <b>Donor References</b> Akerblom	1990, Bolmstedt1990, M	VEQMHEDIISLWDQSLKPCV  Wahren and Jorma Hinkula oore1994c, Moore1994d gp120 is .27 – mutations 113 D/R, 106	Vaccine E/A, and 117 D/A impair binding [Moo	murine (IgG)  ore1994c]
317	11/65 (11/65a/5h)	Ab type C1 References McKeatir  11/65: Binds only sol  11/65: Called 11/65a/ immunogenic – these mice injected with ser	ng1992a, McKeating1993b uble gp120, not virion bou 5h – The most variable an changes did not affect the	and – used to quantify gp120 shedding- nino acids in the V3 loop were replaced ability of sCD4 or MAbs to V1/V2, C1 a reduced response relative to wildtype	with serines to make the immunodomi and C4 to bind – 11/65 was not affected	inant V3 loop less ed by V3 serine substitutions –
318	W1	<b>Ab type</b> C1 <b>Donor</b> <b>References</b> Moore 19	94c	EQMHEDIISLWDQSLKPCVK p120 is 6 – mutations 113 D/A, 113 D/I	Vaccine  R, and 117 K/W impair binding [Moore	murine (IgG)
319	T11	Ab type C1 Donor References Earl1994. • T11: Generated durin • T11: The sulfated pol	R. Doms, Univ. of Pennsy Jagodzinski 1996 g a study of the influence	of the oligomeric structure of Env in de te (CRDS), binds to the Envelope of T-		
320	GV1A8	Ab type C1 References Denisova • GV1A8: When anti-V	1996 73 MAb M77 was bound t	HEDIISLWD  *V component: gp120 complexed with N  o gp120 and used as an immunogen, it is enerated in the same experiment [Denis	stimulated many MAbs to linear epitop	murine bes – MAbs GV7A4 and
321	11	gp160 (111–120) Vaccine Strain: LAI Ab type C1	gp120 (101–120 LAI) HIV component: Env	LWDQSLKPCV	Vaccine	murine (IgG)

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizing	Immunogen	Species(Isotype)
		References Thiriart1 • 11: The relative affin		o120 is 7.8 – mutation 113 D/	R impairs binding [Moore19	94c]	
322	12G10	<b>Ab type</b> C1 <b>References</b> Thiriart1		LWDQSLKPCV  ve gp120 is 17 - mutation 117	K/W impairs binding [Moor	Vaccine re1994c]	murine (IgG)
323	135/9 (87-135/9)	Ab type C1 Donor References Niedrig1  135/9: Defines the ep  135/9: The relative a [Moore1994c]  135/9: Substitutions  135/9: Binding is enl predicted alpha-helix  135/9: Does not neut  135/9: A panel of M. core gp120 protein (  135/9: Noted to bind antibodies which bin  135/9: A combinatio trimers (gp140-GNC F91) and CD4i (17b gp140-GNC4 glycop	992b, Moore1994c, Moore of the property of the	e1994d, Moore1996, Trkola1 MHEDIISLWD (core LWD?) e gp120 is 15 – mutation 113 and 117 K/W impair binding, so and anti-C5 antibodies – enhant 120 interaction with CCR-5 in ith similar or greater affinity is such a core protein product DQSLK – blocks gp120 interaction (F105, 388/389, and b12) [IGNC4 trimeric sequences and e some neutralizing epitopes D-GNC4 as well as gp120 or gmpared to gp120 – MAbs dir	weak neutralization of lab D/R impairs binding to native ome substitutions enhance because binding of some anti-V3, as a MIP-1beta-CCR-5 competent similar competition profits a structure closely approximation with CD4+ cells – blockropelin 1998] disruption of the YU2 gp12 while occluding some non-neutralizing MA	strain [Niedrig1992 e and denatured, 11: inding [Moore1994c, anti-C4 and anti-V etition study [Trkola iles to a deglycosyla imating full length focking activity is ad-0-gp41 cleavage site eutralizing epitopes Abs C11, A32, 522-1	3 D/A only to denatured d] 2 MAbs – 135/9 binds to 1996a] ted or variable loop deleted olded monomer [Binley1998] ditive when combined with e resulted in stable gp140
324	7C10	<b>Ab type</b> C1 <b>References</b> Thiriart1		LWDQSLKPCV gp120 is 5.8 - mutation 117	K/W impairs binding [Moore	Vaccine e1994c]	murine (IgG)
325	C4	Ab type C1 Donor References Abaciog C4: Bound preferent C4: C1 region – epito	George Lewis lu1994, Moore1993a, Moo ially to denatured IIIB gp1	20 [Moore1993a] peptide scanning, BH10 core	-	Vaccine	murine (IgG1)

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizing	Immunogen	Species(Isotype)
326	MF46.1	Ab type C1 References Thiriart1		LWDQSLKPCV ive gp120 is 8.5 [Moore1994c]		Vaccine	murine (IgG)
327	6D5	gp160 (122–141) Vaccine Strain: LAI Ab type V2 Donor References Moore 19	gp120 (122–141 LAI) HIV component: Env r S. Nigida and L. Arthur, 1994c, Moore1994d	LTPLCVSLKCTDLKNDTNTN	5 and 125 L/G impair	Vaccine r binding [Moore1994c	murine (IgG)
328	B33	Ab type V2 Donor References Abaciog B33: There are two N B33: Epitope bounda B27: C1 MAb gener	r Daniels lu1994, Bristow1994 MAbs in the literature nam aries mapped by peptide so ated in a study of the humo	TPLCVSLKCTDLGNATNTNS  rain: NL43 HIV component: gp160  ed B33, see also gp160(727-734) [Abanning [Abacioglu1994]  oral immune response to Baculovirus- gent: ARP304, gp160/41 binding	pacioglu1994]	Vaccine d rgp160 IIIB:NL43, M	murine (IgG2bκ) iicroGenSys [Bristow1994]
329	polyclonal (VEI1)	positive subjects, inc	the epitopes in a vaccine luding sera from 6 non-sul	CTDLKNDTNTNSSSGRMMMEK  construct (VEI) containing peptides for type B infections – serum samples for gions, but most consistently against the	rom San Francisco, C	anada and Puerto Rico	cohort showed presence of
330	35D10/D2			NTKSSNWKEMDGEIK  rain: SF162 HIV component: gp120 lic Health Research Institute, Newark			human from transgenic mice (IgG2 $\kappa$ )
		References He2002 • 35D10/D2: Transger create a panel of anti neutralizing the auto	nic mice (strain XenoMous -HIV gp120 MAb-produci	e G2) carrying human genes allowing ing hybridomas by immunization with region was immunodominant in thes	g production of fully n HIV SF162 gp120 -	human IgG2kappa MA – several of the MAbs o	obtained were effective at
331	40H2/C7	gp160 (139–155)	gp120	NTKSSNWKEMDGEIK	L	Vaccine	human from transgenic mice (IgG2κ)

**Vaccine** *Vector/Type:* recombinant protein *Strain:* SF162 *HIV component:* gp120 *Adjuvant:* Ribi adjuvant (MPL+TDM) **Ab type** V1 **Donor** Dr. Abraham Pinter, Public Health Research Institute, Newark, NJ, pinter@phri.org

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizing	Immunogen	Species(Isotype)
		create a panel of anti neutralizing the auto	ic mice (strain XenoMou i-HIV gp120 MAb-produ	use G2) carrying human genes allow ucing hybridomas by immunization V1- region was immunodominant in e specific [He2002]	n with HIV SF162 gp120 -	several of the MAb	s obtained were effective at
332	43A3/E4	gp160 (139–155)	gp120	NTKSSNWKEMDGEIK		Vaccine	human from transgenic mice (IgG2κ)
		V 1	<b>r</b> Dr. Abraham Pinter, P	Strain: SF162 HIV component: gublic Health Research Institute, Ne	C1 9	, ,	
		a panel of anti-HIV aneutralizing the auto	gp120 MAb-producing h	se G2) carrying human genes allow hybridomas by immunization with 1 V1- region was immunodominant in e specific [He2002]	HIV SF162 gp120 – severa	al of the MAbs obtai	ned were effective at
333	43C7/B9	gp160 (139–155)	gp120	NTKSSNWKEMDGEIK	L	Vaccine	human from transgenic mice (IgG2κ)
		Ab type V1 Dono References He2002 • 43C7/B9: Transgeni a panel of anti-HIV neutralizing the auto	r Dr. Abraham Pinter, Po c mice (strain XenoMou gp120 MAb-producing b	Strain: SF162 HIV component: gublic Health Research Institute, Ne se G2) carrying human genes allow hybridomas by immunization with 1/21- region was immunodominant in e specific [He2002]	wark, NJ, pinter@phri.org ving production of fully hu HIV SF162 gp120 – severa	man IgG2kappa MA al of the MAbs obtai	bs were used to rapidly created were effective at
334	45D1/B7	gp160 (139–155)	gp120	NTKSSNWKEMDGEIK	L	Vaccine	human from transgenic mice $(\operatorname{IgG2}\kappa)$
			<b>r</b> Dr. Abraham Pinter, Pr	Strain: SF162 HIV component: qublic Health Research Institute, Ne			
		create a panel of anti- neutralizing the auto	i-HIV gp120 MAb-produ	use G2) carrying human genes allow ucing hybridomas by immunization V1- region was immunodominant in the specific [He2002]	n with HIV SF162 gp120 -	several of the MAb	s obtained were effective at
335	46E3/E6	gp160 (139–155)	gp120	NTKSSNWKEMDGEIK		Vaccine	human from transgenic mice
							$(IgG2\kappa)$

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizing	g Immunogen	Species(Isotype)
		a panel of anti-HIV neutralizing the auto	c mice (strain XenoMous gp120 MAb-producing h	e G2) carrying human genes al ybridomas by immunization wi 1- region was immunodominal specific [He2002]	th HIV SF162 gp120 – seve	ral of the MAbs obta	ained were effective at
336	58E1/B3	gp160 (139–155)	gp120	NTKSSNWKEMDGEIK	L	Vaccine	human from transgenic mice (IgG2κ)
		Ab type V1 Dono References He2002 • 58E1/B3: Transgeni a panel of anti-HIV neutralizing the auto	r Dr. Abraham Pinter, Pu c mice (strain XenoMous gp120 MAb-producing h	Strain: SF162 HIV componer blic Health Research Institute, e G2) carrying human genes all ybridomas by immunization with region was immunodominal specific [He2002]	Newark, NJ, pinter@phri.or lowing production of fully h th HIV SF162 gp120 – seve	g uman IgG2kappa M ral of the MAbs obta	Abs were used to rapidly creation
337	64B9/A6	gp160 (139–155)	gp120	NTKSSNWKEMDGEIK	L	Vaccine	human from transgenic mice $(IgG2\kappa)$
		References He2002  • 64B9/A6: Transgenic create a panel of ant neutralizing the auto	ic mice (strain XenoMous i-HIV gp120 MAb-produ	blic Health Research Institute, se G2) carrying human genes a cing hybridomas by immuniza 1- region was immunodominal specific [He2002]	llowing production of fully better that the state of the	numan IgG2kappa M – several of the MA	bs obtained were effective at
338	69D2/A1	gp160 (139–155)	gp120	NTKSSNWKEMDGEIK	L	Vaccine	human from transgenic mice (IgG2κ)
			<b>r</b> Dr. Abraham Pinter, Pu	Strain: SF162 HIV componer blic Health Research Institute,			\ E /
		create a panel of ant neutralizing the auto	i-HIV gp120 MAb-produ	se G2) carrying human genes a cing hybridomas by immuniza 1- region was immunodominal specific [He2002]	tion with HIV SF162 gp120	- several of the MA	bs obtained were effective at
339	82D3/C3	gp160 (139–155)	gp120	NTKSSNWKEMDGEIK		Vaccine	human from transgenic mice (IgG2κ)
				Strain: SF162 HIV componer blic Health Research Institute,			

gp160 Antibodies

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizing	Immunogen	Species(Isotype)
	•	create a panel of anti neutralizing the autol	-HIV gp120 MAb-produc	ing hybridomas by immuni - region was immunodomin	s allowing production of fully h zation with HIV SF162 gp120- nant in these mice and the ten V	- several of the MAb	s obtained were effective at
340	2H1B	Ab type C3 References Matsush		RNISFKA  ROD  n the cell surface [Matsush	no ita1995]	Vaccine	murine
341		References Gorny 19 Hioe 2000, Nyambi 20 697-D: Conformation substitutions 176/177 binding – mild oxida 697-D: Not neutraliz 697-D: Review: calle 697-D: Partial inhibit 697-D: Study shows bound monomer, did 697-D: Using a whol V2 Abs 697-D, 1361 B clade viruses (CAS 697-D: Called 697-36 but it enhances its ne	94, Forthal 1995, Moore 1900, Edwards 2002, Maksimal with weak reactivity to 7 FY/AT, 179/180 LD/DL, tion of carbohydrate moieing, no ADCC activity, and 697/30D – neutralizes stion of gp120 interaction vneutralization is not predict not bind oligomer or neutralize TCLA strains but ne virion-ELISA method, 1, and 1357 tended to bind 5), and weak binding to vir 0D – deleting the V2 loop	p95b, Trkola1996a, Binley butov2002 vV2 peptide ISTSIRGKVQ 183/184 PI/SG, and 192-1 ties inhibits binding [Gorned no viral enhancing activity ome primary, but not lab activity of the complex of the com	NYU Med. Center) or Cellular F 1997a, Fouts 1997, Parren 1997c, 2KEYAFFYKLD – neutralized 194 YSL/GSS abrogate binding 1994] 19 [Forthal 1995] 19 [Appreciation of the properties of the propert	, Nyambi1998, Stama 3/4 primary isolates, – anti-C4 MAbs G3-: cola1996a] sociated with oligomanel of 9 viruses from bound well to soluble	eric Env binding – 697-D  clades A, B, D, F, G, and H – e gp120: weak binding to 1/4  n in PBMC or macrophages,
	•	<ul> <li>697-D: Binding of pa anti-V3 and CD4BS</li> </ul>	anel of 21 MAbs to soluble	e neutralization by V2 MA e oligomeric gp140 versus the oligomer and V2 and C	bs G3.4, G3.136, or 687-30D [8 gp41 or gp120 monomers was 6 tended to favor the monomer	compared – no MAb	was oligomer specific, though

binding, with the most frequent binding to C and D clades [Nyambi2000]

• 697-D: 26 HIV-1 group M isolates (clades A to H) were tested for binding to 47 MAbs, including 5 anti-V2 MAbs, which showed weak and sporadic

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizing	Immunogen	Species(Isotype)
		bound state of the exite dependent MAb viruses bearing the taurface expression of 697-D: Called 697D gp120 MAb product as controls [He2002	external Envelope, enhancing 2G12 and the anti-gp41 Maruncation were more sense of the mutated proteins [Eco. — Transgenic mice carrying hybridomas by immunical]	ng binding of CD4i MAb MAb 246D – in contrast, itive to neutralization by dwards2002] ng human genes allowing ization with HIV SF162	X4, R5, and X4R5 viruses forces a bit 17b and 48d and of CD4BS MAI binding of the anti-V2 MAb 697D MAbs 48d, b12, and 2G12 – the aug production of fully human MAbs gp120 – the previously described by the prophage colony stimulating factor I	bs F105, b12, and in m and the anti-V3 MAb nti-C5 MAb 1331A wa were used to rapidly c numan MAbs 5145A, 4	ost cases of glycosylation 694/98D were not affected – as used to track levels of cell create a panel of anti-HIV 4117C and 697D were used
342	6C4/S	<b>Donor</b> S. Ranjbar (I <b>References</b> Moore1			0	Vaccine	
343	C108G	References Warrier  C108G: Chimps we disulfide bonds – bin C108G: Strain specin increased epitope ex  C108G: Characteriz  C108G: Synergistic neutralization further  C108G: Viral bindir [Ugolini1997]  C108G: Inhibits HX  C108G: A study of the company of the comp	re infected with HIV-1 IIII anding disrupted by remova ifficity: LAI, BaL, HXB2 – Eposure [Wu1995] ation of MAb variable regneutralization of HIV-1 wer enhanced by presence of in inhibition by C108G was a continuous to both CD4 per anti-Env MAbs and their	tute, NY, NY  95, Warrier1996, Ugolin: B, and this high affinity Mal of N-linked glycans – p-conformational character  cion [Warrier1995] Then combined with antifoth 1125H and 0.5beta as correlated with neutral  cositive and negative HeL  r ability to bind or direct	lization (all other neutralizing MA	HIV-1 IIIB – binding n glycosylated Env [War al – mutation of conser nti-CD4BS MAbs, 112 os tested showed some	rrier1994] ved glycosylation site at 156 25H and 5145A – correlation except 2F5)
344	10/76b	References McKeat  10/76b: R to L subs  10/76b: Cross-comp  10/76b: Included in  10/76b: HX10 strain  10/76b: Neutralizes	petes with MAbs 10/76b and cross-competition and new a specificity – binds native	Strain: BH10 HIV comp 3a, Shotton1995, Wu199 — human sera recognize and 11/4b — HXB2 neutral attralization studies [Shot b, deglycosylated, or dena- lize chimeric virus with §	25, McKeating1996b epitope [McKeating1993b] lization escape mutant has the subston1995]		
345	11/41e	gp160 (162–170)	gp120 (162–171) e: recombinant protein S	STSIRGKVQ	L (HXB10)	Vaccine	rat (IgG1)

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizing	Immunogen	Species(Isotype)
		<ul><li>11/41e: R to L abro</li><li>11/41e: Included in</li></ul>	cross-competition and neu	Vu1995 a recognize the epitope [McKeating1993b atralization studies [Shotton1995] and deglycosylated gp120 [Wu1995]	<b>b</b> ]		
346	11/4b	References McKea  11/4b: A change fro  11/4b: Cross-comp  11/4b: HXB10 stra  11/4b: Linear V2 e	ating 1993b, Shotton 1995, Wom R to L abrogated binding etes with MAbs 10/76b and in specificity – binds native pitope – reciprocal binding	STSIRGKVQ  train: BH10 HIV component: gp120  Vu1995, Moore1996  ng – human sera recognize epitope [McKeth 11/4c – HXB2 neutralization escape mutter, deglycosylated, or denatured gp120 [With enhancement of anti-V2 discontinuous epiding – inhibits CRA-3 binding CRA-3 do	tant has the substi u1995] pitope antibodies	(in contrast to BAT0	
347	RSD-33	gp160 (162–170) Vaccine Vector/Typ Donor R. Daniels ( References Moore		STSIRGKVQ  HIV component: gp120		Vaccine	
348	11/4c (11/4c/1j/4j)	Ab type V2 References McKea  11/4c: R to L subst  11/4c: HX10 strain  11/4c: Cross-comp  11/4c: Called 11/4c immunogenic – the mice injected with	ating 1993b, Wu1995, Shotte itution abrogated binding – specificity – binds native, of etes with MAbs 10/76b and c/1j/4j – The most variable is se changes did not affect th	human sera recognize epitope [McKeatin deglycosylated, or denatured gp120 [Wu1 l 11/4b – HXB2 neutralization escape mulamino acids in the V3 loop were replaced to ability of sCD4 or MAbs to V1/V2, C1 ld a reduced response relative to wildtype,	995] tant has the substitute with serines to mand C4 to bind —	ake the immunodon 11/4c was not affect	ninant V3 loop less ed by V3 serine substitutions
349	8.22.2	V 1		TTSIRDKVQKEYALFYK  train: SF162 HIV component: gp120  blic Health Research Institute, Newark, N	0	•	human from transgenic mice ( $IgG2\kappa$ )
		References He2002 • 8.22.2 : Transgenic panel of anti-HIV g neutralizing the aut with BaL and JR-F.	2, Maksiutov2002 mice (strain XenoMouse C p120 MAb-producing hybrologous strain – 8.22.2 was L, two B clade R5 strains, b	G2) carrying human genes allowing production with HIV SF16 sthe only V2-specific MAb created and it but not B clade X4 or E clade viruses, and f the human protein macrophage colony st	ction of fully hum 2 gp120 – several could cross-comp l it could weakly i	nan IgG2kappa MAb of the MAbs obtain pete with MAb 697L neutralize autologou	ned were effective at D – 8.22.2 could cross-react s strain SF162 [He2002]

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizing	Immunogen	Species(Isotype)
350	12b	Ab type V2 References Shotton • 12b: V2 MAb neutr • 12b: Neutralizes HX	1995, McKeating1996b, alized HXB2 – position 1 KB2, but fails to neutraliz	79-180 LD to DL abrogates binding – e chimeric virus with gp120 from prim	competes with 60b, bary isolates in an HX	B2 background [Mc	Keating1996b]
351	G3-136 (G3.136)	gp160 (170–180)  Vaccine Vector/Type Ab type V2 Dono References Fung19 Poignard1996a, Bin G3-136: V2 region- sCD4 binding inhibi G3-136: Conformat gp120 [Moore1993a G3-136: Binding en binding site MAbs [ G3-136: HIV-1 RF G3-136: The bindin with differences in c gp120 monomer as i G3.136 don't bind to G3-136: Bound pref G3-136: Called G3. primary macrophage G3-136: Called G3. primary macrophage G3-136: Called G3. but it enhances its not through F – deletion G3-136: Called G3. revealed that these s 391-95D) – V2-regio	gp120 (170–180 IIIB) are recombinant protein for Tanox Biosystems Inc. 192, Pirofski1993, Thali19 ley1997a, Stamatatos199 binds and neutralizes II at similar to peptide, binding to make the form of the first binding (contrast with ional, does not bind well in inding to peptide, binding hanced by selected antibout Moore 1993b] W2 substitutions 177 Y/H g of conformation-dependent tropism was studied indicated by an increase in the first tropic SF2 [Stam Ferentially to the monome epitope as STSIRGKVKI from virus or expose the grand Fab binding to the olimation of Ab sites occuping 136 – deleting the V2 loce cutralization sensitivity to 136 – SF162 is a neutralities prevent neutralization on glycosylation site mut	Strain: IIIB HIV component: gp120 and David Ho, ADARC, NY 293, Moore1993a, Moore1993b, Yoshiy 7, Ditzel1997, Wyatt1997, Parren1998; IB and RF in CEM-SS cells, but not M BAT085) – deglycosylation or reduction to denatured gp120 – not reactive with g inhibited by 183/184 PI/SG substitution to compose the compose of RF reduced and 179 L/P in the V2 loop of RF reduce	L  rama1994, Sattentau1 a, Stamatatos1998, Ly N – neutralization aco on of gp120 by DTT of SF-2 gp120, and does on [Moore1993b] binding site MAbs – of ace affinity [Yoshiyar MAbs to monomeric ded in the oligomeric facrophage-tropic iso gp120 – neutralizes of to anti-V3 MAbs G3- of to anti-V3 MAbs [Pointi-V2 MAb G3-4 – its gp120 epitope is a finity [Yoshiyar MAbs G3-4 – its gp120 epitope finity [Yoshiyar MAbs G3-4 – its gp120 epi	Vaccine  1995b, Stamatatos 19 y2000 tivity against a few programmer of the programme	murine (IgG)  95, Moore1996,  orimary isolates in PBMC –  [Fung1992]  sera from binding to IIIB  selected V3, C4 and anti-CD4  ed gp120 from HIV-1 isolates the virion surface relative to the 28a – anti-V2 MAbs G3-4 and  entau1995b] 23 did not significantly alter  SF162 or SF128A in either  binding [Wyatt1997] test that neutralization is on in PBMC or macrophages, sitivity to sera from clades A  oop of the SF162 gp120 by V3 MAbs (447-D and CD4i MAbs (17b and 48d) –

gp160 Antibodies

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizing	Immunogen	Species(Isotype)
352	G3-4 (G3.4)	gp160 (170–180) <b>Vaccine</b> <i>Vector/Type:</i>	gp120 (170–180 BH10) protein <i>Strain:</i> IIIB <i>HI</i>		L	Vaccine	murine (IgG2bκ)
		V 1	Tanox Biosystems Inc and	1 21			
		References Ho1991a	, Ho1992, Fung1992, McK	eating1992a, Moore1993a, Sullivan1993	, Sattentau 1993,	Thali1993, Moore199	93b, Moore1994b,

**References** Ho1991a, Ho1992, Fung1992, McKeating1992a, Moore1993a, Sullivan1993, Sattentau1993, Thali1993, Moore1993b, Moore1994b, Gorny1994, Thali1994, Yoshiyama1994, Stamatatos1995, Wu1995, Sattentau1995b, Jagodzinski1996, Moore1996, Poignard1996a, Binley1997a, Stamatatos1997, Ditzel1997, Wyatt1997, Parren1998a, Stamatatos1998, Ly2000, Srivastava2002

- G3-4: Binding is sensitive to removal of glycans by endo H 50% neutralization of 4/9 primary isolates has conformational features [Ho1991a]
- G3-4: Neutralizes IIIB and RF, not MN blocks sCD4-gp120, not as potent as MAb 15e V2 binding MAbs BAT085 and G3-136 block G3-4 gp120 binding sensitive to reduction of gp120 by DTT [Ho1992]
- G3-4: Substitutions in residues 176 to 184 affect MAb recognition substitutions in V2 can result in gp120-gp41 dissociation [Sullivan1993]
- G3-4: Increased binding in the presence of sCD4 [Sattentau1993]
- G3-4: Conformational, does not bind well to denatured gp120 not reactive with SF-2 gp120, and does not inhibit HIV-1 sera from binding to IIIB gp120 [Moore1993a]
- G3-4: V2 region, marginal binding to peptide, binding inhibited by 183/184 PI/SG substitution [Moore1993b]
- G3-4: Conformationally sensitive sporadic cross-reactivity among, and outside, B clade gp120s [Moore1994b]
- G3-4: Weakly neutralizing, IC 50 = 53 mug/ml [Gorny1994]
- G3-4: gp41 mutation (582 A/T) that reduces neutralization of anti-CD4 binding site MAbs does not alter G3-4s ability to neutralize [Thali1994]
- G3-4: Neutralizes RF substitutions 177 Y/H and 179 L/P in the V2 loop of RF reduce affinity and result in neutralization escape [Yoshiyama1994]
- G3-4: The binding of conformation-dependent anti-V2, anti-V3, and anti-CD4BS MAbs to monomeric and virion-associated gp120 from HIV-1 isolates with differences in cell tropism was studied V2 loop epitopes are somewhat occluded in the oligomeric gp120 epitopes on the virion surface relative to the gp120 monomer as indicated by an increase in the half-maximal binding values to macrophage-tropic isolates SF162 and SF128a anti-V2 MAbs G3-4 and G3.136 don't bind to T-cell tropic SF2 [Stamatatos1995]
- G3-4: Reactive with BH10, RF, and MN binds native, but not denatured or deglycosylated gp120, binds to deglycosylated V1V2 fusion protein, suggesting importance of glycans outside the V1V2 region [Wu1995]
- G3-4: Bound preferentially to the monomeric rather than oligomeric form of LAI gp120 neutralizes Hx10 cell-free virus [Sattentau1995b]
- G3-4: The sulfated polysaccharide curdlan sulfate (CRDS) binds to the Envelope of T-tropic viruses and neutralizes virus deletion of the V3 loop from gp120 results in more potent G3-4 binding inhibition by CRDS – G3-4 epitope described as 176-184 FYKLDIIPI and 191-193 YSL [Jagodzinski1996]
- G3-4: Binding enhanced by selected antibodies to C1, C4, C5, V3 and anti-CD4 binding site MAbs enhances binding of selected V3, C4 and anti-CD4 binding site MAbs [Moore1996]
- G3-4: Described epitope as STSIRGKVKEYAFFYKLDI binds oligomer binding of V2 MAbs G3-136, G3-4 or BAT085 did not significantly alter gp120 dissociation from virus or expose the gp41 epitope of MAb 50-69, in contrast to anti-V3 MAbs [Poignard1996a]
- G3-4: Called G3.4 mediates gp120 virion dissociation in contrast to anti-V2 MAb G3-136 not neutralizing for SF162 or SF128A in either primary macrophages or PBMC [Stamatatos1997]
- G3-4: Binds both gp120 and soluble gp120+gp41 complex efficiently, suggesting its gp120 epitope is not blocked by gp41 binding [Wyatt1997]
- G3-4: The MAb and Fab binding to the oligomeric form of gp120 and neutralization were highly correlated authors suggest that neutralization is determined by the fraction of Ab sites occupied on a virion irrespective of the epitope [Parren1998a]
- G3-4: Called G3.4 Deleting the V2 loop of neutralization-resistant HIV-1 isolate SF162 does not abrogate its replication in PBMC or macrophages, but it enhances its neutralization sensitivity to sera from patients with B clade infection up to 170-fold, and also enhances sensitivity to sera from clades A through F deletion of V1 or V2 did not enable neutralization by V2 MAbs G3.4, G3.136, or 687-30D [Stamatatos1998]

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutr	ralizing Immunogen	Species(Isotype)
		that these sites prev V2-region glycosyla glycosylation site m [Ly2000] • G3-4: Called G3.4	ent neutralization by CD41 ation site mutations did no nodification allows infection—Oligomeric gp140 (o-gp)	BS MAbs (IgG1b12 and talter neutralization resion of macrophages, probable) derived from R5 pri	IgGCD4), and protect again stance to V2 MAbs (G3.4 a ably due to glycosylated for imary isolate US4 was characteristics.	odifications in the V2 loop of nst neutralization by V3 MA and G3.136) or CD4i MAbs of rms requiring fewer CCR5 materized for use as a vaccine erized MAbs – G3.4 recognizer	bs (447-D and 391-95D) – (17b and 48d) – V2 colecules for viral entry
353	BAT085 (BAT-085)	Donor Tanox Biosy References Fung 19 Wu1995, Sattentau 1 BAT085: V2 region reduction of gp120 BAT085: Called BA binding to IIIB gp1: BAT085: 7/8 V2 mi BAT085: Peptide af neutralization [Moo BAT085: Multi-lab BAT085: Neutralization [Yoshiyama1994] BAT085: HXB10 st BAT085: Bound pro BAT085: Binding is MAb 48d binding [ BAT085: Epitope st dissociation from vi BAT085: The MAb	1995b, Moore 1996, Poignal – sCD4 does not block – sdoes not diminish reactivit XT-85 – conformational, do 20 [Moore 1993a] urine MAbs required gp12 finities of G3-136 and G3-re 1993b] study for antibody charact with two overlapping pepties RF – substitution 177 Yearain specificity – binds nate after the specificity – binds nate after the specificity of the monomes blocked by other V2 region Moore 1996] suggested to be QKEYAFF irus or expose the gp41 epi and Fab binding to the oli	ADARC, NY Ba, Pirofski1993, Thali19 ard1996a, Binley1997a, Ineutralizes IIIB and som by [Fung1992] bees not bind well to dena 0 native structure to bind 4 are 100-fold less than berization and assay com des with region of overla by H in the V2 loop of RF beive, deglycosylated, or or by the cive, deglycosylated, or or by the cive, deglycosylated, or or by the cive of matibodies, enhanced by KLD – binds oligomer by tope of MAb 50-69, in or by gomeric form of gp120	p93, Moore1993b, D'Souza Ditzel1997, Parren1998a are primary isolates, but not I tured gp120 – not reactive v1, but BAT085 was the exce BAT085, but BAT085 has I parison – did not bind MN ap KEYAFFYKLD [Gornyl does not inhibit neutralization of LAI gp120 – neu by several anti-C1 MAbs, a – binding of V2 MAbs G3-contrast to anti-V3 MAbs [F	ion, in contrast to MAbs G3- atralizes cell free Hx10 [Satte and anti-V3 MAb G511 – rec -136, G3-4 or BAT123 did n Poignard1996a] hly correlated – authors sugg	elycosylation or DDT ot inhibit HIV-1 sera from e1993b] 00 and is weaker at 4 and SC258 entau1995b] ciprocal enhancement of CD4 ot significantly alter gp120
354	60b	<ul><li>References Shotton</li><li>60b: V2 MAb did n</li></ul>		train: BH10 HIV com	- substitutions 179-180 LD/	Vaccine DL and 191-193 YSL/GSS	rat (IgG2b) abrogate binding, as do
355	74	gp160 (172–181) Vaccine Vector/Typ References Shotton	gp120 (172–181)  e: recombinant protein S	EYAFFYKLDI train: BH10 HIV com	no ponent: gp120	Vaccine	rat (IgG1)

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizing	Immunogen	Species(Isotype)
				t bind rgp120 ELISA – position 179 nd is enhanced by two conformation			nges outside the minimum
356	38/12b	References Wu1995	e: protein Strain: BH10	) EYAFFYKLDIIPIDNDTTSY  HIV component: gp120  - binds native and deglycosylated g	p120 [Wu1995]	Vaccine	rat
357	38/60b	References Wu1995	e: protein Strain: BH10	HIV component: gp120 e and deglycosylated gp120 [Wu199	95]	Vaccine	rat
358	polyclonal (VEI2)	positive subjects, in	o the epitopes in a vaccine cluding sera from 6 non-su	FYKLDIVPIDNTTTSYRLISC construct (VEI) containing peptides btype B infections – serum samples egions, but most consistently against	from San Francisco, C	anada and Puerto Rico	cohort showed presence of
359	322-151	<b>Donor</b> G. Robey, A <b>References</b> Moore1	994c, Moore1994d	EPIPIHYCAPA IV component: Env gp120 is 30 [Moore1994c]		Vaccine	murine (IgG)
360	3D3.B8	References Bolmste	gp120 (211–220 LAI) e: recombinant protein Hedt1990, Moore1994c e affinity denatured/native	EPIPIHYCAPA  IV component: Env  gp120 is greater than 10 [Moore199	4c]	Vaccine	murine (IgG)
361	4C11.D8	References Bolmste	gp120 (211–220 LAI) e: recombinant protein H edt1990, Moore1994c ve affinity denatured/native	EPIPIHYCAPA  IV component: Env e gp120 is greater than 10 [Moore19	94c]	Vaccine	murine (IgM)
362	493-156	<b>Donor</b> G. Robey, A <b>References</b> Moore1	994c	EPIPIHYCAPAGFAILKCNN  IV component: Env  gp120 is >10 [Moore1994c]		Vaccine	murine (IgG)
363	110.1	References Pincus 1	gp120 (200–217) e: recombinant protein H 993a, Pincus1996, Valenzu her antibody with this ID the		no 0 in LAI, see [Gosting	Vaccine	human

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizing	Immunogen	Species(Isotype)
					ricin A – immunotoxins mediat 4 has no effect [Pincus1993a, l		lling was not directly
364	GV4H3	References Denisov			lexed with MAb M77 munogen, it stimulated many M	Vaccine  1Abs to linear epitopo	murine es [Denisova1996]
365	J1	Donor J. Hoxie, U. 1 References Moorel!  J1: The relative affin  J1: MAbs against the	994c, Moore1994d, Cook19 hity denatured/native gp120 e glycosphingolipid GalCer	is 30 [Moore1994c] block HIV infection of no	rmally susceptible CD4 negativ ling of GalCer to gp120 does n		
366	J3	Donor J. Hoxie, U. J References Moorel! • J3: The relative affin • J3: MAbs against the	994c, Cook1994 iity denatured/native gp120 e glycosphingolipid GalCer	block HIV infection of no	rmally susceptible CD4 negativ ling of GalCer to gp120 does n		
367	1006-30-D	Ig from HIV+ indivi [Hioe2000] • 847-D: 26 HIV-1 gro to isolates from clade	onses, because of their capa duals inhibited proliferative oup M isolates (clades A to	e responses of gp120 speci H) were tested for binding y did not not bind to isolat	and processing, can influence ic T cells – C2 MAbs 1006-30-to 47 MAbs, including two C2 es from subtypes A and H – epi	-D and 847-D did not MAbs – the binding	effect proliferation of anti-C2 MAbs was weak
368	847-D	from HIV+ individua • 847-D: 26 HIV-1 group to isolates from clade	s, because of their capacity als inhibited proliferative re oup M isolates (clades A to	sponses of gp120 specific H) were tested for binding y did not not bind to isolat	processing, can influence help Γ cells – C2 MAbs 1006-30-D to 47 MAbs, including two C2 es from subtypes A and H – epi	and 847-D did not ef MAbs – the binding	fect proliferation [Hioe2000] of anti-C2 MAbs was weak
369	MF169.1	gp160 (252–261) Vaccine Strain: LAI	gp120 (242–261 LAI)  HIV component: Env	RPVVSTQLLL		Vaccine	murine (IgG)

No.	MAb ID	<b>HXB2</b> Location	<b>Author's Location</b>	Sequence	Neutralizing	Immunogen	Species(Isotype)
			989, Moore1994c, Moore we affinity denatured/native	1994d gp120 is 11 – mutations 252	R/W, 257 T/G, and 257 T/R	impair binding [Mo	ore1994c]
370	MF170.1	References Thiriart1 • MF170.1: The relative	gp120 (242–261 LAI) HIV component: Env 1989, Moore1994c, Moore1 we affinity denatured/native 1281 A/V to only native gp	gp120 is 15 – mutations 252	R/W, 257 T/G, and 257 T/R	Vaccine impair binding to de	murine (IgG) enatured and native gp120, ar
71	MF87.1	References Thiriart1		RPVVSTQLLL gp120 is 10 – mutations 252	R/W, 257 T/G, and 257 T/R i	Vaccine Impair binding [Moo	murine (IgG) re1994c]
372		Ab type C2 Donor References Thiriart I • 213.1: Bound prefere • 213.1: The relative a	1989, Moore1993a, Moore1 entially to denatured IIIB a	1994c nd SF2 gp120 [Moore1993a] 120 is 100 – mutations 252 R	/W, 257 T/G or T/R impair b	Vaccine  binding [Moore1994c	murine (IgG1)
73		Ab type C2 References Moore 19 • B12: C2 region – the	994c, Maksiutov2002 e relative affinity for denatu	RPVVSTQLLLNGSLAEER rain: LAI HIV component: ured/native gp120 is 27 – mut man protein lymphatic endot	gp160 ations 257 T/R and 262 N/T		
374	B13 (Bh13, Chessie B13)	Ab type C2 Donor References Pincus 19 • B13: Bound preferer • B13: The relative aff • B13: C2 region – ep. • B13: Called Bh13 – [Pincus 1993a, Pincu	r George Lewis, Institute of 1993a, Moore 1993a, Moore 1993a, Moore 1993a, Moore 1993a, Moore 1993a, Moore 1994a, Moore 1993a, Moore 1994a, Moore 1993a, Moore 1994 1994a, Moore 1993a, Moore 1994 1994a, Moore 1994a, Moore 1994 1994a, Moore 1994a, Moore 1994a, Moore 1994 1994a, Moore 1994a, M	RPVVSTQLLLNGSLAEER rain: LAI HIV component: f Human Virology, Baltimore 1994c, Abacioglu1994, Moor 120 [Moore1993a] pp120 is 30 – mutations 257 y peptide scanning, core epit nfected cells – when linked to man protein lymphatic endotes.	gp160 MD, USA e1994d, Pincus1996, Connor F/R and 269 E/L impair bind ope: TQLLLN [Abacioglu19 oricin A, the immunotoxin di	ing [Moore1994c] 194] id not mediate cell k	illing – sCD4 has no effect
75	C13	gp160 (252–271)		RPVVSTQLLLNGSLAEER		Vaccine	murine (IgG1)

No. MAb ID	HXB2 Location	<b>Author's Location</b>	Sequence	Neutralizin	g Immunogen	Species(Isotype)
	<ul> <li>C13: Bound preferen</li> <li>C13: The relative aff</li> <li>C13: Epitope bounda</li> <li>C13: This epitope is [Maksiutov2002].</li> </ul>	tially to denatured IIIB grainity for denatured/native ary extended to RPVVSTO	gp120 is 36 – mutations 25 QLLLNGSLAEEEVVIR, to uman protein lymphatic en	7 T/R, 267 E/L, and 269 E/L io take into account the effect odothelium-specific hyaluronan	f a point mutation [A	Abacioglu1994]
376 M89	Ab type C2 Donor References diMarzo • M89: Immunoblot re • M89: C2 region – the	active, RIP negative, for se relative affinity for dena	e 94c, Moore1994d, Maksiuto strains IIIB, 451, MN, RF, a tured/native gp120 is >30 –		/L impair binding [M	
377 B21	Ab type C2 References Abaciog	lu1994	TQLLLN train: LAI HIV componer y peptide scanning [Abacio	<u>.</u>	Vaccine	murine (IgG1)
378 B23	<b>Ab type</b> C2 <b>References</b> Abaciog	lu1994	TQLLLN  train: LAI HIV component  y peptide scanning [Abacio	-	Vaccine	murine (IgG2a)
379 B24	<b>Ab type</b> C2 <b>References</b> Abaciog	lu1994	TQLLLN  train: LAI HIV componer  y peptide scanning [Abacio	-	Vaccine	murine (IgG2a)
380 B25	<b>Ab type</b> C2 <b>References</b> Abaciog	lu1994	TQLLLN  train: LAI HIV component  y peptide scanning [Abacio	-	Vaccine	murine (IgG1)
381 B3	gp160 (257–262)  Vaccine Vector/Type.  Ab type C2  References Abaciog	-	) TQLLLN train: LAI HIV componer	nt: gp160	Vaccine	murine (IgG1)

No. MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizing	Immunogen	Species(Isotype)
	• B3: C2 region, epi	tope boundaries mapped by	peptide scanning [Abacioglu1994	]		
882 B26	Ab type C2 References Abacie	oglu1994	) TQLLLNG train: LAI HIV component: gp1 y peptide scanning [Abacioglu199		Vaccine	murine (IgG1)
883 B29	Ab type C2 References Abacie	oglu1994	TQLLLNG train: LAI HIV component: gp1 y peptide scanning [Abacioglu199		Vaccine	murine (IgG2a)
384 B36	Ab type C2 References Abaci	oglu1994	TQLLLNG train: LAI HIV component: gp1 y peptide scanning [Abacioglu199		Vaccine	murine (IgG1)
85 110.E	Ab type C2 Dor References Moore • 110.E: The relative	or F. Traincard 1994c, Moore1994d, Maksi affinity for denatured/nativ	NGSLAEEEVVIRSVNFTDNA train: LAI HIV component: Envutov2002 e gp120 is 7.3 [Moore1994c] human protein lymphatic endothe	lium-specific hyaluronan	Vaccine receptor LYVE-1, T	murine (IgG) TRLLVQGSLRAEE
86 110.C	Ab type C2 Dor References Moore • 110.C: The relative	or F. Traincard, Hybridolab e1994c, Moore1994d, Valenz e affinity for denatured/nativ	zuela1998	ela1998]	Vaccine	murine (IgG)
87 IIIB-V3-20	Vaccine Vector/Ty <sub>1</sub> Ab type V3 References Lamar • IIIB-V3-26: Binds	epitope is similar to a fragme	SVEINCTRPNNNTRKSI on denatured gp120 [Laman1992] ent of the FasI receptor precursor	no Apptosis-mediating surfa	Vaccine  ace antigen fas) (APO	murine (IgG1)  O- 1 antigen) (CD95 antigen
388 IIIB-V3-2	gp160 (294–299) <b>Vaccine</b> <i>Vector/Ty</i>	gp120 (299–304 IIIB)	INCTRP	no	Vaccine	murine (IgG1)

No.	MAb ID	HXB2 Location Aut	hor's Location	Sequence	Neutralizing	Immunogen	Species(Isotype)
		<ul> <li>IIIB-V3-21: Binds to the ba</li> <li>IIIB-V3-21: Binds to NP40</li> <li>IIIB-V3-21: Does not block</li> <li>IIIB-V3-21: A rare mutatio by MAbs directed against the 2/12 anti-V3 MAbs tested (and 2F5 – thus multiple epihighly sensitive MN-TCLA</li> </ul>	aman1993, Valenzuela ase of the V3 loop on treated gp120, and ep at HIV-1 LAI binding on in the neutralization the CD4 binding site (e 19b and 694/98-D) no topes on R2 are funct a strain and the typical as similar to a fragment 2002] esearch Council AID		08] ab of the V3 regions, soluble CD4 (soluble CD4) be included in the control of	on caused Env to become se CD4), and HNS2, a broadly G1b12), 2/2 CD4i MAbs (1' sitivity profile of R2 is inte	neutralizing sera – 7b and 4.8D), and 2G12 rmediate between the
389	polyclonal	Ab type V3 References FitzGerald1998 • Polyclonal response to MN	, or Thai E V3 loop in by disulfide bond – s	CNYNKRKRIHIGPGRAFYTTKNIIG TIC serted into Pseudomonas Exotoxin for era from vaccinated rabbit were reactive	vaccination – ins		
390	polyclonal	Vaccine Vector/Type: lipop Ab type V3 References Pialoux2001  28 subjects were vaccinated adjuvant QS21 – HIV-speci	l with six HIV-1 pepti fic Ab responses were	TRPNNNTRKSIHIGPGRAFYATGEI IGDIRQAH HIV component: V3 Adjuvant: QS2 des that were selected to be particularly e detected in 25/28 (89%), proliferative peptide (E), 7/24 had proliferative responses	21 y rich in CTL epi in 19/28 (79%),	and CTL in 13/24 (54%) of	testable volunteers –
391	MO97/V3	gp160 (299–308) gp15 <b>Ab type</b> V3 <b>References</b> Ohlin1992	20 (299–308 IIIB)	PNNNTRKSIR  uninfected-donor lymphocytes with rp	no	in vitro stimulation	human (IgM)
392	polyclonal	Vaccine Vector/Type: peptid Ab type V3 References Neurath1990		PNNNTRKSIRIQRGPGRAFVTIGKI GNMRQAHC were tested and serological cross-react		Vaccine  vith divergence [Neurath199	rabbit (IgG)

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No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutraliz	zing Immunogen	Species(Isotype)
393	55/11	did not affect the ab	iable amino acids in the Vility of sCD4 or MAbs to	NNNTRKRIRIQRGPGR?  /3 loop were replaced with serines to V1/V2, C1 and C4 to bind, and anted gp120 had a reduced response re	i-V3 MAb 55/11 bin	ding was abrogated by V	3 serine substitutions in the
394	8/38c (8/38/1c)	Ab type V3 Dono References McKeat  8/38c: Binds to virio 8/38c: Binds equally lab strains [Sattentat 8/38c: Deletion of th 8/38c: The MAb and determined by the fi 8/38c: Called 8/38/1 these changes did no substitutions C-term immunogenicity of or	or C. Dean and C. Shotton ting 1992a, Sattentau 1995 on gp 120 and neutralizes by well to monomer and ol u 1995b] he V1V2 regions did not d Fab binding to the oligo raction of Ab sites occuping the control of the sites occuping the control of the ability of sCI		rey, UK 3 eating1992a] nan other anti-V3 an then compared to inta tion were highly con itope [Parren1998a] ed with serines to m b bind, and anti-V3 N	act rec gp120 [Jeffs1996] rrelated – authors suggest ake the immunodominan MAb 8/38c binding was o	t that neutralization is at V3 loop less immunogenic only diminished by V3 serine
395	8/64b	Ab type V3 References McKeat  8/64b: Binds to virio  8/64b: The most var did not affect the ab to the tip of the loop conserved regions [1]	ting1992a, Peet1998 on gp120 and neutralizes riable amino acids in the villity of sCD4 or MAbs to to – mice injected with ser	NNNTRKRIRIQRGPGR  Strain: BH10 HIV component: gp only in the presence of sCD4 [McKV3 loop were replaced with serines V1/V2, C1 and C4 to bind, and ant ine substituted gp120 had a reduced reagent: ARP3036	eating1992a] to make the immuno i-V3 MAb 8/64b bin	ding was abrogated by V	73 serine substitutions C-term
396	polyclonal	gp160 (300–321) Vaccine Vector/Type Ab type V3 References Bartlett		NYNKRKRIHIGPGRAFYTTK ail HIV component: V3	L	HIV-1 infection, Va	accine human

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizing	Immunogen	Species(Isotype)
				OA) with a C4 helper T cell epitope were us crease in HIV-1 RNA levels or increase in C			patients – V3 Ab levels and
397	polyclonal	gp160 (300–321)	gp120	NYNKRKRIHIGPGRAFYTTK		HIV-1 exposed seronegative	human (IgA)
		Ab type V3 References Kaul199 • HIV-1 Env-specific responses [Kaul1999	mucosal IgA found in gen	ital track of 16/21 HIV-1 resistant chronica	lly exposed Ken	yan sex workers – 11/2	1 had detectable Th
398	polyclonal	References Allaway		CNNTRKSIRIQRGPGRAFVTIGK tthews, Duke University lecules in inhibition of HIV-1 Env mediated	L d cell fusion [Al	laway1993]	guinea pig (IgG)
399	polyclonal (VEI3)	gp160 (300–328)	Env	NNNTRKSIRIGPGRAFYTTGDIGNI- RQ		HIV-1 infection	human
				construct (VEI) containing peptides from			
		antibodies against al [Carlos1999]	l five VEI hypervariable re	ubtype B infections – serum samples from Segions, but most consistently against the V	3 region peptide	NNNTRKSIRIGPGRA	AFYTTGDIGNIRQ
400	9284 (NEA 9284)	antibodies against al [Carlos1999]  gp160 (301–312)  Vaccine Vector/Type Ab type V3 Dono References Skinner VanCott1994, Thali Binley1997a, Parren  9284: IIIB type-spec  9284: Two fold incre  9284: Single amino neutralization—posit  9284: Increased bind  9284: Inhibits C4 re  9284: Peptide RIQR  9284: Does not bind  9284: gp41 mutation MAb [Thali1994]  9284: MAbs against inhibit gp120 bindin	gp120 (307–318 IIIB) e: inactivated virus Strain r Dupont de Nemours, Le 1988b, Skinner1988a, Satt 1994, Cook1994, Okada19 1998a, Schonning1998 eific binding and neutralize ease in binding to gp120 in acid substitutions in the C cion 427 is also important in ding in the presence of scl gion antibodies (G3-299, oc. GPGRAFVTIGKIGNMR I MN gp120, just IIIB [Van that confers resistance to the glycosphingolipid Ga g to GalCer in vitro [Cook	NNTRKSIRIQRG  n: IIIB HIV component: virus s Ulis, France or Wilmington, Delaware tentau1991, Wyatt1992, McKeating1992a, 1994, Sorensen1994, Sattentau1995b, VanCo ation [Skinner1988b] in the presence of bound sCD4 [Sattentau19 4 region (427 W/V or W/S) or at the base of for CD4 binding and anti-CD4 binding site D4 [Sattentau1993] G3-519) which have conformational require QA – Reacts with three human brain prote inCott1994] o neutralization by anti-CD4 binding site an	Sattentau1993, 1 ott1995, Fontence 1991] of the V3 loop (2 of MAbs [Wyatt19] ements [Moore I of 35, 55, 11 ottbodies does not be the content of the content	Vaccine  Vaccine  Moore1993c, Trujillo19  911995, Moore1996, Poi  298 R/G) can significan  992]  993c]  0 kd – called NEA-928  ot reduce neutralizing elative cells from the brai	murine (IgG1)  993, Thali1993, ignard1996a, Cao1997b,  tly increase binding and  4 [Trujillo1993]  fficiency of this V3 region  n and colon – this MAb car

No.	MAb ID	HXB2 Location	Author's Location	Sequence		Neutralizing	g Immunogen	Species(Isotype)
		<ul> <li>9284: Binds equally [Sattentau1995b]</li> <li>9284: Used to monity of the second of the sec</li></ul>	well to monomer and oligitor HIV-1 Env expression up — anti-C1 MAbs 133/29 84, BAT123, 110.5, and 10-69, in contrast to anti-V2 e V1-V2 loop deleted was BS MAb F105 or sCD4 [Cd Fab binding to the oligo raction of Ab sites occupithe influence of the glycat Env and anti-V3 MAbs w	s viable and more susceptib	nd potent neutralizes native and reduceing – reciprocal billy increase gp120 ble to neutralization were of the epitope [Parloop on MAb reco	ed gp120s siminding inhibition dissociation from by CD4i MA highly correlarren1998a] ognition, 9284	larly [VanCott1995] n of other anti-V3 MAb om virus, mimicking sC ab 17b, and anti-V3 MA ated – authors suggest th was found to have an in	s [Moore1996] D4, and expose the gp41 bs 1121, 9284, and 110.4, at neutralization is
401	polyclonal	gp160 (301–325)  Vaccine Vector/Typ  Ab type V3  References Bukawa  Polyclonal secretory	gp120 (IIIB) e: peptide Strain: IIIB a1995 y IgA antibody raised by 1	NNTRKSIRIQRGPGF Adjuvant: cholera toxin a mucosal immunization is a peptide immunogen [Buk	djuvant ble to neutralize II	L IIB, SF2, and M	Vaccine ЛN – HIV-1 neutralizati	murine (IgA) on may be due to V3, CD4
402	polyclonal	Ab type V3 References Sasaki I  An anti-env response	998 se was sought, and co-exp	NNTRKSIRIQRGPGHHV component: Env, Rev ression of Rev was require conse mediated via Th1 cyt	d – intramuscular			murine (IgA22a) ccine with a QS21 adjuvant
403	polyclonal	gp160 (302–317) <b>Ab type</b> V3 <b>References</b> Morris?  • Ab responses before who were classified and four subtype B	Env (B consensus)  2001  e HAART therapy and aft as HAART failures – V3 clinical isolates were testes stained viral suppression t	NTRKSIHIGPGRAF	e measured in 8 in titers to the B-cons nti-V3 and NAb h	dividuals that v sensus and MN umoral immuno	HIV-1 infection were classified HAART I and SF2 variants, and e responses before start	
404	polyclonal	gp160 (302–318) <b>Ab type</b> V3 <b>References</b> Bonger	Env tz2001	NTRKSIHIGPGRAF	ľ	LP	HIV-1 infection	human

**HIV Antibodies Tables** 

No.	MAb ID	HXB2 Location	<b>Author's Location</b>	Sequence	Neutralizing	Immunogen	Species(Isotype)
		pregnant women), co	ompared to plasma from tra tes from transmitting moth	uency of high neutralizing plasma Abnsmitting mothers (0/8 pregnant womeers, but neutralization of autologous vi	en) – non-transmitti	ng mothers also had	more potent neutralization
405	MAG 109	Ab type V3 References Kang199	sCD4-gp120 complex S	NTRKSIRIQRGPGRAFVTIG  Strain: HXB2 HIV component: gp120  to both V3 loop mutations and a mutat		Vaccine ne V1/V2 loop struct	murine ture (120/121 VK/LE)
406		Vaccine Vector/Type Ab type V3 References Kang 199 MAG 49: Binds a V3 [Kang 1994] MAG 49: Called #49	s sCD4-gp120 complex S 94, Moore1996 3 loop peptide – sensitive to 9 in this text. Binding enhan	NTRKSIRIQRGPGRAFVTIG  Strain: HXB2 HIV component: gp120  b both V3 loop mutations and a mutation  need by anti-C1 MAbs 133/290, 135/9,  ibition of anti-V3 MAbs [Moore1996]	on at the base of the	•	
407	MAG 53	Ab type V3 References Kang199	sCD4-gp120 complex S	NTRKSIRIQRGPGRAFVTIG  Strain: HXB2 HIV component: gp120  b both V3 loop mutations and a mutation		Vaccine e V1/V2 loop structu	murine are (120/121 VK/LE)
408	MAG 56	Ab type V3 References Kang199	94	NTRKSIRIQRGPGRAFVTIG  Strain: HXB2 HIV component: gp126  b both V3 loop mutations and a mutation		Vaccine e V1/V2 loop structu	murine are (120/121 VK/LE)
409	1324-E (1324E)	gp160 (303–308)  Ab type V3 Donor  References Gorny19  1324-E: A human M  peptide from clade E  with B and D clade V	98, Zolla-Pazner1999a, Zo Ab was derived from an Hl - cross-reactive with V3 p V3 peptides or rgp120 – net	TRTSVR as01@mcrcr6.med.nyu) (NYU Med. Colla-Pazner1999b, Nyambi2000 IV-1 E clade infection from a US service eptides, and gp120 from E, C and A clatralizes E clade virus adapted for grow	ce man who had se ades, as well as cel with in H9 cells, but	ls infected with a C- not 5 primary E clad	clade primary isolate, but not

autologous isolate - kinetic parameters were measured, 1324E was comparable to 447-52D [Gorny1998]

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizing Immunogen	Species(Isotype)
		stimulated Abs can oreactivity with B pep  1324-E: MAb reacte 1324-E: Called 1324 tested, and of 494 coisolates, less to E, F,	cross-react with some pept ptides and most D peptides ed with peptides from E cla 4E – A panel of 47 human pmbinations, 44% displaye	ides from other clades – the [Zolla-Pazner1999a] ade, while B clade derived MAbs was tested against 2 d some viral binding – V3 d poor cross-reactivity, and	es nor did B clade derived peptides with an E clade V3 his Ab showed strong binding to several E, A and F peptides MAbs could not [Zolla-Pazner1999b] 26 HIV-1 group M primary isolates from clades A through MAbs tended to have the most cross-reactive binding it was the only MAb tested that was derived from a non-	tides, one C peptide, and no 19 H – 19 V3 MAbs were to clade A, B, C, and D
410	polyclonal		gp120 (subtype C)	CKRKIHIGPGQAFYT  osome HIV component:	Vaccine V3 Adjuvant: ISCOM	murine (IgG2a, IgG2b)
			nodified to resemble an Inc		corporated into ISCOMS (immune stimulating complex y the presentation in the ISCOM suggestive of a Th1 re	•
411	MO99/V3	gp160 (304–308) <b>Ab type</b> V3 <b>References</b> Ohlin19  • MO99: Generated th		RKSIR of uninfected-donor lymp	no in vitro stimulation hocytes with rpB1 (IIIB Env 286-467) [Ohlin1992]	human (IgM)
412	C311E	[Warrier1996] • C311E: A study of 6	re infected with HIV-1 IIIB	ability to bind or direct A	L HIV-1 infection gave synergistic neutralization of HIV-1 when combined DCC against target cells infected with IIIB, MN, SF-2,	
413	907	<ul><li>References Chesebu</li><li>907: Strain specific</li><li>907: Coupled to rici</li><li>907: Epitope sequen</li></ul>	nce is based on database co nunotoxins were generated	s1991, Pincus1996 of only the LAV strain [C i7 inhibited protein synthe unt of a specified location	L Vaccine  Chesebro 1988] sis and cell growth in HIV-infected cells [Pincus 1989]  – 924-RAC immunotoxin is IIIB strain-specific [Pincus icin A – immunotoxins mediated cell killing, but killing	
414	924	<b>Ab type</b> V3 <b>References</b> Chesebr	gp120 (309–318 IIIB) e: vaccinia Strain: IIIB ro1988, Pincus1991, Pincu n specific [Chesebro1988]		Vaccine ok1994, Pincus1996, Pincus1998	murine (IgG1κ)

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizing Immunogen	Species(Isotype)
		<ul> <li>924: MAb was coup immunotoxins in vit</li> <li>924: Ab response in vaccinia gp160 vacc</li> <li>924: MAbs against inhibit gp120 bindin</li> </ul>	led to ricin A chain (RAC) ro increased 30-fold by sCl IIIB lab workers was compine had strong V3 MAb reshe glycosphingolipid GalCg to GalCer in vitro [Cook nunotoxins were generated]	– immunotoxin efficacy was D4 [Pincus1993a] pared to gp160 LAI vaccine reponse, but alum absorbed re er block HIV infection of no 1994]	224-RAC immunotoxin is IIIB strain-specific [Pincus not significantly decreased by sCD4, although the exception of the except	ed lab workers and a 93b] a and colon – this MAb can
415	polyclonal	gp160 (304–318) <b>Ab type</b> V3 <b>References</b> Chin199  • Mimicking the humo		RKSIRIQRGPGRAFV tro supports isotype switchin	in vitro stimulation g – human IgG MAbs were generated from naive do	human (IgG, IgM) nors [Chin1995]
416	polyclonal	Ab type V3 References Zafiropo • IgG to IgM isotype			Vaccine vaccinations was studied – the immunogen containe	human (IgG, IgM) and a V3 loop fragment and a
417	10F10	Ab type V3 References Duarte1 • 2C4: Putative epitop		. 0.	L Vaccine  ope polypeptide immunization – recognize MN and	murine (IgG1) SC (TRSIHIGPGRAFYTT)
418	2C4	Ab type V3 References Duarte1 • 2C4: Putative epitop	e lies within IHIGPGRAF	RKRIHIGPGRAFYTT  YT – neutralizes MN, not III lower affinity for SF2 [Duart	L (MN) Vaccine  B and SF2 – generated by multi-epitope polypeptide e1994]	murine (IgG2a) immunization – recognize
419	412-D (412-10D, 412, 412D)	<ul><li>References Gorny 19</li><li>412-D: Neutralizes 1</li><li>412-D: Mediated de</li><li>412-D: Called 412-D</li></ul>	993, Spear1993, VanCott19 MN, does not bind SF2 or I position of complement cor 0D – relatively rapid disso	IXB2 – not reactive with her mponent C3 on HIV infected ciation and weak homologou	L HIV-1 infection (U Med. Center) (18, Nyambi1998, Zolla-Pazner1999a, Zolla-Pazner198, as or heptapeptides by Pepscan [Gorny1993] (cells, enhanced by second Ab binding, rabbit anti-has neutralization [VanCott1994] (one – higher valency correlates with stronger affinity)	uman IgG [Spear1993]

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutraliz	zing Immunogen	Species(Isotype)
		has a relatively fast  412-D: Using a who 412-D was bound o  412-D: Review of c  412-D: MAb peptid acids HIGPGR tend  412-D: A panel of 4 combinations, 44%	dissociation, thus low affir ble virion-ELISA method, nly to B clade virions and lade specificity and anti-V le-reactivity pattern cluster led to be critical for reactiv to human MAbs was tested	nity among V3 MAbs [Gori 18 human MAbs were tested to D clade MAL [Nyambi] 3 HIV-1-Abs [Zolla-Pazner ed with immunological rela- tity in this group [Zolla-Paz 1 against 26 HIV-1 group M ng – V3 MAbs tended to h	ed for their ability to bind to 998] 1999a] ated MAbs: 391.5, 412 and 4 aner1999b] I primary isolates from clade	a panel of 9 viruses from a 418, all selected with MN es A through H – 19 V3 M	clades A, B, D, F, G, and H – V3 peptide – the core amino IAbs were tested, and of 494 and D isolates, less to E, F, G,
420	polyclonal		serum that can bind to nati	RKRIHIGPGRAFYTT  ive viral proteins on MN-in n HIV infected cells [Spear		HIV-1 infection  by the peptide RKRIHIGF	human PGRAFYTT, which can also
421	CGP 47 439	Ab type V3 References Liou19 CGP 47 439: passiv BAT123-human Ig CGP 47 439: Phase serum t_1/2 was 8- CGP 47 439: Post-enot elicited by CGP cobra venom factor.	re transfer to Hu-PBS-SCII chimera [Safrit1993] I/IIA clinical trial studying 16 days, and a virus burden exposure passive transfer of 47 439, suggesting that the which inactivates serum of	994, Gauduin1998, Jacobso O mice confers protection a g multidose tolerability, im a reduction was noted in so f murine BAT123 can confe e protection is mediated by omplement – in this circum	on 1998 Igainst challenge with homo munogenicity and pharmaco me patients [Gunthard 1994] er protection to hu-PBL-SCI	okinetic responses – GP 47 D mice challenged with He ability of BAT123 is lost on provided a protective a	7 439 was well tolerated, IIV-1 LAI – this protection is when mice were treated with
422	polyclonal	gp160 (304–322) <b>Ab type</b> V3 <b>References</b> Cheing  • The Ab response of studies – the Ab bin	(MN) song-Popov1992 829 HIV-1 infected subjections pattern was highly va	RKRIHIGPGRAFYTT) ets from eight geographic auriable, depended on the geo	reas to a set of different V3 p	HIV-1 infection reptides was determined by 297 sera were tested in	human  y ELISA and cross-inhibition a neutralization assay – there Cheingsong-Popov1992]
423	178.1 (178.1.1)	Ab type V3 Dono References Thiriart • 178.1: Reacts to gp	or C. Thiriart, Smith Kline 1989, Back1993, Moore19 120 and gp160 in RIPA EL	train: IIIB HIV compone and MRC AIDS reagent p	roject t1989]	Vaccine	murine (IgG2a)

No.	MAb ID	<b>HXB2</b> Location	<b>Author's Location</b>	Sequence	Neutralizing	Immunogen	Species(Isotype)			
		• 178.1: gp41 amino a	·	S) and 675 (I/M) in gp41 i	nterfere with 5023s neutralization	potency, region 662-6	75 is			
		• 178.1: MAbs against the glycosphingolipid GalCer block HIV infection of normally susceptible CD4 negative cells from the brain and colon – this MAb								
		can inhibit gp120 bi	inding to GalCer in vitro -	- binding of GalCer to gp1	20 inhibited but did not complete	ly block MAb binding[	Cook1994]			
		• 178.1: UK Medical	Research Council AIDS 1	reagent: ARP331						
124	257-D (257,	gp160 (305-309)	gp120 (MN)	KRIHI	L	HIV-1 infection	human (IgG1λ)			
	257-2-D-IV,	Ab type V3 Dono	or Susan Zolla-Pazner (Zo	ollas01@mcrcr6.med.nyu)	(NYU Med. Center)					
	257-D-IV,	References Gorny1	991, D'Souza1991, Karw	owska1992b, Gorny1993,	Cavacini1993a, Spear1993, D'So	uza1994, VanCott1994	, Stamatatos 1995,			
	257, 257-2D,	D'Souza1995, Zolla-Pazner1995a, Schutten1995a, Schutten1995b, Fontenot1995, Wisnewski1996, Schutten1996, Schutten1997, Stamatatos1997,								
	257D,	Hill1997, Hioe1997	b, LaCasse1998, Yang199	98, Gorny1998, Stamatatos	1998, Zolla-Pazner1999a, Zolla-	Pazner1999b, Beddows	1999, Oggioni 1999,			
	ARP3023)	Nyambi2000, Park2	2000, York2001, Zhang200	02						
		• 257-D: Called 257-2	2-D-IV – potent neutralizi	ng MAb [D'Souza1991]						
		• 257-D: Reacts with	MN, NY5, CDC4 and SF	2, does not cross-react wit	h RF, WM52, or HXB2 [Karwow	ska1992b]				
		• 257-D: Neutralizes	MN – binds SF2: KSIYI -	- specificity: MN, SF2, N	Y5, RF. [Gorny1993]					
					inding site MAb F105 – does not	neutralize RF [Cavacin	i1993a]			
					cted cells, enhanced by second A					

- 257-D: Included a multi-lab study for antibody characterization and assay comparison best NAb against MN, but not IIIB [D'Souza1994]
- 257-D: Potent MN neutralization, slow dissociation constant [VanCott1994]

mediated virolysis of MN, but not in the presence of sCD4 [Spear1993]

- 257-D: The binding of conformation-dependent anti-V2, anti-V3, and anti-CD4BS MAbs to monomeric and virion-associated gp120 from HIV-1 isolates with differences in cell tropism was studied V3 loop epitopes were less accessible to Ab binding on the virion surface than in the gp120 monomer, particularly for macrophage-tropic isolates SF162 and SF128a, relative to T-cell tropic SF2 sCD4 association with gp120 better revealed this V3 epitope on TCLA SF2 and dual tropic (MU3) viruses than on macrophage tropic isolates [Stamatatos1995]
- 257-D: Called 257-D-IV could neutralize MN and closely related JRCSF, but not 2 B subtype and 1 D subtype primary isolates in a multi-laboratory study involving 11 labs [D'Souza1995]
- 257-D: In serotyping study using flow-cytometry, bound only to virus with KRIHI [Zolla-Pazner1995a]
- 257-D: Only inhibition of SI phenotype virus, and strong enhancement of NSI phenotype chimeric viruses, that incorporated different envs from the same donor [Schutten1995a]
- 257-D: Comparable affinity for SI and NSI viruses, in contrast to MAb MN215 [Schutten1995b]
- 257-D: 257-D is V H5 V-region heavy chain usage was examined and a bias of enhanced V H1 and V H4, and reduced V H3, was noted among HIV infected individuals [Wisnewski1996]
- 257-D: IIIB neutralizing MAbs in vitro fail to neutralize in a mouse model it in vivo [Schutten1996]
- 257-D: Neutralized (>90%) an SI-env chimeric virus and enhanced (>200%) an NSI-env chimeric virus [Schutten1997]
- 257-D: Binds less extensively than MAb 391-95D on the surface of HIV-1 isolates SF162 and SF128A neutralizes less potently than 391-95D stronger neutralization of primary macrophage targets than PBMC [Stamatatos1997]
- 257-D: Called 257 gp120 can inhibit MIP-1alpha from binding to CCR5, but this inhibitory effect is blocked by pre-incubation of gp120 with three anti-V3 MAbs: 447, 257, 1027 MAb 670 which binds in the C5 region had no effect [Hill1997]
- 257-D: A T-cell line-adapted (TCLA) derivative of SI primary isolate 168P acquired the ability to be neutralized by anti-V3 MAbs the primary isolate
  could use either CCR5 or CXCR4, and was not neutralized when infection was directed via either pathway, however the TCLA derivative uses CXCR4 only
  and is neutralized [LaCasse1998]

No. MAb ID HXB2 Location Author's Location Sequence Neutralizing Immunogen Species(Isotype)

• 257-D: A neutralization assay was developed based on hemi-nested PCR amplification of the LTR (HNPCR) – LTR-HNPCR consistently revealed HIV DNA and was shown to be a rapid, specific and reliable neutralization assay based on tests with 6 MAbs and 5 isolates [Yang1998]

• 257-D: Kinetic parameters were measured, and the association rates were similar, but dissociation rate constants were quite variable for V3 MAbs, 257-D has a slow dissociation, thus the highest affinity among V3 MAbs [Gorny1998]

• 257-D: Called 257D – deleting the V2 loop of neutralization-resistant HIV-1 isolate SF162 does not abrogate its replication in PBMC or macrophages, but it

through F – deletion of V1 or V2 did not enable neutralization by V3 MAbs 391-95D or 257D [Stamatatos1998]

- 257-D: Review of clade specificity and anti-V3 HIV-1-Abs [Zolla-Pazner1999a]
- 257-D: MAb peptide reactivity pattern clustered with immunological related MAbs: 1108, 386, 268, 311, 257, 694.8 the amino acids HI tended to be critical for reactivity in this group [Zolla-Pazner1999b]

enhances its neutralization sensitivity to sera from patients with B clade infection up to 170-fold, and also enhances sensitivity to sera from clades A

- 257-D: rgp120 derived from a R5X4 subtype B virus, HIV-1 W61D, was used to vaccinate healthy volunteers and the resulting sera were compared with sera from HIV-1 positive subjects and neutralizing MAbs 257-D bound rgp120 W61D but could only neutralize the W61D isolate following T-cell line adaptation [Beddows1999]
- 257-D: Study of a live-vector mucosal vaccine that expresses HIV-1 V3 domains using the bacterium Streptococcus gordonii which can express heterologous Ag and can colonize the oral cavity and vagina of mice 268-D and 257-D recognized S. gordonii expressing the V3 domain of MN the vaccine stimulated V3-specific IgG2a in mice [Oggioni1999]
- 257-D: A panel of 47 human MAbs was tested against 26 HIV-1 group M primary isolates from clades A through H 19 V3 MAbs were tested, and of 494 combinations, 44% displayed some viral binding V3 MAbs tended to have the most cross-reactive binding to clade A, B, C, and D isolates, less to E, F, G, and H 257-D showed intermediate reactivity [Nyambi2000]
- 257-D: Called 257D six mutations in MN change the virus from a high-infectivity neutralization resistant phenotype to low-infectivity neutralization sensitive V3, CD4BS, and CD4i MAbs are 20-100 fold more efficient at neutralizing the sensitive form the mutation L544P reduced binding of all MAbs against gp120 by causing conformational changes [Park2000]
- 257-D: Abs against the V3 loop (50.1, 58.2, 59.1, 257-D, 268-D, 447-52D), CD4BS (IgG1b12, 559-64D, F105), CD4i (17b), and to gp41 (2F5, F240) each showed similar binding efficiency to Env derived from related pairs of primary and TCLA lines (primary: 168P and 320SI, and TCLA: 168C and 320SI-C3.3), but the TCLA lines were much more susceptible to neutralization suggesting that the change in TCLA lines that make them more susceptible to NAbs alters some step after binding [York2001]
- 257-D: Called ARP3023: Herpesvirus saimiri-immortalized CD4+ T lymphocytes (HVS T cells) were used to isolate virus and perform HIV-1 neutralization assays, and compared with a standard PBMC protocol neutralization sensitivities to a panel of MAbs and to homologous or heterologous plasma/sera were similar for HVS T cells (CN-2 cells) and PBMCs [Vella2002]
- 257-D: A rare mutation in the neutralization sensitive R2-strain in the proximal limb of the V3 region caused Env to become sensitive to neutralization by MAbs directed against the CD4 binding site (CD4BS), CD4-induced (CD4i) epitopes, soluble CD4 (sCD4), and HNS2, a broadly neutralizing sera 2/12 anti-V3 MAbs tested (19b and 694/98-D) neutralized R2, as did 2/3 anti-CD4BS MAbs (15e and IgG1b12), 2/2 CD4i MAbs (17b and 4.8D), and 2G12 and 2F5 thus multiple epitopes on R2 are functional targets for neutralization and the neutralization sensitivity profile of R2 is intermediate between the highly sensitive MN-TCLA strain and the typically resistant MN-primary strain [Zhang2002]
- 257-D: UK Medical Research Council AIDS reagent: ARP3023
- 257-D: NIH AIDS Research and Reference Reagent Program: 1510

425 311-11-D (311-11D, 311, 311D.

311-D)

gp160 (305–313) gp120

KRIHIGP

L HIV-1 infection

human (IgG1λ)

Ab type V3 Donor Susan Zolla-Pazner (Zollas01@mcrcr6.med.nyu) (NYU Med. Center)

References Gorny1991, Gorny1993, Spear1993, Gorny1998, Zolla-Pazner1999a, Zolla-Pazner1999b, Nyambi2000

- 311-11-D: Neutralizes MN binds SF2: KSIYIGP [Gorny1993]
- 311-11-D: Mediated deposition of complement component C3 on HIV infected cells, enhanced by second Ab binding, rabbit anti-human IgG [Spear1993]

No.	MAb ID	<b>HXB2</b> Location	Author's Location	Sequence	Neutralizing	Immunogen	Species(Isotype)			
		<ul> <li>311-11-D: MAb per critical for reactivity</li> <li>311-11-D: A panel of 494 combinations, 4</li> </ul>	otide reactivity pattern clu in this group [Zolla-Paz of 47 human MAbs was t	ner1999b] ested against 26 HIV-1 gro binding – V3 MAbs tend	Pazner1999a] al related MAbs: 1108, 386, 268, 3  oup M primary isolates from clade ed to have the most cross-reactive	s A through H – 19 V3	3 MAbs were tested, and of			
426	41148D	<ul> <li>41148D: A study of directed lysis agains</li> </ul>	s less potently than 41176 6 anti-Env MAbs and the st strains IIIB, MN, SF-2,	comparable to 4117C, ho	L  F2 [Pinter1993b]  ADCC against target cells infecte wever 41148D is 10x less efficient					
427	391/95-D (391-95D, 391.5, 391/95D)	Ab type V3 Donor Susan Zolla-Pazner (Zollas01@mcrcr6.med.nyu) (NYU Med. Center) References Gorny1991, Gorny1993, Fontenot1995, Stamatatos1995, Seligman1996, Stamatatos1997, Stamatatos1998, Zolla-Pazner1999a,								

- from clades A through F deletion of V1 or V2 did not enable neutralization by V3 MAbs 391-95D or 257D [Stamatatos1998]

   391/95-D: Review of clade specificity and anti-V3 HIV-1-Abs [Zolla-Pazner1999a]
- 391/95-D: Called 391.5 MAb peptide-reactivity pattern clustered with immunological related MAbs: 391.5, 412 and 418, all selected with MN V3 peptide the core amino acids HIGPGR tended to be critical for reactivity in this group [Zolla-Pazner1999b]

• 391/95-D: Called 391-95D – deleting the V2 loop of neutralization-resistant HIV-1 isolate SF162 does not abrogate its replication in PBMC or

• 391/95-D: Called 391-95D – SF162 is a neutralization-resistant HIV-1 isolate – N-linked glycosylation modifications in the V2 loop of the SF162 gp120 revealed that these sites prevent neutralization by CD4BS MAbs (IgG1b12 and IgGCD4), and protect against neutralization by V3 MAbs (447-D and 391-95D) – V2-region glycosylation site mutations did not alter neutralization resistance to V2 MAbs (G3.4 and G3.136) or CD4i MAbs (17b and 48d) – V2 glycosylation site modification allows infection of macrophages, probably due to glycosylated forms requiring fewer CCR5 molecules for viral entry [Ly2000]

macrophages, but it enhances its neutralization sensitivity to sera from patients with B clade infection up to 170-fold, and also enhances sensitivity to sera

• 391/95-D: Called 391/95D – six mutations in MN change the virus from a high-infectivity neutralization resistant phenotype to low-infectivity neutralization sensitive – V3, CD4BS, and CD4i MAbs are 20-100 fold more efficient at neutralizing the sensitive form – the mutation L544P reduced binding of all MAbs against gp120 by causing conformational changes [Park2000]

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizing	Immunogen	Species(Isotype)
		enhanced, not X4 – critical – tests with enhanced or neutral  • 391/95-D: The pher demonstrated infect presence of 391/95-in the post-seroconv  • 391/95-D: A rare m by MAbs directed a 2/12 anti-V3 MAbs and 2F5 – thus multi	the V3 region was the mair MAbs anti-V3 391/95-D an ized, rather the phenotype value of viral ivity of clones derived presupersion 391/95-D enhanced utation in the neutralization gainst the CD4 binding site tested (19b and 694/98-D) tiple epitopes on R2 are fun	an determinant of Ab-mediate of CD4BS-specific GP68 incomes determined by Env configures determined by Env configures services were studied services where the services were not influenced (See [Guillon2002]) [In sensitive R2-strain in the process of the process of the services of the s	d enhancement and modulation dicate that Ab specificity did not permation [Guillon2002] di over a period of seroconversi uenced by MAb 391/95-D, but hange in the CD4-binding site Lawson2002] coximal limb of the V3 region D4i) epitopes, soluble CD4 (soluti-CD4BS MAbs (15e and IgC tion and the neutralization sen	n of the interaction of determine whether the don in one individual the post-seroconversic was observed (NL-caused Env to beco CD4), and HNS2, a G1b12), 2/2 CD4i M	er or not infectivity was  1 – Env trans-complementation on clones were enhanced in the 43 427 Glu->Lys) to be present the sensitive to neutralization broadly neutralizing sera – (Abs (17b and 4.8D), and 2G12
428	Aw	Ab type V3 References McKnig • Aw: Rat antibodies		tides that represent either the	L e wildtype (wt), or brain-cell to	Vaccine ropic variant (v) of the second ropic variant (v) of t	rat he isolate Gun-1 – Aw gives
429	Bw	Ab type V3 References McKnig • Bw: Rat antibodies	were raised against V3 pep		L e wildtype (wt), or brain-cell to cKnight1995]	Vaccine ropic variant (v) of	rat the isolate Gun-1 – Bw gives
430	DO142-10 (DO 142-10	<ul> <li>References Seligma</li> <li>DO142-10: Fab frag</li> <li>DO142-10: Phage egp120 [Ditzel1997]</li> <li>DO142-10: Neutral</li> <li>DO142-10: Binds to all [Parren1997a]</li> <li>DO142-10: The ran was markedly differ &gt; b3 &gt; b13) and bin</li> </ul>	gment – competition ELISA expression libraries panned sizes TCLA strains but not po gp120 MN and an MN V3 k order of Fab binding affinite that Fab binding affinited ding to oligomeric form and	against MN peptide were us brimary isolates [Parren1997 B peptide with equal affinity, with the monomeric gp120 (Low to the mature oligomeric for	ed the epitope KRIHIGPGRA ed to select Fab DO142-10 – F c] but binds a consensus B pepti cop 2 > 3B3 > b12 = DO8i > b orm (3B3 > b12 > DO142-10 > ted for both Fabs and MAbs –	Tab binds MN gp120  de and JRCSF less  old > b3 > b14 > b1  > Loop 2 > b11 > L	o, but not a primary isolate rec well, and to IIIB gp120 not at 3 > DO142-10 > DA48 > L17) 17 > b6 > DO8i > b14 > DA48

No.	MAb ID	HXB2 Location	<b>Author's Location</b>	Sequence	Neutralizing	Immunogen	Species(Isotype)
		entry state could be concentrations of sC	conferred on HxB2 by intro CD4 and the effect is depend	oducing the YU2 V3 loop, odent of CCR5 – Fab Ab frag	to the CD4BS, V3 loop, and Or the YU2 V3 and V1/V2 loop ment DO124-10 also enhances ld, it neutralizes HXBc2 under	os – a similar effec s YU2 entry, rulin	t is observed by sub-neutralizing g out Fc interactions or Env
431	Dv	Ab type V3 References McKnig Dv: Rat antibodies	were raised against V3 pept	•	L wildtype (wt), or brain-cell tr ht1995]	Vaccine opic variant (v) of	rat  f the isolate Gun-1 —
432	Fv	Ab type V3 References McKnig • Fv: Rat antibodies v	vere raised against V3 pepti		L wildtype (wt), or brain-cell tro	Vaccine opic variant (v) of	rat the isolate Gun-1 –
433	Gv	Ab type V3 References McKnig Gv: Rat antibodies	were raised against V3 pept		L e wildtype (wt), or brain-cell tr ht1995]	Vaccine opic variant (v) of	rat  • the isolate Gun-1 –
434	Hv	Ab type V3 References McKnig • Hv: Rat antibodies	were raised against V3 pept	•	L e wildtype (wt), or brain-cell tr ht1995]	Vaccine opic variant (v) of	rat f the isolate Gun-1 –
435	polyclonal	Ab type V3 References Barnett	2001		yes eltaV2 HIV component: gp1	·	
		neutralization – whe neutralizing Ab titer SF162DeltaV2, but non-homologous iso	en incorporated into a codor is against SF162 than did SI not intact SF162, was used plates decreased, but anti-V	n-optimized DNA vaccine w F162 itself, and Abs that cro as the immunogen – NAbs 3 peptide binding Abs were	-	d by gene gun, SF as primary isolates sed with multiple stinction because a	162DeltaV2 gave higher s were obtained only when immunizations, while titers for anti-V3 titers were much lower

No.	MAb ID	HXB2 Location	<b>Author's Location</b>	Sequence	Neutralizing	Immunogen	Species(Isotype)			
136	50.1	gp160 (306-310)	gp120 (MN)	RIHIG	L	Vaccine	murine (IgG1κ)			
	(R/V3-50.1,	Vaccine Vector/Type	e: peptide Strain: MN	HIV component: V3						
	Fab 50.1)	Ab type V3 Donor Mary White-Scharf, Repligen Corporation, Cambridge, MA								
		References D'Souz	a1991, White-Scharf199	3, Potts1993, Ghiara1993, Ri	ni1993, Bou-Habib1994, VanCo	ott1994, Robert-Guro	ff1994, Moore1994b,			
		VanCott1995, Fonte	not1995, Seligman1996,	Berman1997, LaCasse1998,	Stanfield1999, Hoffman1999, F	Park2000, York2001,	Zhang2002			
		• 50.1: Called R/V3-5	50.1 – potent neutralizing	of lab strains[D'Souza1991]						
					o acid substitutions – epitope R	HIGP [White-Schar	f1993]			
					1Ab F105 – isotype stated to be					
					to 59.1 and 50.1 Fab fragment		[Ghiara1993]			
					the left of GPG, heavy chain b					
					d neutralization of T cell tropic					
		[Bou-Habib1994]	1 5	2	1	,				
			utralization, slow dissoci	ation rate [VanCott1994]						
					CS signal, Ab affinity, and vira	l neutralization [Robe	ert-Guroff19941			
				B clade gp120s, little outside						
				in infected H9 cells [VanCo						
					mate of epitope length to crysta	al structure and alanin	e substitution – KRIHIG			
		<ul> <li>[Seligman1996]</li> <li>50.1: Binds to 6/7 isolates from breakthrough cases from a MN gp120 vaccine trial [Berman1997]</li> </ul>								
		• 50.1: A T-cell line-a	ndapted (TCLA) derivative CXCR4, and was not new	e of SI primary isolate 168P	acquired the ability to be neutra lirected via either pathway, how					
		• 50.1: The crystal str	_	es bound to Fabs was obtaine	d – conformational changes in t	the tip of the V3 loop	(GPGR) were observed v			
		• 50.1: Called R/V3-50.1 – six mutations in MN change the virus from a high-infectivity neutralization resistant phenotype to low-infectivity neutralization sensitive – V3, CD4BS, and CD4i MAbs are 20-100 fold more efficient at neutralizing the sensitive form – the mutation L544P reduced binding of all MAbs against gp120 by causing conformational changes – 50.1 could only neutralize the sensitive form [Park2000]								
		• 50.1: Abs against the showed similar bind	ne V3 loop (50.1, 58.2, 59 ling efficiency to Env der	0.1, 257-D, 268-D, 447-52D) ived from related pairs of pri	CD4BS (IgG1b12, 559-64D, F mary and TCLA lines (primary:	7105), CD4i (17b), and 168P and 320SI, and	d TCLA: 168C and			
					ation suggesting that the change 60.1 for the cell associated primary					
					_	-	-			
		• 50.1: Called R/V3-50.1 – A rare mutation in the neutralization sensitive R2-strain in the proximal limb of the V3 region caused Env to become sensitive to neutralization by MAbs directed against the CD4 binding site (CD4BS), CD4-induced (CD4i) epitopes, soluble CD4 (sCD4), and HNS2, a broadly neutralizing sera – 2/12 anti-V3 MAbs tested (19b and 694/98-D) neutralized R2, as did 2/3 anti-CD4BS MAbs (15e and IgG1b12), 2/2 CD4i MAbs (17b and 4.8D), and 2G12 and 2F5 – thus multiple epitopes on R2 are functional targets for neutralization and the neutralization sensitivity profile of R2 is								
		intermediate betwee	en the highly sensitive MI	N-TCLA strain and the typic	ılly resistant MN-primary strain	[Zhang2002]				
		• 50.1: NIH AIDS Re	esearch and Reference Re	agent Program: 1289						
37	polyclonal	gp160 (306–318)	gp120 (NY5)	KKGIAIGPGRTLY			(IgM)			

References Metlas1999b, Metlas1999a

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizing	Immunogen	Species(Isotype)
		Auto-Abs that react	with the V3 loop of NY5 a	are present in the sera of HI	/- individuals, and are predomi	nantly IgM [Metlas19	999b]
438	BAT123 (BAT-123, CGP 47 439)		CI .	) RIRIQRGPGRAFVTIG a: IIIB HIV component: v d David Ho, ADARC, NY		Vaccine	murine (IgG1κ)
		Andrus 1998, Parren	1998a, Gauduin1998	Moore1993a, Safrit1993, Th at has a human IgG1 Fc don	ali1993, Pirofski1993, Gauduii	n1995, Sattentau1995	b, Poignard1996a,
		<ul> <li>BAT123: Anti-idiot</li> <li>BAT123: Called BA binding to IIIB gp12</li> <li>BAT123: Passive tra</li> <li>BAT123: Passive tra mice from infection</li> <li>BAT123: Binds with</li> <li>BAT123: Epitope do virus (BAT123 less</li> <li>BAT123: Post-expo declined to 50% if of that could protect de</li> <li>BAT123: The MAb determined by the fi</li> <li>BAT123: Post-expo elicited by CGP 47</li> </ul>	ypic MAb, AB19-4i, stimu (T-123 – conformational, do 20 [Moore1993a] ansfer to Hu-PBS-SCID mi egion sequenced – heavy cl ansfer of BAT123 to hu-PB – the protection, like the Martin high affinity to monomer escribed as RGPGRAFVTI so than the others), mimick sure prophylaxis was effect delivered 4 hours post infection and Fab binding to the oligonaction of Ab sites occupied sure passive transfer of murating that 439, a BAT123 chimera that	lates anti-anti-ID which neu- bes not bind well to denature ce confers protection agains nain: V 3660-SB32, D unkn L-SCID mice 1 hour prior to IAb, was specific for the vir- and oligomer, rapid associa GK – V3 MAbs 9284, BAT- ting sCD4, and expose the gaive when MAb 694/98-D was the grive when MAB 694/98-D was the gr	tralizes MN and IIIB [Fung 1995 ed gp120 – not reactive with SF et challenge with homologous cown, J H3 – light chain: V kap to inoculation with HIV-1 LAI, al strain LAI [Gauduin1995] tion and potent neutralization of 123, 110.5, and 110.I could eac p41 epitope for MAb 50-69, in as delivered 15 min post-exposaints have been observed for H neutralization were highly corrected epitope [Parren1998a] tection to hu-PBL-SCID mice eain, suggesting that the protect	F-2 gp120 – does not ell-free virus [Safrit1 pa21, J kappa2 [Pirof or up to four hours post flab strain [Sattentauth significantly increased contrast to anti-V2 Marre to HIV-1 LAI in ElVIG, 2F5 and 2G12 elated – authors suggesthallenged with HIV-tion is mediated by co	993] Sski1993] Ost-exposure, could protect 11995b] Use gp120 dissociation from MAbs [Poignard1996a] hu-PBL-SCID mice, but , in contrast to MAb BAT123 est that neutralization is 1 LAI – this protection is not complement – the protective
120	020 D (020)	so an IgG2 MAb mi	ght perform better [Gaudui	n1998]	which inactivates serum comp		
439	838-D (838)	References Gorny1  838-D: Five human cross-reactive with  838-D: Four primar inhibited by all poly anti-CD4bd (559/64 (419-D, and 447-52 at all by MAbs indiv [Hioe1997b]  838-D: Using a who 838-D bound B clace	997, Hioe 1997b, Nyambi 19 MAbs against were derived V3 peptides from clade A at y isolates showed distinct proclonal sera and plasma test I-D, 654-D and 830-D and cluster II gp41 (98-6 vidually or by a cocktail of the virions but had limited clade specificity and anti-V3	I from HIV-infected North And C, and could bind to 5/8 patterns of sensitivity to neured, and was also neutralized a cluster II of gp41 directed MAbs at higher concentraten MAbs consisting of 419 8 human MAbs were tested coss-reactivity with other class	L YU Med. Center) Ila-Pazner1999b, Gorny2000a, American subjects after selectic B clade V3 peptides – 50% ne ralization by polyclonal sera or I by 8/17 MAbs, in particular a MAb (98-6) – isolates 92HT59 tions – US4 was neutralized by -D, 447-52D, 782-D, 838-D, 5 for their ability to bind to a pa des, with low levels of binding ed strong binding to many A, I	on by the V3 RF pepti utralization of RF wa r plasma and MAbs – nti-V3 loop (419-D, 4 93 and 91US056 were r some of the polyclor 59/64-D, 654-D, 450 nel of 9 viruses from g to A and D virions [	ide – 838-D was s obtained [Gorny1997] BZ167 was the only isolate 447-52D, 782-D, and 838-D), e neutralized by V3 loop nal sera/plasma tested and no -D, 670-D, 1281-D and 98-6 clades A, B, D, F, G, and H - Nyambi1998]

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Ne	utralizing Immunogen	Species(Isotype)
		core amino acids K.  838-D: Binding of panti-V3 and CD4B5 with a 7-10 fold pre 838-D: A panel of 4 combinations, 44% and H – 838-D show 838-D: Called 838-gp120 MAb produc others, V3) and 697 838-D: A rare muta MAbs directed again anti-V3 MAbs tested 2F5 – thus multiple	SITK tended to be critical panel of 21 MAbs to solub 3 MAbs reacted better with ference for the oligomer [47 human MAbs was tested displayed some viral bind wed intermediate reactivity – Transgenic mice carrying ing hybridomas by immun D (and SC258, V2) were ution in the neutralization s nst the CD4 binding site (d d (19b and 694/98-D) neu	for reactivity in this le oligomeric gp140 in the oligomer and V Gorny2000a] d against 26 HIV-1 g ling – V3 MAbs tendy [Nyambi2000] g human genes allow a controls [Heisensitive R2-strain in CD4BS), CD4-inductralized R2, as did 2 anal targets for neutr	group [Zolla-Pazner1999b] versus gp41 or gp120 mono 2 and C5 tended to favor the roup M primary isolates from ed to have the most cross-reading production of fully huma [162 gp120 – the previously 2002] the proximal limb of the V3 ted (CD4i) epitopes, soluble [3] anti-CD4BS MAbs (15e and alization and the neutralization	1027, 908, and 1006, all selected mers was compared – no MAb were monomer – V3 MAbs 447-52D, and clades A through H – 19 V3 M active binding to clade A, B, C, a man MAbs were used to rapidly credescribed human MAbs 5145A(Coregion caused Env to become se CD4 (sCD4), and HNS2, a broadend IgG1b12), 2/2 CD4i MAbs (1 on sensitivity profile of R2 is interested mercal mercal materials.)	ras oligomer specific, though 838-D, and 1334 bound  Abs were tested, and of 494 and D isolates, less to E, F, G, eate a panel of anti-HIV CD4BS), 4117C (plus insitive to neutralization by lly neutralizing sera – 2/12 7b and 4.8D), and 2G12 and
440	1006-15D (1006)	References Gorny1  1006-15D: Five hur cross-reactive with 1006-15D: Review reactivity with A pe 1006-15D: MAb pe the core amino acid 1006-15D: A panel 494 combinations, 4 F, G, and H – 1006- 1006-15D: Called 1 gp120 MAb produc	V3 peptides from clade A, of clade specificity and an eptides – no binding was ol ptide-reactivity pattern clus s KSITK tended to be criti of 47 human MAbs was to 44% displayed some viral 15D showed strong cross-006 – Transgenic mice can	Zolla-Pazner1999b, lerived from HIV-infe C and other B clade ti-V3 HIV-1-Abs – t beserved with D and lastered with immuno ical for reactivity in lested against 26 HIV binding – V3 MAbs reactivity [Nyambi2 trying human genes sization with HIV SF	Nyambi2000, He2002 ceted North American subject to V3 peptides, but not E clade his Ab showed strong bindin E peptides [Zolla-Pazner1999] logical related MAbs: 838, 7 this group [Zolla-Pazner1999] -1 group M primary isolates tended to have the most cros 000] allowing production of fully 162 gp120 – the previously	ts after selection by the V3 RF per e [Gorny1997] g to several B and F peptides, on Pa] 782, 1027, 908, and 1006, all sele	e C peptide, and some cted with RF V3 peptide –  3 MAbs were tested, and of C, and D isolates, less to E, ly create a panel of anti-HIV
441	782-D (782)	References Gorny1 • 782-D: Five human	997, Hioe1997b, Zolla-Pa MAbs against were derive V3 peptides from clade A	zner1999a, Zolla-Pa ed from HIV-infected	l North American subjects af	HIV-1 infection  fter selection by the V3 RF peptic and 1/2 C clade V3 peptides – 50	

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizing	Immunogen	Species(Isotype)
		inhibited by all poly anti-CD4bd (559/64 (419-D, and 447-52) at all by MAbs indiv [Hioe1997b]  • 782-D: Review of cl with A and D peptide core amino acids KS  • 782-D: A panel of 4 combinations, 44% of the core and the core and the combinations of the core and the core and the core amino acids KS	clonal sera and plasma test-D, 654-D and 830-D and D)and cluster II gp41 (98-cidually or by a cocktail of ade specificity and anti-Vest [Zolla-Pazner1999a] e-reactivity pattern cluster ITK tended to be critical if human MAbs was tested	ted, and was also ne a cluster II of gp41 6) MAbs at higher conference and the mass and the mass at higher conference and the mass and the mass at higher the mass at higher the mass at higher than t	y to neutralization by polyclonal sera of putralized by 8/17 MAbs, in particular a directed MAb (98-6) – isolates 92HT59 concentrations – US4 was neutralized by ag of 419-D, 447-52D, 782-D, 838-D, 50 Ab showed strong binding to several B cal related MAbs: 838, 782, 1027, 908 group [Zolla-Pazner1999b] roup M primary isolates from clades A ed to have the most cross-reactive binding	nti-V3 loop (419-D, 4 93 and 91US056 were 7 some of the polyclon 59/64-D, 654-D, 450- and F peptides, one C 1, and 1006, all selected through H – 19 V3 M	47-52D, 782-D, and 838-D), neutralized by V3 loop al sera/plasma tested and not D, 670-D, 1281-D and 98-6 peptide, and some reactivity d with RF V3 peptide – the Abs were tested, and of 494
442	908-D (908, 908-12D)	References Gorny 19  908-D: Five human cross-reactive with Vobtained [Gorny 199  908-D: Review of cl peptides [Zolla-Pazr  908-D: MAb peptide core amino acids KS  908-D: A panel of 4 combinations, 44% of	297, Zolla-Pazner1999a, Z MAbs against were derive WAS against were derive WAS peptides from clade E, Tollar ade specificity and anti-Valer1999a] E-reactivity pattern cluster WAS ETK tended to be critical of Thuman MAbs was tested displayed some viral bindi	Colla-Pazner1999b, Node from HIV-infected but could bind to 6/8 and HIV-1-Abs — this Act and with immunological for reactivity in this Lagainst 26 HIV-1 gray — V3 MAbs tend	L.nyu) (NYU Med. Center) Nyambi2000 I North American subjects after selection B B clade V3 peptides, 2/4 A clade, and Ab showed strong binding to several A, cal related MAbs: 838, 782, 1027, 908. group [Zolla-Pazner1999b] roup M primary isolates from clades A ed to have the most cross -reactive bind by 50% neutralization on 2/5 isolates tes	B, C and F peptides, and 1006, all selected through H – 19 V3 M ling to clade A, B, C,	eutralization of RF was and poor binding to E and D d with RF V3 peptide – the Abs were tested, and of 494
443	1027-15D (1027, 1027-D, 1027D)	References Gorny 19 1027-15D: Five hum cross-reactive with V 1027-15D: Review of reactivity with A, D 1027-15D: MAb per the core amino acids 1027-15D: A panel of 494 combinations, 4	297, Zolla-Pazner1999a, Zonan MAbs against were de 373 peptides from clade A of clade specificity and ant and E peptides [Zolla-Pazotide-reactivity pattern clus KSITK tended to be critiof 47 human MAbs was te	Colla-Pazner1999b, Norived from HIV-infector E, but could bind in Li-V3 HIV-1-Abs — the collapse of the collap	icted North American subjects after selected North American subjects after selected 3/8 B clade V3 peptides, and 1/2 C chis Ab showed moderate binding to sevel logical related MAbs: 838, 782, 1027, whis group [Zolla-Pazner1999b] -1 group M primary isolates from clade tended to have the most cross-reactive.	clade V3 peptides [Go eral B and F peptides, 908, and 1006, all sele s A through H – 19 V	one C peptide, and was not ected with RF V3 peptide –  3 MAbs were tested, and of

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizing	Immunogen	Species(Isotype)
		to neutralization by neutralizing sera – 2 and 4.8D), and 2G12	MAbs directed against the /12 anti-V3 MAbs tested (2 and 2F5 – thus multiple 6	CD4 binding site (CD4BS 19b and 694/98-D) neutral epitopes on R2 are function	e R2-strain in the proximal limb ), CD4-induced (CD4i) epitoped ized R2, as did 2/3 anti-CD4BS and targets for neutralization and ally resistant MN-primary strain	s, soluble CD4 (sCD- MAbs (15e and IgG the neutralization se	4), and HNS2, a broadly 1b12), 2/2 CD4i MAbs (17b
444	F19.26-4	Ab type V3 References Boudet1	994	IRIQRGPGRAFVT  train: IIIB HIV compone  liotype antibodies [Boudet		Vaccine	murine (IgG2aκ)
445	F19.48-3	Ab type V3 References Boudet1	994	IRIQRGPGRAFVT train: IIIB HIV compone liotype antibodies [Boudet		Vaccine	murine (IgG2aκ)
446	F19.57-11	Ab type V3 References Boudet1 • F19.57-11: MAb F1 • F19.57-11: Anti-ant	991, Boudet1994, Boudet 9.57-11 is strain specific for i-idiotypic antibodies (Abs)	or LAI – used to raise anti-	idiotype rabbit antibodies (calle ice that had greater breadth of r		
447	M77	<ul> <li>References Pal1992</li> <li>M77: IIIB-specific M</li> <li>M77: Antibody bind native gp120 binding</li> <li>M77: MAbs against inhibit gp120 bindin</li> <li>M77: Reacted with M</li> <li>M77: Conformation</li> <li>M77: Stated to be a sera – M77 neutraliz</li> <li>M77: Used M77 bot immunogen generate</li> <li>M77: Native M77 is</li> </ul>	, diMarzo Veronese 1992, of MAb, immunoprecipitates ling to viral isolates from I g, but not peptide binding by the glycosphingolipid Galg to GalCer in vitro [Cook both reduced and non-redual rearrangements upon bin murine MAb – a neutralization was only slightly record to gp 120 as an immuned MAbs to more linear ephighly strain specific, and	deglycosylated form [diMa IIIB infected lab worker fol [diMarzo Veronese1993] (Cer block HIV infection of 1994] (ced covalently cross-linked anding of M77 to gp120 ger lation escape mutant (HXB) duced by this mutation [Wa logen – analysis of polyclor bitopes than gp120 alone or 1 V3 binding is primarily de	atkins1993, Cook1994, DeVicolarzo Veronese1992] Illowed through time – A to T su f normally susceptible CD4 negative from the susceptible CD4 regative from the susceptible CD4 complex [DeVicolariates novel epitopes called me 2 A281V) was selected by grow	bstitution resulted in ative cells from the b 1995] tatopes [Denisova199 th of HXB2 in the provere generated) responsa 1996] light chain switched	the loss of neutralization and rain and colon – this MAb can [95] resence of broadly neutralizing onse suggests the M77-gp120 [Fab version of M77 could]

No.	MAb ID	<b>HXB2</b> Location	<b>Author's Location</b>	Sequence	Neutralizing	Immunogen	Species(Isotype)
				anti-idiotypic Abs directed aga prolong the primary response a			
448	SP.BAL114	gp160 (308–317) <b>Ab type</b> V3	gp120 (BAL)	SIHIGPGRAF	L		murine? (IgG2aκ)
		References Arendru	p1995				
		Authors suggest that	during in vivo immunosele	ection of escape virus, the V3 d	omain gains increasing res	emblance to that of lab	strains [Arendrup1995]
449	SP.SF2:104	gp160 (308–317) <b>Ab type</b> V3	gp120 (SF2)	SIYIGPGRAF	L	HIV-1 infection	(IgG2a\kappa)
		References Arendru	p1993, Arendrup1995				
			•	alize primary virus isolated from	n a time point of neutraliza	tion resistance of autolo	ogous virus [Arendrup1993
			•	immunoselection of escape vi			
		[Arendrup1995]		•		, and the second	
450	polyclonal	gp160 (308–319)	gp120 (304–318 LAI)	RIHIGPGRAFYT		HIV-1 infection	human (IgG, IgM)
	1 7	Ab type V3					(0,70,7
		References Langedij	k1995				
		-		eactivity against a panel of pep pediik19951	tides based on autologous	sequences provide evide	ence for immunological
		escape mutations in t	the tip of the v3 loop [Lang	5001,111//0]			
<del></del> 451	19b	gp160 (308–320)	gp120	-IGFY-T	L	HIV-1 infection	human (IgG1)
<del></del> 451	19b	gp160 (308–320)		-IGFY-T	L	HIV-1 infection	
<del></del> 451	19b	gp160 (308–320) <b>Ab type</b> V3 <b>Donor</b>	gp120 James Robinson, Univers	-IGFY-T	_		human (IgG1)

Kolchinsky2001, Schulke2002, Zhang2002, Poignard2003

- 19b: V3 loop binding MAb that is more broadly clade cross-reactive than most (binds to 19/29 clade B and 10/12 clade E gp120s) [Moore1994b]
- 19b: Competition studies with human sera from seroconverting individuals showed that anti-CD4 BS antibodies can arise very early in infection, comparable or prior to anti-V3 antibodies [Moore1994a]
- 19b: Formalin inactivation of virus at 0.1% formalin for 10 hours at 4 degrees was optimal for inactivation of virus while maintaining epitope integrity [Sattentau1995c]
- 19b: Binds to some gp120s from clades A,B,C,E, and F weakly neutralized some B and one C clade virus [Moore1995c]
- 19b: Despite broad gp120 binding reactivity, not broadly neutralizing [Moore1995a]
- 19b: Review: more broadly cross-reactive than anti-V3 tip MAb 447-D [Moore1995b]
- 19b: Not as effective as IgG1b12 at neutralization ex vivo of virus direct from plasma of HIV-1 infected individuals [Gauduin1996]
- 19b: MIP-1alpha binding to CCR-5 expressing cells can be inhibited by gp120-sCD4 binding of 19b blocks this inhibition [Wu1996]
- 19b: Inhibits gp120 interaction with CCR-5 in a MIP-1beta-CCR-5 competition study [Trkola1996a]
- 19b: In a multilaboratory blinded study, failed to consistently neutralize any of nine B clade primary isolates there were four sequences with variations in the defined epitope among the 9 isolates tested [D'Souza1997]
- 19b: Study shows neutralization is not predicted by MAb binding to JRFL monomeric gp120, but is associated with oligomeric Env binding 19b bound monomer, did not bind oligomer or neutralize JRFL [Fouts1997]
- 19b: Viral binding inhibition by 19b was weakly correlated with neutralization (all other neutralizing MAbs tested showed some correlation except 2F5) [Ugolini1997]

No. MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizing Immunogen	Species(Isotype)
NO. MADID	<ul> <li>19b: Abs that recog V3 loop, with 5 or 6 and some tolerated bind with out the color 19b: Neutralizes TC</li> <li>19b: Neutralizes TC</li> <li>19b: Used as a cont</li> <li>19b: The MAb and determined by the f</li> <li>19b: No detectable</li> <li>19b: The MAbs with in an immune responsimic the native color also by anti-V3 MA bind C11, 23A, and very strongly induction to SOSgp140,</li> <li>19b: Six mutations CD4BS, and CD4i Ineutralize either for</li> <li>19b: Mutations in the become CD4-indepincluding to 19b [K</li> <li>19b: Ab binding challed IgG1b12, CD4 induction gp41 in gp140unc)</li> <li>19b: A rare mutation MAbs directed again anti-V3 MAbs teste 2F5 – thus multiple sensitive MN-TCLA</li> <li>19b: Virion capture</li> </ul>	nize discontinuous epitopes of essential amino acids distributed for the turn [Boots19]. CLA strains but not primary rol in this Hx10 binding at Fab binding to the oligomeraction of Ab sites occupies neutralizing activity among the broadest neutralizing neutralizing neutralizing activity among the properties of Env and explose 19b and 83.1 – SOSgp. M90, MAbs that bind to get by CD4 in SOS gp140-in contrast to 2F5, which be in MN change the virus from MAbs are 20-100 fold morm [Park2000] wo glycosylation sites in the endent and able to enter ceolchinsky2001].  Baracteristics of SOS gp140 cible 17b, and 19b bound and 23A (binds gp120) dictible 17b, and 19b bound and 23A (binds gp120) dictible 17b, and 19b bound and 23A (binds gp120) dictible 17b, and 19b bound and 23A (binds gp120) dictible 17b, and 19b bound and 23A (binds gp120) neutralization sense the CD4 binding site (0d (19b and 694/98-D) neutralization sense and the typically reassays are not a good precedent and about a good precedent and and a good precedent and a good preceden	es can identify mimotopes fuributed within a 12 amino and be I, V, or L, the Y can be 197]  y isolates [Parren1997c]  and neutralizing MAb study eric form of gp120 and neutralizing material study eric form of gp120 and neutralized study. IgG1b12, 2G12 and virion surface rather than depoined its potential as an immunitation of material	om a phage peptide display library – 19b has an epit cid stretch – the previously determined binding site Y, F, or W – probably a beta-turn is required for FY probably and probably and the region of TCL probably a disulfined for FY probably a beta-turn is required for FY probably a disulfined for FY probably and probably a beta-turn is required for FY probably and FY probably a beta-turn is required for FY probably and the probably a beta-turn is required for FY probably and probably and probably a beta-turn is required for FY probably and probably and probably a beta-turn is required for FY probably and probably a beta-turn is required for FY probably and probably and probably a beta-turn is required for FY probably and probably and probably and probably a beta-turn is required for FY probably and probably and probably a beta-turn is required for FY probably and probably and probably a beta-turn is required for FY probably and probably and probably a beta-turn is required for FY probably and probably and probably a beta-turn is required for FY probably and probably and probably and probably a beta-turn is required for FY probably and probably and probably and probably and probably and p	ope involving the tip of the was confirmed -I—G–FY-T or FF binding, but WY in can nat neutralization is  A strains [Trkola1998] dicating that they were raised SOS gp140) was created to 2, 2G12, and CD4-IgG2, and -42 and G3-519 – nor did it epitopes, 17b and A32 were 4, T15G1 and 4D4, did not xes [Binley1999] dization sensitive – V3, red around 950 ng/ml to 199) cause the virus to ation sensitivity of the virus, fide bond – NAbs 2G12, 2F5, izing MAbs 2.2B (binds to sitive to neutralization by addy neutralizing sera – 2/12 17b and 4.8D), and 2G12 and termediate between the highly be different from that of
		neutralization – while b12 oor neutralizers [Poignard2		the three primary virions JR-CSF, A DA, and 89.6, the	e Abs F105, 19b, and Fab b6
452 4G10	Ab type V3 Dono References vonBru • 4G10: A 25 amino	nn1993	, Max-von-Pettenkofer-Inst eed to HBcAg enhanced V3	Vaccine tut, Ludwig-Maximilians-Universitat Munchen, Ger immunogenicity [vonBrunn1993]	murine

**HIV Antibodies Tables** 

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizing	Immunogen	Species(Isotype)
453	5F7		gp120 (308–322 LAI) e: HBcAg fusion HIV con	RIQRGPGRAFVTGK  mponent: V3  Max-von-Pettenkofer-Institut, Lu	dwig-Maximilians-Univ	Vaccine	murine
		References vonBru		with-von-rettenkorer-mettut, Le	awig-waxiiiiiaiis-Oiiiw	ersitat ivianenen, Germa	my
				to HBcAg enhanced V3 immuno	genicity [vonBrunn1993]	]	
45.4	G2 522		search and Reference Reag				
454	G3-523	gp160 (308–322) <b>Ab type</b> V3	gp120 (308–322)	RIQRGPGRAFVTIGK			murine
			hita1988, Jagodzinski1996				
		• G3-523: The sulfate binding [Jagodzinsk		sulfate (CRDS) binds to the Envel	ope of T-tropic viruses ar	nd neutralizes virus – C	RDS inhibits G3-523
455	MN215	gp160 (308–322) <b>Ab type</b> V3	gp120 (MN)	RIHIGPGRAFYTTKN	L	HIV-1 infection	human (IgG1)
		References Schutte	n1995b				
				Dutch consensus is AFYTTGE,			V transformation of PBM
		– displayed higher a	*	glycoproteins – amino acids HIG	were essential for bindi	ng [Schutten1995b]	
456	Nea 9301	gp160 (308–323)	gp120 (IIIB)  or Dupont, commercial	RIQRGPGRAFVTIGKI			murine
		References Wagner	-				
457	4117C	gp160 (309–315) <b>Ab type</b> V3	gp120	IXIGPGR	L	HIV-1 infection	human (IgG1λ)
		References Tilley 19		Veronese1993, Pinter1993a, Pinter			
				N, SF-2, and NY-5 – synergy with		•	0021
			•	y combined with anti-CD4 binding ipitate soluble gp120, does react	2	_	992]
		• 4117C: A study of 6		ability to bind or direct ADCC ag	O.	-	nd RF – bound and directe
		•		s allowing production of fully hur	nan MAbs were used to r	apidly create a panel of	anti-HIV gp120 MAb
			nas by immunization with F V2) were used as controls [	HIV SF162 gp120 – the previousl He2002]	y described human MAbs	s 5145A(CD4BS) , 411	7C (plus others, V3) and
458	419-D (419,	gp160 (309–315)	gp120 (MN)	IHIGPGR	L	HIV-1 infection	human (IgG1λ)
	419D)	Ab type V3 Dono References	or Susan Zolla-Pazner (Zol	las01@mcrcr6.med.nyu) (NYU N	Ied. Center)		

- 419-D: MN, NY5 and SF2 strain specific, does not cross-react with RF, CDC4, WM52 or HXB2 [Karwowska1992b]
- 419-D: Neutralizes MN binds SF2: IYIGPGR [Gorny1993]
- 419-D: Mediated deposition of complement component C3 on HIV infected cells, enhanced by second Ab binding, rabbit anti-human IgG [Spear1993]

No.	MAb ID	HXB2 Location	<b>Author's Location</b>	Sequence	Neutralizing	Immunogen	Species(Isotype)		
NO. MAD ID		<ul> <li>419-D: Four primary isolates showed distinct patterns of sensitivity to neutralization by polyclonal sera or plasma and MAbs – BZ167 was the only isolate inhibited by all polyclonal sera and plasma tested, and was also neutralized by 8/17 MAbs, in particular anti-V3 loop (419-D, 447-52D, 782-D, and 838-D), anti-CD4bd (559/64-D, 654-D and 830-D and a cluster II of gp41 directed MAb (98-6) – isolates 92HT593 and 91US056 were neutralized by V3 loop (419-D, and 447-52D) and cluster II gp41 (98-6) MAbs at higher concentrations – US4 was neutralized by some of the polyclonal sera/plasma tested and not at all by MAbs individually or by a cocktail of ten MAbs consisting of 419-D, 447-52D, 782-D, 838-D, 559/64-D, 654-D, 450-D, 670-D, 1281-D and 98-6 [Hioe1997b]</li> <li>419-D: Using a whole virion-ELISA method, 18 human MAbs were tested for their ability to bind to a panel of 9 viruses from clades A, B, D, F, G, and H – 419-D bound to 3/4 B clade virions, and to D clade MAL [Nyambi1998]</li> <li>419-D: Review of clade specificity and anti-V3 HIV-1-Abs – epitope is described as KRIHIGP [Zolla-Pazner1999a]</li> <li>419-D: MAb peptide-reactivity pattern clustered with immunological related MAbs: 1334, 419, 504, 447, 453 and 537 – the core amino acids GP tended to be critical for reactivity in this group [Zolla-Pazner1999b]</li> <li>419-D: A panel of 47 human MAbs was tested against 26 HIV-1 group M primary isolates from clades A through H – 19 V3 MAbs were tested, and of 494 combinations, 44% displayed some viral binding – V3 MAbs tended to have the most cross-reactive binding to clade A, B, C, and D isolates, less to E, F, G, and H – 419-D showed intermediate reactivity, and no neutralization when tested against five strains – discrepancy between the epitope as described in earlier papers and as described here, KRIHIGP [Nyambi2000]</li> <li>419-D: Called 419 – Transgenic mice carrying human genes allowing production of fully human MAbs were used to rapidly create a panel of anti-HIV gp120 MAb producing hybridomas</li></ul>							
459	453-D (453)	gp160 (309–315) Ab type V3 Donc References Gorny1  • 453-D: Neutralizes  • 453-D: Moderate ho  • 453-D: Review of c  • 453-D: MAb peptic be critical for reactiful strating that cont  • 453-D: A panel of 4 combinations, 44%	gp120 (MN)  or Susan Zolla-Pazner (Zo 991, Gorny1993, VanCott MN – binds SF2: IYIGPC omologous neutralization, epitope described as KRI ontenot1995] lade specificity and anti-V de-reactivity pattern cluste vity in this group – MAb 2 text can be critical [Zolla- 17 human MAbs was teste	IHIGPGR Illas01@mcrcr6.me 1994, Fontenot199 GR – specificity: M moderately slow d HIGPGR – the tip  Ta HIV-1-Abs [Zoll bred with immunole 268, with a previou Pazner1999b] d against 26 HIV-1 ing – V3 MAbs ter	L ed.nyu) (NYU Med. Center) 5, Zolla-Pazner1999a, Zolla-Pazner1999b, N, SF2, NY5, RF [Gorny1993] issociation rate [VanCott1994] of the V3 loop was presented in a mucin ba	ackbone – higher va 453 and 537 – the c HIGPGR), was not p brough H – 19 V3 M	ore amino acids GP tended to art of this reactivity group,  IAbs were tested, and of 494		
460	504-D (504, 504-10D)	gp160 (309–315) <b>Ab type</b> V3 <b>Dono References</b> Gorny1  • 504-D – Neutralizes	gp120 (MN)	IHIGPGR illas01@mcrcr6.me Zolla-Pazner1999b GR [Gorny1993]	ed.nyu) (NYU Med. Center) , Nyambi2000	HIV-1 infection	human (IgG1κ)		

- 504-D: Review of clade specificity and anti-V3 HIV-1-Abs [Zolla-Pazner1999a]
- 504-D: MAb peptide-reactivity pattern clustered with immunological related MAbs: 1334, 419, 504, 447, 453 and 537 the core amino acids GP tended to be critical for reactivity in this group [Zolla-Pazner1999b]

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizi	ng Immunogen	Species(Isotype)
		combinations, 44%		ding – V3 MAbs tended to h			MAbs were tested, and of 494 and D isolates, less to E, F, G,
461	83.1 (MAb 83.1)	Ab type V3 Don References White • 83.1: Neutralizes S • 83.1: Study of syn	-Scharf1993, Potts1993, Jo SF2 [White-Scharf1993] ergism of neutralization ar	epligen Corporation, Cambri elonek1999, Keller1999, Bin and binding comparing F105			
		mice [Jelonek 1999]  83.1: 19 day old m response, suggesti  83.1: The MAbs w in an immune resp mimic the native c also by anti-V3 M bind C11, 23A, an very strongly indu	pinice injected with 83.1 having that prior treatment with with the broadest neutralizing onse to the oligomer on the conformation of Env and example Abs 19b and 83.1 – SOSgl d M90, MAbs that bind to ced by CD4 in SOS gp140	e a shift in IgG1 response aw h a MAb can mask immunog ng activity, IgG1b12, 2G12 a e virion surface rather than c cplore its potential as an imm b140 is not recognized by C4 gp120 C1 and C5, where it is a anti-gp41 MAbs that bind	ay from the V3 loop upon vac tenic sites and shift the immurand 2F5, all have high affinity issociated subunits – a disulfi	ecination, without decrease response to vaccinate for the native trimer, in de linked gp120-gp41 gnized by NAbs IgG1b only TCLA strains, Gatat bind CD4 inducible ith gp120, 7B2, 2.2B, 7	ndicating that they were raised (SOS gp140) was created to 12, 2G12, and CD4-IgG2, and 3-42 and G3-519 – nor did it epitopes, 17b and A32 were F4, T15G1 and 4D4, did not
462	5023B	Ab type V3 References Lange			no	Vaccine	murine (IgG)
463	F58/D1 (F58	Vaccine Vector/Ty Ab type V3 References Akerb • F58/D1: Binding t [Moore1993c] • F58/D1: The inter mass spectrometry • F58/D1: A 17 ami	to native gp120 1-3 fold graction of a 17-amino-acid [Millar1998] no acid MicroAB was made of mass than the original	Moore1993c, Millar1998, Jac eater than to denatured – 31 <sup>4</sup> neutralizing microantibody (	G/W substitution abolishes b MicroAB) based on F58 and l tarity-determining region of the	HIV-1 env was studied the heavy chain of MAb	•
464	P1/D12	gp160 (309–316) <b>Vaccine</b> <i>Vector/Ty</i>	gp120  pe: virus derived protein	IxxGPGRA Strain: IIIB HIV compone	L ent: gp120	Vaccine	murine (IgG)

No.	MAb ID	HXB2 Location	<b>Author's Location</b>	Sequence	Neutralizing Immunogen	Species(Isotype)
			m1990, Moore1993c native gp120 1-3 fold grea	nter than to denatured – 314G	W substitution abolishes binding, changes outside	the loop have little effect
465	P4/D10 (P4D10)	Ab type V3 References Akerblom1990, Bro P4/D10: Neutralizin P4/D10: Variable do P4/D10: Binding to [Moore1993c] P4/D10: Primary iso P4/D10: Used for pa MAb F58/H3 [Hink P4/D10: Called P4E neutralize an HIV-B [Schonning1998] P4/D10: Called P4E all or none, i.e., each	liden1990, Broliden1991, g and ADCC activity [Broomain sequenced and is idenative gp120 3 fold greate plates from different time passive immunotherapy in foula1994] passive immunotherapy, sup10 – In a study of the influ RU mutant virus that lacks pl10 – the stoichiometry of a envelope oligomer binds	oliden1990] entical to F58/H3 [Marks1992] r than to denatured – 314G/W entities from one individual we cour late-stage HIV-infected parametrizing [Hinkula1994] in the late of the glycan at position is the V3 loop glycan more efform.  MAb neutralization was tested a single MAb and each Envice.	endrup1993, Hinkula1994, Jacobson1998, Schonn	me loop have little effect endrup1993] any of these four – see also  MAbs were found to tested to be 314-323 of BRU tion was was incremental not MAb BC1071 was used for
466	IIIB-13 V3 (1044-13 IIIB-V3-13 1727)	Ab type V3 References Laman1 IIIB-13 V3: Also kn IIIB-13 V3: Neutral IIIB-13 V3: Include other than IIIB [D'S IIIB-13 V3: Called sera – IIIB-V3-13 nd IIIB-13 V3: Called mimic a fusion inter	nown as 1044-13 and as III izes IIIB but not MN [Lam d in a panel of antibodies uouza1994] [IIIB-V3-13 – a neutralizatioutralization was only slight 1727: Used as a standard f	on escape mutant (HXB2 A2 at the property of t	ntibody characterization and assay comparison, so 81V) was selected by growth of HXB2 in the present	ence of broadly neutralizing

highly sensitive MN-TCLA strain and the typically resistant MN-primary strain [Zhang2002]

and 2F5 - thus multiple epitopes on R2 are functional targets for neutralization and the neutralization sensitivity profile of R2 is intermediate between the

No.	MAb ID	HXB2 Location	<b>Author's Location</b>	Sequence	Neutralizing	Immunogen	Species(Isotype)
			lical Research Council AII OS Research and Reference				
467		Ab type V3 References Laman 19 IIIB-34 V3: Neutrali IIIB-34 V3: Called I native and denatured	zes IIIB but not MN – QX0 IIB-V3-34 – IIIB strain spe	IQRGPGRAF  GPG are critical amino acids for becific neutralization – binding is reported by the property of th			murine (IgG1)  Industry to the desired by NP40, but binds to
468	A47/B1	gp160 (309–318) Vaccine Vector/Type. Ab type V3 References Akerbloo	gp120 (307–316 IIIB) : protein <i>Strain:</i> IIIB <i>H</i> m1990	IQRGPGRAFV IV component: gp120	L	Vaccine	murine (IgG)
469	D59/A2	gp160 (309–318) Vaccine Vector/Type Ab type V3 References Akerbloi	gp120 (307–316 IIIB) protein <i>Strain:</i> IIIB <i>H</i>	IQRGPGRAFV IV component: gp120	L	Vaccine	murine (IgG)
470	G44/H7	gp160 (309–318) Vaccine Vector/Type. Ab type V3 References Akerbloi	gp120 (307–316 IIIB) protein <i>Strain:</i> IIIB <i>H</i>	IQRGPGRAFV IV component: gp120	L	Vaccine	murine (IgG)
471	M096/V3	gp160 (309–318 + 329–338) <b>Ab type</b> V3 <b>References</b> Ohlin199 • M096: Generated in 329-338 [Ohlin1992]	response to IIIB Env 286-4	IQRGPGRAFV+AHCNISRAKW		in vitro stimulation	human (IgM) eptides: 309-318 +
472		• mu5.5: Rmu5.5 is a l	loss of IIIB type-specificity	IHIGPGRAFYT  y for MAb 0.5beta, allowing bind use MAb m5.5 – neutralized primoto1998]			
473	loop 2 (Loop 2, IgG1 Loop 2)	References Barbas I		SISGPGRAFYTG rch Institute, La Jolla, CA 996, Ditzel1997, Ugolini1997, Pa s a obtained by engineering Fab lo			human Fab 98a, Sullivan1998a

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizing	g Immunogen	Species(Isotype)
		<ul> <li>loop 2: Called Loop</li> <li>loop 2: MIP-lalpha</li> <li>loop 2: Binds to gp</li> <li>loop 2: Viral bindin except 2F5) [Ugolin</li> <li>loop 2: Epitope is stage [Parren1997a]</li> <li>loop 2: Neutralizes</li> <li>loop 2: The rank or markedly different to b13) and binding fraction of Ab sites loop 2, suggesting to loop 2: The HIV-lastate could be conferenced</li> </ul>	o 2 – shows modest cross-ibinding to CCR-5 express 120 from MN and SF2 but g inhibition by loop 2 MA 11997] uggested to be GPGRAF - TCLA strains but not prinder of Fab binding affinity than Fab binding affinity to oligomeric form and ne occupied on a virion irrespective in the IgG1 form may bind wirus YU2 entry can be entered on HxB2 by introduction.	reactivity among B c sing cells can be inh t not LAI [Ditzel199 Ab or Fab was correlated by the correl	atted with neutralization (all other neutralization) (all other neutralizat	op 2 blocks this inhibition of 2 blocks this inhibition alizing MAbs tested slam can neutralize MN at $> b3 > b14 > b13 > D0$ oop $2 > b11 > L17 > b1$ hors suggest that neutration 2 is only 2-fold great epitopes – the activation is similar effect is observed.	nowed some correlation and 2 primary isolates tested 0142-10 > DA48 > L17) was 5 > DO8i > b14 > DA48 > b3 alization is determined by the ater than monovalent Fab tion for this enhanced entry wed by sub-neutralizing
474	(268-11-D-IV 268D, 268, 268-11D, 268-10D, MAb 268, 268-10-D, ARP3024)	gp160 (310–315)  Ab type V3 Donc References Gorny1 McKeating1996b, V Laisney1999, Hioe2  268-D: Called 268-  268-D: Neutralizes  268-D: Mediated de  268-D: Moderate di  268-D: Serotyping s  268-D: The binding with differences in a particularly for mac 268-D: Failed to ne  268-D: 268-D is V infected individuals  268-D: Poor reactiv  268-D: A T-cell line could use either CC and is neutralized [1]	gp120 (MN)  or Susan Zolla-Pazner (Zo 991, D'Souza1991, Karwe Visnewski1996, Hioe1997 2000, Nyambi2000, Park20 11-D-IV – strain specific v MN, NY5, CDC4, RF and MN – binds SF2: YIGPG reposition of complement c ssociation rate and homole study using flow-cytometr of conformation-dependence cell tropism was studied – rophage-tropic isolates SF ociated gp120, although so utralize HXB2 and chimer H4 – V-region heavy chair [Wisnewski1996] ity against HIV-1 isolates e-adapted (TCLA) derivati R5 or CXCR4, and was no	HIGPGR bllas01@mcrcr6.med owska1992b, Gorny b, Stamatatos1997, 000, York2001, Vella weakly neutralizing d SF2, does not cross R – specificity: MN, component C3 on HI ogous neutralization y, if H of HIGPGR v ent anti-V2, anti-V3, V3 loop epitopes w F162 and SF128a, re CD4 binding did alte ric virus with gp120 n usage was examine SF162 and SF128A ive of SI primary iso ot neutralized when	L.nyu) (NYU Med. Center) 1993, Spear1993, VanCott1994, Stama LaCasse1998, Zolla-Pazner1999a, Zolla 2002, Zhang2002 D'Souza1991] s-react with WM52 or HXB2 [Karwow SF2, NY5, RF, CDC4 [Gorny1993] V infected cells, but not in the presence titer [VanCott1994] vas substituted in virus, 268-D did not and anti-CD4BS MAbs to monomeric ere less accessible to Ab binding on the lative to T-cell tropic SF2 – sCD4 assorate pitope exposure for other anti-V3 M from primary isolates in an HXB2 bace and and a bias of enhanced V H1 and V and no neutralization, in contrast to M late 168P acquired the ability to be neutralization was directed via either pathw	HIV-1 infection  atatos1995, Zolla-Pazne la-Pazner1999b, Beddo  vska1992b]  e of sCD4 [Spear1993]  bind [Zolla-Pazner199  and virion-associated e virion surface than in ciation with gp120 did Abs [Stamatatos1995] kground [McKeating19 H4, and reduced V H3  (Abs 391/95-D and 257 atralized by anti-V3 M.	human (IgG1 $\lambda$ ) er1995a, Fontenot1995, ows1999, Oggioni1999,  5a] gp120 from HIV-1 isolates the gp120 monomer, not influence the binding of [ 996b] , was noted among HIV  7-D [Stamatatos1997] Abs – the primary isolate

No. MAb ID HXB2 Location Author's Location Sequence Neutralizing Immunogen Species(Isotype)

• 268-D: Peptide reactivity pattern clustered with immunological related MAbs: 1108, 386, 268, 311, 257, 694.8 – the amino acids HI tended to be critical for reactivity in this group – MAb 453, with an identical core epitope to 268 based on prior experiments (HIGPGR), was not part of this reactivity group, illustrating that context can be critical [Zolla-Pazner1999b]

• 268-D: rgp120 derived from a R5X4 subtype B virus, HIV-1 W61D, was used to vaccinate healthy volunteers and the resulting sera were compared with

- 268-D: rgp120 derived from a R5X4 subtype B virus, HIV-1 W61D, was used to vaccinate healthy volunteers and the resulting sera were compared with sera from HIV-1 positive subjects and neutralizing MAbs 268-D bound rgp120 W61D but could only neutralize the W61D isolate following T-cell line adaptation [Beddows1999]
- 268-D: Called 268-11D Study of a live-vector mucosal vaccine that expresses HIV-1 V3 domains using the bacterium Streptococcus gordonii which can express heterologous Ag and can colonize the oral cavity and vagina of mice 268-D and 257-D recognized S. gordonii expressing the V3 domain of MN the vaccine stimulated V3-specific IgG2a in mice [Oggioni1999]
- 268-D: Called MAb 268 To identify potential mimotopes of V3, a hexapeptide phage library was screened with MAb 268 two hexamers were identified,
  HLGPGR or KAIHRI that bind to 268 with the same binding site as the V3 loop and inhibit 268 MN gp120 KLH conjugated hexamer KAIHRI stimulates
  Abs in rabbits that cross-react with ML gp120 [Laisney1999]
- 268-D: Ab responses, because of their capacity to alter antigen uptake and processing, can influence helper T cell responses CD4BS MAbs or serum Ig
  from HIV+ individuals inhibited proliferative responses of gp120 specific T cells V3 MAbs 447-52-D and 268-10-D did not effect proliferation
  [Hioe2000]
- 268-D: A panel of 47 human MAbs was tested against 26 HIV-1 group M primary isolates from clades A through H 19 V3 MAbs were tested, and of 494 combinations, 44% displayed some viral binding V3 MAbs tended to have the most cross-reactive binding to clade A, B, C, and D isolates, less to E, F, G, and H 268-D showed weak reactivity [Nyambi2000]
- 268-D: Called 268D six mutations in MN change the virus from a high-infectivity neutralization resistant phenotype to low-infectivity neutralization sensitive V3, CD4BS, and CD4i MAbs are 20-100 fold more efficient at neutralizing the sensitive form the mutation L544P reduced binding of all MAbs against gp120 by causing conformational changes [Park2000]
- 268-D: Abs against the V3 loop (50.1, 58.2, 59.1, 257-D, 268-D, 447-52D), CD4BS (IgG1b12, 559-64D, F105), CD4i (17b), and to gp41 (2F5, F240) each showed similar binding efficiency to Env derived from related pairs of primary and TCLA lines (primary: 168P and 320SI, and TCLA: 168C and 320SI-C3.3), but the TCLA lines were much more susceptible to neutralization suggesting that the change in TCLA lines that make them more susceptible to NAbs alters some step after binding one of the TCLA V3 viruses 320SI-C3.3 shows reduced binding with this MAb, the sequence of the epitope in 320SI is HIGPGR and in 320SI-C3.3 is RIGPGR [York2001]
- 268-D: Called ARP3024: Herpesvirus saimiri-immortalized CD4+ T lymphocytes (HVS T cells) were used to isolate virus and perform HIV-1 neutralization assays, and compared with a standard PBMC protocol neutralization sensitivities to a panel of MAbs and to homologous or heterologous plasma/sera were similar for HVS T cells (CN-2 cells) and PBMCs [Vella2002].
- 268-D: A rare mutation in the neutralization sensitive R2-strain in the proximal limb of the V3 region caused Env to become sensitive to neutralization by MAbs directed against the CD4 binding site (CD4BS), CD4-induced (CD4i) epitopes, soluble CD4 (sCD4), and HNS2, a broadly neutralizing sera—2/12 anti-V3 MAbs tested (19b and 694/98-D) neutralized R2, as did 2/3 anti-CD4BS MAbs (15e and IgG1b12), 2/2 CD4i MAbs (17b and 4.8D), and 2G12 and 2F5—thus multiple epitopes on R2 are functional targets for neutralization and the neutralization sensitivity profile of R2 is intermediate between the highly sensitive MN-TCLA strain and the typically resistant MN-primary strain [Zhang2002].
- 268-D: UK Medical Research Council AIDS reagent: ARP3024
- 268-D: NIH AIDS Research and Reference Reagent Program: 1511

475 386-D (386, 386-10D, 386D) gp160 (310-315) gp120 (MN)

HIGPGR

L

HIV-1 infection

human (IgG1λ)

References Karwowska1992b, Gorny1993, VanCott1994, Fontenot1995, Zolla-Pazner1999a, Zolla-Pazner1999b, Nyambi2000

Ab type V3 Donor Susan Zolla-Pazner (Zollas01@mcrcr6.med.nyu) (NYU Med. Center)

- 386-D: Neutralizes MN binds SF2: YIGPGR specificity: MN, SF2, NY5, RF, CDC4 [Gorny1993]
- 386-D: Slow dissociation rate, potent homologous neutralization [VanCott1994]

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizing	Immunogen	Species(Isotype)
		<ul> <li>386-D: Peptide reac reactivity in this gro</li> <li>386-D: A panel of 4 combinations, 44%</li> </ul>	up [Zolla-Pazner1999b] 7 human MAbs was tested :	immunological related Magainst 26 HIV-1 group Mg – V3 MAbs tended to ha	Abs: 1108, 386, 268, 311, 257, primary isolates from clades A we the most cross-reactive bindi	through H – 19 V3 M	Abs were tested, and of 494
476	5042A	Ab type V3 References Langed	gp120 (310–315 BH10) e: peptide Strain: BH10 jk1991, Gorny1991 and fine mapping of murine	HIV component: V3	L	Vaccine	murine (IgG)
477	5042B	Ab type V3 References Langedi	gp120 (310–315 BH10) e: peptide Strain: BH10 jk1991 and fine mapping of murine	HIV component: V3	no	Vaccine	murine (IgG)
478	418-D (418, 418D)	References Karwow  418-D: MN strain sp  418-D: Neutralizes 1  418-D: Review of cl  418-D: Called 418 - the core amino acids  418-D: A panel of 4 combinations, 44% and H - 418-D show  418-D: A rare mutat MAbs directed again anti-V3 MAbs tested 2F5 - thus multiple	pecific, does not cross-react MN, does not bind to SF2 of ade specificity and anti-V3 of MAb peptide-reactivity pass HIGPGR tended to be crit human MAbs was tested a displayed some viral binding dintermediate reactivity [ ion in the neutralization sents the CD4 binding site (Cld (19b and 694/98-D) neutralization contents the CD4 binding site (Cld (19b and 694/98-D) neutralization sents the CD4 binding site (Cld (19b and 694/98-D) neutralization sents the CD4 binding site (Cld (19b and 694/98-D) neutralization sents the CD4 binding site (Cld (19b and 694/98-D) neutralization sents the CD4 binding site (Cld (19b and 694/98-D) neutralization sents the CD4 binding site (Cld (19b and 694/98-D)) neutralization sents the CD4 binding site (Cld (19b and 694/98-D))	la-Pazner1999a, Zolla-Paz with SF2, NY5, RF, CDC4 r HXB2 [Gorny1993] HIV-1-Abs [Zolla-Pazner1 ttern clustered with immur ical for reactivity in this gragainst 26 HIV-1 group M g – V3 MAbs tended to ha Nyambi2000] sitive R2-strain in the prop D4BS), CD4-induced (CD4 alized R2, as did 2/3 anti-Cal targets for neutralization	ner1999b, Nyambi2000, Zhang WM52 or HXB2 [Karwowska 1999a] sological related MAbs: 391.5, pup [Zolla-Pazner1999b] primary isolates from clades A we the most cross-reactive bindi- timal limb of the V3 region cau ki) epitopes, soluble CD4 (sCD 194BS MAbs (15e and IgG1b1) and the neutralization sensitive	412 and 418, all selecthrough H – 19 V3 Ming to clade A, B, C, and seed Env to become see 4), and HNS2, a broad 2), 2/2 CD4i MAbs (1	IAbs were tested, and of 494 nd D isolates, less to E, F, G, nsitive to neutralization by fly neutralizing sera – 2/12 7b and 4.8D), and 2G12 and
479	5021	Ab type V3 References Durda19 • 5021: Generation ar	gp120 e: peptide Strain: BH10 988, Durda1990, Langedijk ad fine mapping of murine M tive gp120 100-300 fold gre	1991, Moore1993c //Abs [Langedijk1991]	L  4G/W substitution abolishes by	Vaccine inding, changes outsic	murine (IgG) le the loop have little effect

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizing	Immunogen	Species(Isotype)
480	5025B	<b>Ab type</b> V3 <b>References</b> Langedi	gp120 (310–316 BH10) e: peptide Strain: BH10 ijk1991 and fine mapping of murine	HIV component: V3	no	Vaccine	murine (IgG)
81	5042		988, Durda1990, Moore199	QRGPGRA  3c eater than to denatured – 314G/W	L substitution abolishes by	Vaccine inding, changes outs:	murine ide the loop have little effect
82	110.3	Ab type V3 References Thomas • 110.3: Included as a • 110.3: MAb variable	s 1988, Evans 1989, Langedij a control [Evans 1989] e region sequenced – heavy	QRGPGRAF  tin: BRU HIV component: virus  kk1992, Pirofski1993, Connelly19  chain: V 7138(40), D deletion, J  t 110.3 both mimics and binds to	994 H4 – light chain: V kapp		
883	110.4	Ab type V3 Dono References Thomas Valenzuela1998, Ca  110.4: 313 P/S subs  110.4: MAb variable [Pirofski1993]  110.4: Primary isola  110.4: gp41 mutatio MAb [Thali1994]  110.4: An anti-idiot  110.4: Neutralizes F  110.4: Neutralizatio  110.4: Virus with th but not to and CD4F	or Genetic Systems Corp, Soc 1988, Thali 1992b, Langedi o 1997b, Guillerm 1998 titution in the V3 region dise region sequenced – heavy ates from different time point that confers resistance to the Sypic MAb generated against HV-1 LAI [McDougal 1996] on of LAI in CEM cells by a see V1-V2 loop deleted was vas MAb F105 or sCD4 [Cac	nti-V3 MAbs 110.4 and N11-20 in tisk and more susceptible to new	Arendrup1993, Thali19 o DSP2.3, 2.4 and .6, J F susceptible to neutralizati ng site antibodies does no 0.4 [Connelly1994] is through inhibition of v utralization by CD4i MA	I2 – light chain: V ka ion by 110.4 [Arenda of reduce neutralizing iral binding to the ce b 17b, and anti-V3 M	appa21, J kappa2 rup1993] g efficiency of this V3 region rup1 [Valenzuela1998] MAbs 1121, 9284, and 110.4,
184	110.5	gp160 (310–317) Vaccine Vector/Type	gp120 (308–328 BRU) e: infected-cell lysate Stra or E. Kinney-Thomas or Gen	QRGPGRAF  uin: BRU HIV component: virus  netic Systems, Seattle WA	L s	Vaccine	murine (IgG1κ)

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutra	alizing Immunogen	Species(Isotype)
		Klasse 1993a, Sattent 110.5: Did not induce detection, as the gp1 110.5: Binding inser 110.5: Two fold incr 110.5: Variable regio 110.5: Thrombin cle requirements (G3-29 110.5: The gp41 murneutralizing MAbs – 110.5: Pretreatment 110.5: Binds with hi [Sattentau1995b] 110.5: Reciprocal bi MAbs [Moore1996] 110.5: V3 MAbs 928 epitope for MAb 50- 110.5: Neutralizes H 110.5: Deletion of th 110.5: Viral binding [Ugolini1997] 110.5: The MAb and	au 1995c, Sattentau 1995be edissociation of gp120, a 20-MAb complex was desitive to gp120 reduction ease in binding to gp120 on sequenced – heavy chavage of V3 loop betwee 19) – binding to native gptation 582 (Ala to Thr) respectively of HX10-infected H9 celling affinity to monomer and and inhibition with other 184, BAT123, 110.5, and 1869, in contrast to anti-V2 IV-1 LAI [McDougal199] are V1V2 regions did not a sinhibition by 110.5 was delable to the oligo	o, Moore1996, Poign as sCD4 did – discrete continued in the Poign [Cordell1991] in the presence of buin: V 3660-SB32, In R-315 and A-316 120 100-300 fold grouts in conformation of 110.5 is not affect lis with sCD4 decrea and oligomer, rapid a ler anti-V3 MAbs – of the MAbs [Poignard19 26] affect anti-V3 Abs a correlated with neutroneric form of gp12	p91, Langedijk1992, McKeating Inard1996a, McDougal1996, Jeffs epancy with [Poignard1996a], that ard study [Moore1990b]  ound sCD4 [Sattentau1991]  o closest to DSP2.3, 2.4 and .6, Jabrogates binding – can inhibit Ceater than to denatured [Moore1911] all changes in gp120 that conferenced [Reitz1988, Klasse1993a] ses signal from 110.5 at 37 degrees sociation and potent neutralization enhances binding of some anti-Valificantly increase gp120 dissociation and potent neutralization (all other neutralizing Management of the epitope [Parren1998] ective of the epitope [Parren1998]	1996, Binley1997a, Ugolin at was suggested to be due to the Washington and the Burney 1998. H2 – light chain: V kappa2 (24 region antibody which have 1993c) neutralization resistance to the session of lab strains – neutralization of lab strains – neutralization from virus, mimicking that the control of the property o	i1997, Parren1998a o MAb interference with  i1, J kappa2 [Pirofski1993] as conformational conformationally sensitive i120-gp41 [Sattentau1995c] as cell-free Hx10 i1 by some CD4 binding site sCD4, and expose the gp41 correlation except 2F5)
485	58.2	Ab type V3 Donoi References White-S 58.2: Epitope defined [White-Scharf1993] 58.2: Did not synerg 58.2: Modest cross-r 58.2: Competition E significance of non-c 58.2: The crystal strucker MAb 58.2: 58.2's epitope CD4i (17b), and to g and 320SI, and TCL	charf1993, Potts1993, Mod by peptide reactivity an istically neutralize MN ir eactivity among B clade LISAs with serial deletio contact residues [Seligman acture of Fab 58.2 bound s were bound – 58.2's epiwas noted to be IGPGRAp41 (2F5, F240) each sho	oore1994b, Seligmad changes in affinity a combination with gp120s, little outsidns produced longer n1996] to V3 loop peptides itope was defined as uF – Abs against the towed similar binding), but the TCLA line	n1996, Stanfield1999, York2001 with amino acid substitutions — MAb F105 — there was synergistic B clade — core epitope as I-IHIC estimates of epitope length, RIHIC was obtained — conformational of KRKRIHIGPGRAFY [Stanfield V3 loop (50.1, 58.2, 59.1, 257-D g efficiency to Env derived from the swere much more susceptible to	c neutralization when comb G [Moore1994b] GPGRAFY, than Alanine s changes in the tip of the V3 1999] b, 268-D, 447-52D), CD4BS related pairs of primary and	ubstitution, suggesting loop (GPGR) were observed S (IgG1b12, 559-64D, F105), TCLA lines (primary: 168P

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizing	Immunogen	Species(Isotype)
486	polyclonal	gp160 (310–318)	gp120	QRGPGRAFV?	L	Vaccine	murine (IgA, IgG1, IgG2a)
			MN HIV component: V	us (Ba) conjugate, peptide keyh	ole limpet hemocyanin (KLH	) conjugate, peptide l	ipopolysaccharide (LPS)
		• Internasal (i.n.) imminduce serum and mainly restricted to	nunization with V3-Ba in nucosal IgA and IgG in B. IgG1, and to V3-Ba, IgG	duced mucosal anti-V3 NAbs a ALB/c mice – i.n. plus i.p. imn 2a – class II KO mice (CD4+-d nses in HIV-1 infected individu	nunizations gave higher titers leficient) did not respond to V	than i.n. alone – the rage of	esponse to V3-KLH was ond to V3-Ba, suggesting the
187	537-D (537)	gp160 (311–315)	gp120 (MN)	IGPGR bllas01@mcrcr6.med.nyu) (NY	L	HIV-1 infection	human (IgG1λ)
		<ul> <li>537-D: Reacts with</li> <li>537-D: MN type sp</li> <li>537-D: Moderate ho</li> <li>537-D: Review of c</li> <li>537-D: MAb peptid be critical for reacti</li> <li>537-D: A panel of 4 combinations, 44%</li> </ul>	MN, NY5, CDC4, RF, We ecific neutralization obseromologous neutralization lade specificity and anti-Vereactivity pattern cluster vity in this group [Zolla-I47 human MAbs was tested	ed against 26 HIV-1 group M pr ling – V3 MAbs tended to have	oss-react with HXB2 [Karwov [Gorny1992, Gorny1993] onstant [VanCott1994] 99a] 1 MAbs: 1334, 419, 504, 447, rimary isolates from clades A	vska1992b]  453 and 537 – the co	ore amino acids GP tended to
488	5020	Ab type V3 References Langed	gp120 (311–316 BH1 e: peptide <i>Strain:</i> BH10 ijk1991 nd fine mapping of murin	) HIV component: V3	no	Vaccine	murine (IgG)
189	RC25		amanized MAb that recog	IGPGRA nizes the epitope IGPGRA – it a study of NAb activity in patie			humanized murine virus) and weak against
490	5023A (5023, NEA-9205, NEA 9205)	Vaccine Vector/Type Ab type V3 Dono	gp120 (311–317 BH1 e: peptide Strain: BH10 or Paul Durda, Du Pont do iik1991, D'Souza1991, B	) HIV component: V3	L	Vaccine	murine (IgG)

**HIV Antibodies Tables** 

No.	MAb ID	HXB2 Location	<b>Author's Location</b>	Sequence	Neutralizing	Immunogen	Species(Isotype)
		as an immunogen [Ro 5023A: Called NEA-	ovinski1995]	precipitate gp160 in immunoblots in a an of the V3 loop makes the tip of the ng1998]			
491	110.6	Ab type V3 References Thomas 1	988, Pirofski 1993, Lai	RGPGRAFV  Strain: BRU HIV component: virus  ngedijk1992  hain: V J558-146b.1alpha, D closest to	L (weak)  DSP16.2, J H3 – light	Vaccine chain: V lambda1,	murine (IgG1λ)  J lambda1 [Pirofski1993]
492	polyclonal	gp160 (311–318) Vaccine Vector/Type: Ab type V3 References Golding1 Ab is evoked even in	995	IGPGRAFY  Strain: SF2, MN HIV component: g + cells	L gp120	Vaccine	murine (IgG2a)
493		Ab type V3 References McKeatin 10/36e: Binding to vi 10/36e: The most var did not affect the abili	ng 1992a, McKeating 19 rion gp 120 enhanced b iable amino acids in th ity of sCD4 or MAbs t	RGPGRAFVTIG  Strain: BH10 HIV component: gp1  993b, Peet1998 by sCD4 [McKeating1992a] e V3 loop were replaced with serines to V1/V2, C1 and C4 to bind, but anti- estituted gp120 had a reduced response	to make the immunodo V3 MAb 10/36e bindin	g was dramatically o	diminished by V3 serine
494	•	gp160 (311–321)  Vaccine Vector/Type: Ab type V3 References McKeatir 10/54: Binding to viri 10/54: Studied in the 10/54: Called 10/54o immunogenic – these diminished by V3 ser	ng1992a, McKeating19 ion gp120 enhanced by context of a neutraliza w/6i/6i: The most varia changes did not affect	RGPGRAFVTIG  Strain: BH10 HIV component: gp1  993a, McKeating1993b, Peet1998  y sCD4 [McKeating1992a]  tion escape mutant [McKeating1993a]  able amino acids in the V3 loop were in the ability of sCD4 or MAbs to V1/V te injected with serine substituted gp12  1998]	 replaced with serines to 2, C1 and C4 to bind, b	out anti-V3 MAb 10/	54 binding was dramatically
495	11/85b (11/85b/14I/14	gp160 (311–321) I)	gp120 (311–321 HXB10)	RGPGRAFVTIG  Strain: BH10 HIV component: gp1	L (HXB2)	Vaccine	rat (IgG2b)

gp160 Antibodies

Vaccine Vector/Type: recombinant protein Strain: BH10 HIV component: gp120

**Ab type** V3

lo.	MAb ID	HXB2 Location	<b>Author's Location</b>	Sequence	Neutralizing	Immunogen	Species(Isotype)
			ing1992a, McKeating199 virion gp120 enhanced by	93b y sCD4 [McKeating1992a]			
96	polyclonal	gp160 (311–322)	gp120 (MN)	IGPGRAFYTTKN	L (MN ALA-1)	Vaccine	guinea pig
		Vaccine Vector/Type Ab type V3	e: human rhinovirus 14	Strain: MN HIV component: V3			
		120 type (					
		References Smith19					
	•	References Smith 19 The tip of the MN V	<sup>7</sup> 3 loop (IGPGRAFYTTK	KN) was inserted into cold-causing huma loop antibodies – chimeric viruses elicit			
7	$0.5\beta$ (0.5 beta,	References Smith19 The tip of the MN V chimeric viruses wer gp160 (311–324)	73 loop (IGPGRAFYTTK re neutralized by anti-V3 gp120 (316–330 HXE	loop antibodies – chimeric viruses elicit 32) RGPGRAFVTIGKIG			
7		References Smith19 The tip of the MN V chimeric viruses wer gp160 (311–324) Vaccine Vector/Type	73 loop (IGPGRAFYTTK re neutralized by anti-V3 gp120 (316–330 HXE 2: protein <i>Strain</i> : IIIB	loop antibodies – chimeric viruses elicit 32) RGPGRAFVTIGKIG HIV component: Env	ed potent NAbs aga	inst ALA-1 and MN [	Smith1998]
7	$0.5\beta$ (0.5 beta,	References Smith 19 The tip of the MN V chimeric viruses were gp160 (311–324) Vaccine Vector/Type Ab type V3 Dono	73 loop (IGPGRAFYTTK) re neutralized by anti-V3 gp120 (316–330 HXE) e: protein Strain: IIIB or Shuzo Matsushita or To	loop antibodies – chimeric viruses elicit  32) RGPGRAFVTIGKIG  HIV component: Env oshio Hattori of Kumamoto University	L (IIIB)	inst ALA-1 and MN [ Vaccine	Smith1998] murine (IgG1 $\kappa$ )
7	$0.5\beta$ (0.5 beta,	References Smith 19 The tip of the MN V chimeric viruses were gp160 (311–324) Vaccine Vector/Type Ab type V3 Dono	73 loop (IGPGRAFYTTK) re neutralized by anti-V3 gp120 (316–330 HXE) e: protein Strain: IIIB or Shuzo Matsushita or To	loop antibodies – chimeric viruses elicit 32) RGPGRAFVTIGKIG HIV component: Env	L (IIIB)	inst ALA-1 and MN [ Vaccine	Smith1998] murine (IgG1 $\kappa$ )
7	$0.5\beta$ (0.5 beta,	References Smith 19 The tip of the MN V chimeric viruses wer gp160 (311–324) Vaccine Vector/Type Ab type V3 Dono References Matsush	73 loop (IGPGRAFYTT) re neutralized by anti-V3 gp120 (316–330 HXE) e: protein <i>Strain:</i> IIIB or Shuzo Matsushita or To nita1988, Skinner1988b,	loop antibodies – chimeric viruses elicit  32) RGPGRAFVTIGKIG  HIV component: Env oshio Hattori of Kumamoto University	L (IIIB)  Souza1991, Matsush	Vaccine vita1992, Emini1992,	Smith1998] murine (IgG1 $\kappa$ ) Maeda1992,

- 0.5beta: Type-specific neutralization of IIIB does not neutralize MN or RF [Matsushita1988, Skinner1988b]
- 0.5beta: Emergence of virus resistant to MAb 0.5beta and autologous sera neutralization in IIIB infected chimps [Nara1990]
- 0.5beta: Potent neutralizing activity [D'Souza1991]
- 0.5beta: Chimeric mouse-human MAb Cbeta1 was constructed by combining the human Cgamma1 and Ckappa constant regions with the 0.5beta murine MAb ADCC and neutralizing activity[Matsushita1992]
- 0.5beta: sCD4 causes loss of IIIB type-specificity, allowing binding and neutralization of MN, in contrast to MAb mu5.5 [Maeda1992]
- 0.5beta: Monoclonal anti-idiotype antibodies that mimic the 0.5beta epitope were generated [Sperlagh1993]
- 0.5beta: Neutralization of virus carrying an A to T substitution (contrast with MAb M77) [diMarzo Veronese1993]
- 0.5beta: Binding to native gp120 100-300 fold greater than to denatured [Moore1993c]

Tugarinov1999, Fortin2000, Jagodzinski2000, Tugarinov2000, Zvi2000

- 0.5beta: The gp41 mutation 582(Ala to Thr) results in conformational changes in gp120 that confer neutralization resistance to some antiserum and conformationally sensitive neutralizing MAbs neutralization efficiency of 0.5beta is not affected [Reitz1988, Klasse1993a]
- 0.5beta: A neutralization escape mutant (HXB2 A281V) was selected by growth of HXB2 in the presence of broadly neutralizing sera of the MAbs tested , 0.5beta neutralization was the most profoundly affected by this mutation [Watkins1993]
- 0.5beta: MAbs against the glycosphingolipid GalCer block HIV infection of normally susceptible CD4 negative cells from the brain and colon this MAb can inhibit gp120 binding to GalCer in vitro [Cook1994]
- 0.5beta: gp41 mutation that confers resistance to neutralization by anti-CD4 binding site antibodies does not reduce neutralizing efficiency of this V3 region MAb [Thali1994]
- 0.5beta: Binding domain aa 310-319: RGPGRAFVTIGKIG mutations in the V3 loop from basic residues can destroy virus infectivity and syncytium formation: R306T, R309T and R313G can also reduce binding of V3 MAbs with two different binding sites: 9284 and 0.5beta [Okada1994]
- 0.5beta: Type-specific neutralization of IIIB does not neutralize SF2 [Broder1994]
- 0.5beta: The interactions of the peptide RKSIRIQRGPGRAFVT 0.5beta were studied by NMR, and hydrophobic interactions between the two Is and the V form the base of a 12 amino acid loop with GPGR at the apex[Zvi1995b]
- 0.5beta: NMR of 0.5beta bound NNTRKSIRIQRGPGRAFVTIGKIG suggests that the bound amino acids are in the region SIRIQRGPGRAFVT [Zvi1995a]

No.	MAb ID	HXB2 Location	<b>Author's Location</b>	Sequence		Neutraliz	zing Immunogen	Species(Isotype)
	MAN ID	0.5beta: The sulfate binding – 0.5beta e     0.5beta: Synergistic     0.5beta: Deletion o     0.5beta: Deletion o     0.5beta: Relative to beta-glucosamine n     0.5beta: The struct     0.5beta: Binds both     0.5beta: The Fv fra     0.5beta: NMR struct     0.5beta: Host encomodify virus sensit lymphocyte functio     0.5beta: MAbs 0.5b results in reduction [Jagodzinski2000]     0.5beta: 14/18 resida beta-hairpin turn     0.5beta: NMR and contribute to the bin interacts with Arg1	ed polysaccharide curdlan pitope described as GPGF concutralization of HIV-1 of the V1V2 regions did not the native peptide, an O-modified peptide showed rare of a 17 amino acid V3 and gp120 and soluble gp120 gment was purified and the cure reveals that Ab bounded intercellular adhesion ivity to antibodies 0.5beta an-association antigen-1 (I beta and G3-42 were used of oligomeric gp120 at the	sulfate (CRDS) bin RAFVTIG [Jagodzir when combined with of affect anti-V3 Abilinked alpha-galactor educed binding [Huppetide bound to the D+gp41 complex efficient temperature depend IIIB-V3 peptide a molecule (ICAM-1) as or 4.8D or sCD4, but LFA-1) Ab [Fortin 20] to study synthesis of the cell surface and of the CSIRIQRGPGRAFV g pocket [Tugarinov ployed to generate a with the peptide – F-RGPG retains hair	aski1996] h anti-V2 MAb C108G s ability to bind when c becamine modified V3 pe ang 1997] he Fab was studied usin diciently, suggesting its indence and effect of me dopts an unexpected ty is incorporated by the but neutralizing ability of 000] of oligomeric and mono f monomer in the cytop VTIG, were shown to b v2000] model of the peptide-a v96(L) of 0.5beta binds pin conformation binds	G-tropic viruse  G-trop	s and neutralizes virus —  s and s a	CRDS inhibits 0.5beta  26] While an N-linked  binding [Wyatt1997]  21999] Ctivity – ICAM-1 does not ring virions in the presence of cycosylation by tunicamycin glycosylated Env precursor asing NMR – QRGPGR forms as that interact or do not
498	<b>C</b> β1, 0.5β	gp160 (311–324)  Vaccine Vector/Typ Ab type V3 References Emini I	gp120 (316–330 HXI)  e: protein Strain: IIIB  992, Matsushita1992, Kinnsfer to chimpanzees cont	32) RGPGRAFVTI  HIV component: E	GKIG Env li2002	L	Vaccine ree virus – mouse 0.5bet	humanized murine (IgG1) a human IgG1 chimera
		<ul> <li>[Emini1992]</li> <li>Cbeta1: Chimeric r MAb – ADCC and</li> <li>Cbeta1: Defines ep study of NAb activi</li> <li>Cbeta1: Review of</li> </ul>	nouse-human MAb Cbeta neutralizing activity [Mat itope as IQRGPGRA – str ity in patients undergoing	al was constructed b tsushita1992] rong neutralizing ac HAART [Kimura20 xis with human NAI	by combining the human tivity against NL4-3 (X 1002] os that also includes thi	n Cgamma1 a	nd Ckappa constant regi	ons with the 0.5beta murine irus) – used as a control in a g it protected 2/2 Chimpanzees
499	NM-01	gp160 (312–315) Vaccine Vector/Typ Ab type V3 Don References Ohno19	gp120 (MN) e: human rhinovirus 14	GPGR Strain: MN HIV 1998	component: V3	L presence of N	Vaccine  VM-01 [Yoshida1997]	murine (IgG)

No.	MAb ID	<b>HXB2</b> Location	<b>Author's Location</b>	Sequence	Neutrali	izing Immunogen	Species(Isotype)
			anti-V3 loop antibodies,	rted into cold-causing huma and NM-01 was among the			
500	1026	Ab type V3 References Nakamu  1026: Bound diverse	ra1993, Bou-Habib1994 e strains, neutralizing act	GPGRAF  Strain: MN HIV compone.  ivity against MN, close to G T-CSF, derived from JR-CSI	PGRAF [Nakamura1993]	Vaccine e JR-CSF [Bou-Habib199	murine (IgG) 4]
501	1034	Ab type V3 References Bou-Hal • 1034: Greater affinit	bib1994, Berman1997 y for T cell tropic T-CSI	GPGRAF  Strain: MN HIV compone.  F, derived from JR-CSF, than the cases from a MN gp120 variable.	to the primary isolate JR-C	Vaccine CSF, close to GPGRAF [B	murine (IgG) ou-Habib1994]
502	59.1 (R/V3-59.1)	Ab type V3 Donor References D'Souza Stanfield1999, York2  59.1: Called R/V3-5  59.1: Epitope defined  59.1: Synergistic net  59.1: Crystal structu  59.1: Greater affinity  59.1: Multi-lab study  59.1: Competition E RIHIGPGRAFYTT,  59.1: A conformatio  59.1 and an MN pep retaining the Fab bot  59.1: The tip of the N neutralized by anti-V [Smith1998]  59.1: The crystal stru different MAbs were  59.1: Abs against the showed similar bindi 320SI-C3.3), but the	a1991, White-Scharf199 2001 9.1 – potent neutralizing d by peptide reactivity a stralization of MN when re of a 24 amino acid per of the for T-cell tropic strain by for antibody characterical LISAs with serial deletical suggesting significance and seriod and 59.1 and the mound form [Ghiara1997] MN V3 loop was inserted an loop of the form [Ghiara1997] MN V3 loop was inserted an loop of the form [Ghiara1997] MN V3 loop was inserted and seriod seriod seriod [Stanfield1999] E V3 loop (50.1, 58.2, 59) Stang efficiency to Env der	HIV component: V3 d A. Profy, Repligen Corpora 3, Potts1993, Ghiara1993, B  3 MAb [D'Souza1991] Ind binding affinity with amir combined with sCD4 or the ptide from the V3 loop boun F-CSF than the primary isola zation and assay comparison ons produced longer estimate of non-contact residues [Selif the tip of the V3 loop was obtained d into cold causing human rh 59.1 was among the Abs used es bound to Fabs was obtained 0.1, 257-D, 268-D, 447-52D) ived from related pairs of pri more susceptible to neutrali	to acid substitutions – GPG CD4BS MAb F105 [Potts1 d to 59.1 Fab fragment – cotte JR-CSF, from which T-C – neutralizes MN and IIIB of epitope length than x-ragman1996] constructed and bound with at NMR studies reveal that the inovirus 14 (HRV14) – chird – chimeric viruses elicited and conformational change , CD4BS (IgG1b12, 559-64 mary and TCLA lines (prince in the inovirus (prince in the inovirus (IgG1b12, 559-64 mary and TCLA lines (prince in the inovirus (IgG1b12, 559-64 mary and TCLA lines (prince in the inovirus (IgG1b12, 559-64 mary and TCLA lines (prince in the inovirus (IgG1b12, 559-64 mary and TCLA lines (prince in the inovirus (IgG1b12, 559-64 mary and TCLA lines (IgG1b12).	GRAF [White-Scharf1993] [1993] [1993] [1993] [1994] [1975]	[Ghiara1993] bib1994] sine substitution, re shows interactions betwee bre ordered in solution, ed, and chimeric viruses wer gs against ALA-1 and MN (GPGR) were observed whe d to gp41 (2F5, F240) each

**HIV Antibodies Tables** 

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizing	Immunogen	Species(Isotype
503	polyclonal	Ab type V3 References Lu20000 High titer response t CG-GPGRAFY-G-E CG-(ELDKWA-GPO	to ELDKWA and RILAVE ELDKWA-G-RILAVERY	ERYLKD was observed u LKD conjugated to BSA, led, yielding a strong Ab	ipon vaccination with multiple-epit , a weak response to GPGRAFY – response to ELDKWA, weak to G	immunization with	rabbit (Ig) nation yielded strong Al
504	10E3	Ab type V3 References Tian200 10E3: Peptides GPC	)1	hemocyanin (KLH) conj were conjugated to KLH	ugate Strain: IIIB HIV componer and used to raise mouse monoclon [Tian2001]		murine (IgG)  has were generated with
505	polyclonal	Ab type V3 References Yu2000 High levels of epitop		ced by the peptide-BSA	conjugates C-(GPGRAF)_4-BSA o	Vaccine  or C-(TRPNNNTRKSI	murine, rabbit
506	N11-20 (110-H)	References Valenzu			L (LAI) and N11-20 is through inhibition of	f virus binding to the ce	murine (IgG1κ)
507		Ab type V3 Dono References Langedi 5025A: Generation a	gp120 (313–317 BH10 e: peptide Strain: BH10 or Paul Durda, Du Pont de ijk1991, D'Souza1991 and fine mapping of murin - strain specific weakly ne	HIV component: V3 Nemours and Co ne MAbs [Langedijk199]		Vaccine	murine (IgG)
508			gp120 (316–322) on1990a, Scott1990 cificity [Robinson1990a] cific neutralization, ADCO	PGRAFY C directed against MN in	L fected cells [Scott1990]	HIV-1 infection	human (IgG1)
509	902		gp120 (IIIB) e: vaccinia Strain: IIIB or Bruce Chesebro, Rocky			Vaccine	murine (IgG1κ)

No. MAb ID **HXB2** Location Author's Location Sequence **Neutralizing Immunogen** Species(Isotype) References Chesebro 1988, Laman 1993, Broder 1994, Earl 1994, Sakaida 1997 • 902: Strain specific neutralization of HIV [Chesebro1988] • 902: Epitope may be partially masked or altered in the oligomeric molecule [Broder1994] • 902: Used as a control in a study of the influence of oligomeric structure of Env in determining the repertoire of the Ab response [Earl1994] • 902: V3-BH10 peptide with loop-structure inhibits IL-2 induced T-cell proliferation, thought to be due to altering intracellular signaling, and MAb 908 can block the peptide inhibition [Sakaida1997] • 902: NIH AIDS Research and Reference Reagent Program: 522 510 694/98-D gp160 (314-317) gp120 (IIIB) L GRAF HIV-1 infection human ( $IgG1\lambda$ ) (694/98, **Ab type** V3 **Donor** Drs. S. Zolla-Pazner and M. Gorny, NYU Med Center NY, NY 694.8, References Gorny1991, Gorny1992, Gorny1993, Cavacini1993a, Spear1993, Gorny1994, Laal1994, VanCott1994, Cook1994, VanCott1995, 694/98D) Zolla-Pazner1995a, Forthal1995, Li1997, Zolla-Pazner1997, Smith1998, Li1998, Andrus1998, Nyambi1998, Schonning1998, Zolla-Pazner1999a, Zolla-Pazner1999b, Altmeyer1999, Nyambi2000, Park2000, Edwards2002, He2002, Zhang2002 • 694/98-D: This MAb was first described here [Skinner1988b] • 694/98-D: Type-specific lab isolate neutralization was observed – binds with 1-3 fold greater affinity to gp120 than to peptides [Gorny1992] • 694/98-D: Neutralizes MN and IIIB (GRAF) – binds SF2 (GRAF) – binding reactivity: MN, IIIB, SF2, NY5, RF, CDC4, WM52 [Gorny1993] • 694/98-D: Called 694-D – complement mediated virolysis of IIIB, but not in the presence of sCD4 [Spear1993] • 694/98-D: 50% neutralization of HIV-IIIB at a concentration of 0.15mug/ml [Gorny1994] • 694/98-D: Potent neutralization of IIIB – no neutralization synergy in combination with CD4 binding domain MAbs [Laal1994] • 694/98-D: GRVY did not alter peptide binding – GRVI and GQAW enhanced dissociation – GQVF and GQAL did not bind [VanCott1994] • 694/98-D: MAbs against the glycosphingolipid GalCer block HIV infection of normally susceptible CD4 negative cells from the brain and colon – V3 MAbs can inhibit gp120 binding to GalCer in vitro – binding of GalCer to gp120 inhibited but did not completely block MAb binding[Cook1994] • 694/98-D: Human HIV-1 infected sera and MAb 694/98 have high reactivity to MN and RF infected H9 cells, but Genentech rec gp120 IIIB vaccine recipients do not [VanCott1995] • 694/98-D: Serotyping study using flow-cytometry – bound GRAX bearing virus in 10/11 cases – somewhat conformation dependent [Zolla-Pazner1995a] • 694/98-D: ADCC activity, and no viral enhancing activity [Forthal1995] • 694/98-D: One of 14 human MAbs tested for ability to neutralize a chimeric SHIV-vpu+, which expressed HIV-1 IIIB env – could only achieve 50% neutralization alone – all Ab combinations tested showed synergistic neutralization – 694/98-D has synergistic response with MAbs F105, 15e, b12, 2F5, 17b, 2G12, and 48d, and with HIVIG [Li1997]

- 694/98-D: Used to study pre- and post-exposure prophylaxis Hu-PBL-SCID mice infected by an intraperitoneal injection of HIV-1 LAI MAb half-life in plasma in mice is 9 days 2 hours post-694/98-D mice were challenged with LAI, and at an Ab concentration of 1.32 mg/Kg, 50% of the mice were infected one of the infected mice carried the resistant form GRTF rather than GRAF (critical amino acids for binding are GRA) post-exposure prophylaxis was effective if delivered 15 min post-exposure, but declined to 50% if delivered 60 min post-exposure, and similar time constraints have been observed for HIVIG, 2F5 and 2G12, in contrast to MAb BAT123 that could protect delivered 4 hours post infection [Andrus1998]
- 694/98-D: The tip of the MN V3 loop was inserted into cold causing human rhinovirus 14 (HRV14) chimeras were immunoselected, and chimeric viruses were neutralized by anti-V3 loop antibodies, and 694/98-D was among the Abs used chimeric viruses elicited potent NAbs in guinea pigs against ALA-1 and MN [Smith1998]
- 694/98-D: Neutralization synergy was observed when the MAbs 694/98-D (V3), 2F5 (gp41), and 2G12 (gp120 discontinuous) were used in combination, and even greater neutralizing potential was seen with the addition of a fourth MAb, F105 (CD4 BS) [Li1998]
- 694/98-D: Using a whole virion-ELISA method, 18 human MAbs were tested for their ability to bind to a panel of 9 viruses from clades A, B, D, F, G, and H 694/98-D bound only to B and D clade virions and had limited cross reactivity [Nyambi1998]

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Net	ıtralizing Immunogen	Species(Isotype)
		HIV-BRU mutant vi  694/98-D: Review of 694/98-D: MAb per critical for reactivity 694/98-D: A Semlik recognized by the an and 694/98D and not antibodies and not be 694/98-D: A panel of 494 combinations, 444 combinations, 457, G, and H – 694/9 694/98-D: Called 698 neutralization sensitiving of all MAbs 694/98-D: Called 698 the CD4 bound stated glycosylation site do not affected – virused track levels of cell s 694/98-D: Called 698 gp120 MAb productivity	irus that lacks the V3 loop of clade specificity and ant otide reactivity pattern clustrial in this group [Zolla-Pazr ici Forest virus (SFV) expraiti-V3 MAbs K24 and F5. of linear V3 MAbs — express yanti-V3 antibodies [Altrof 47 human MAbs was te 14% displayed some viral 8-D showed intermediate 194/98D — six mutations in tive — V3, CD4BS, and CE is against gp120 by causing 194/98D — Truncation of the expression of the expression of the result of the expression of the mod — Transgenic mice carrier	o glycan more efficienti-V3 HIV-1-Abs [Zistered with immuno ner1999b] ession system carry [5, while gp120 at the ession in rat brain also meyer1999] ested against 26 HIV binding – V3 MAbs reactivity [Nyambi2 MN change the viru [24 i MAbs are 20-10 gronformational characteristic enhancing binding the anti-gp41 MAbs were more sensitive nutated proteins [Edying human genes a nization with HIV S	ntly than HIV-BRU [Schonnin olla-Pazner1999a] logical related MAbs: 1108, 3 mg BX08 env was used to stude plasma membrane was deteror showed that surface-expressional properties of the surface of the s	gnition, anti-V3 MAbs were founding 1998]  886, 268, 311, 257, 694.8 – the amidy the conformation of gp120 – intoted only by conformation dependenced Env was recognized only by the rom clades A through H – 19 V3 Masteriation resistant phenotype to logizing the sensitive form – the mutation of CD4BS MAbs F105, b12, and the anti-V2 MAb 697D and the anti-V3 MAbs were used to rapidly collective of the service of	no acids HI tended to be racytoplasmic gp120 was ent MAbs 2G12, 670-D e conformation-dependent MAbs were tested, and of and D isolates, less to E, w-infectivity ation L544P reduced more closely resembles and in most cases of ati-V3 MAb 694/98D were ab 1331A was used to reate a panel of anti-HIV
511					LGVAPTKAKR stimulation of uninfected-do	in vitro stimulation nor lymphocytes – reacts with pept	human (IgM) tides 314-323 + 494-503
512		4 gp160 (314–323 + 494–503) <b>Ab type</b> V3-C5 <b>References</b> Ohlin19  • MO101: Generated	gp120 (314–323)	on of uninfected-do	LGVAPTKAKR  for lymphocytes with pB1 control  IGKI + LGVAPTKAKR [Ohl	in vitro stimulation  ataining IIIB Env 286-467 – reacts in1992]	human (IgM) with peptides from the V3
513	MO101/V3,C	4 gp160 (314–323 + 494–503) <b>Ab type</b> V3-C5 <b>References</b> Ohlin19	gp120 (494–503)	GRAFVTIGKI	-LGVAPTKAKR	in vitro stimulation	human (IgM)

No.	MAb ID	<b>HXB2</b> Location	Author's Location	Sequence	Neutralizing	Immunogen	Species(Isotype)
				ion of uninfected-donor lymph 3, peptides GRAFVTIGKI + L		B Env 286-467 – re	acts with peptides from the V3
514	9205 (NEA-9205 NEA9205)	Ab type V3 Dono References Durda 19 9205: Also see MAI 9205: Called NEA-9 RAF is the core reac 9205: Synergy with 9205: Neutralizes II 9205: Called NEA-9 enhances neutralizat 9205: Called NEA-9 not all or none, i.e., with a glycosylation 9205: Called NEA-9 glycosylation sites -	b called 5023A  9205, epitope RIQRGPG  ctivity [Trujillo1993]  combinations of CD4-ba  IB but not MN – signific  9205 – The N306 glycan  tion sensitivity [Schonnir  9205 – the stoichiometry  each envelope oligomer ba  a site mutation in the V3 b  205 – gp120 capture ELI  CD4 binding could only	nmercial ay 1993, VanCott1994, Fontend RAFVTIGK – reacts with three ased molecules in inhibition of antly slower dissociation const of the V3 loop makes the tip of	e human brain proteins of 35, HIV-1 Env mediated cell fusic ant for IIIB than MN [VanCot f the V3 loop inaccessible to the ted and the data indicated that any oligomer bound reduces the C-term) or 9205 (anti-V3) were gp120 was bound to the plate	on [Allaway1993] t1994] his MAb in oligome binding for neutrali e chances of infection	eric Env, loss of this glycan zation was was incremental on – 9205 binds only to Env
515	110.I	Ab type V3 Dono References Moore1  110.I: Binds to carb  110.I: Binds equally  110.I: Reciprocal bi anti-CD4 binding si  110.I: Epitope suggo mimicking sCD4, an  110.I: Binds both gg  110.I: The MAb and	oxy-terminal side of the well to monomer and ol nding inhibition with oth the MAbs [Moore1996] ested to be RAFVTIGK and expose the gp41 epitop120 and soluble gp120+1 Fab binding to the oligorous well as the side of the solution of the side of the		24 region MAb G3-299 [Moore potent neutralization of lab strate and enhances binding of some 0.5, and 110.I could each signition anti-V2 MAbs [Poignard 190] esting its gp120 epitope is not ralization were highly correlated	e1993c] nins [Sattentau1995b ne anti-V2 MAbs – b ficantly increase gp [96a] blocked by gp41 bin	pinding enhanced by some 120 dissociation from virus, nding [Wyatt1997]
516	anti-HIV-2 polyclonal	<ul><li>Ab type HIV-2 V3</li><li>References Morner</li><li>Neutralizing Abs ag</li></ul>	1999 ainst HIV-2 V3 are produ	FHSQ+WCR  2 SBL6669-ISY HIV compounded when peptides spanning to the C-term Cys	wo non-contiguous parts of the	Vaccine  V3 loop are used for	guinea pig (IgG) or vaccination including amino

**HIV Antibodies Tables** 

lo. MAb	) ID	HXB2 Location	<b>Author's Location</b>	Sequence	Neutralizing	Immunogen	Species(Isotype)
17 IIIB-V	V3-01	gp160 (320–328) Vaccine Vector/Type Ab type V3 Donor References Laman 19		IGKIGNMRQ HIV component: V3	no	Vaccine	murine (IgG1)
		• IIIB-V3-01: UK Med	dical Research Council A	ank of the IIIB V3 loop – epitope is AIDS reagent: ARP3046 ence Reagent Program: 1726	hidden native gp120, exp	oosed on denaturation	n [Laman1993]
18 D/6D	<b>D</b> 1	gp160 (346–377)	gp120 (351–382 LAI)	IVTHSFN		Vaccine	murine (IgG1)
		<b>Ab type</b> V4 <b>References</b> Bristow	1994	Strain: LAI HIV component: gp1 humoral immune response to Bacul		ded rgp120 and rgp1	60 [Bristow1994]
19 4D7/4	4	Ab type V4 Donor References Moore 19 4D7/4: C3 region – t	r S. Ranjbar, NIBSC, UF 994c	Strain: LAI HIV component: Env  K enatured/native gp120 is >10 [Moor		Vaccine	murine (IgG)
20 36.1(A 329)	ARP	gp160 (361–381)	gp120 (362–381 LAI)		Ξ	Vaccine	murine (IgG)
		Ab type V4 References Thiriart1  • 36.1: The relative aff	989, Moore1994c	Strain: LAI HIV component: Enverge gp120 is >30 – mutations 380 G/I eagent: ARP329		g [Moore1994c]	
21 C12		Ab type V4 Donor References Moore 19 • C12: Bound preferer • C12: The relative aff gp120(380-393 LAI)	r George Lewis 993a, Moore1994c, Abac ntially to denatured IIIB inity for denatured/nativ [Moore1994c]	Strain: LAI HIV component: gp1 cioglu1994, Moore1994d gp120 [Moore1993a] e gp120 is >30 – mutations 380 G/F	60 5, 381 E/P, and 384 Y/E is	Vaccine  mpair binding – also	murine (IgG1) binds GEFFYCNSTQLF
22 110.D	)	gp160 (380–393)	gp120 (380–393 LAI)		no	Vaccine	murine (IgG)
		Ab type C3 Donor	recombinant protein F. Traincard, Pasteur In 194c, Valenzuela 1998	Strain: LAI HIV component: Envisitute, France			

No. MAb	b ID	<b>HXB2</b> Location	<b>Author's Location</b>	Sequence	Neutralizing	Immunogen	Species(Isotype)
		• 110.D: The relative	affinity for denatured/nativ	ve gp120 is >50 [Moore1994	c]		
523 B32		Ab type C3 References Moore I  B32: The relative at	994c, Abacioglu1994 finity for denatured/native	GEFFYCNSTQLFNS train: LAI HIV components gp120 is >100 - mutations by peptide scanning - FFY(	380 G/F, 381 G/P, 382 F/L, 38 <sup>2</sup>	Vaccine  4 Y/E, and 386 N/R in	murine (IgG1)  mpair binding [Moore1994c
524 polyc (VEI		positive subjects, in	to the epitopes in a vaccine cluding sera from 6 non-su	btype B infections - serum	peptides from 5 hypervariable samples from San Francisco, C against the V3 region peptide	Canada and Puerto Ric	co cohort showed presence of
525 B15		Ab type V4 Dono References Moore I • B15: Bound prefere • B15: Binds native E	or George Lewis 993a, Moore1993c, Abaciontially to denatured IIIB glisH10 gp120 with 5 fold les	<i>train:</i> LAI <i>HIV componen</i> oglu1994 p120 [Moore1993a]	oes not bind native or denature	Vaccine od MN gp120 [Moore	murine (IgG2b)
526 B34		<b>Ab type</b> V4 <b>References</b> Abacio	şlu1994	) WFNSTW train: LAI HIV component by peptide scanning [Abacie	-	Vaccine	murine (IgG2b)
527 7F11	I	References Lasky1		nt: gp120 nat binds to integrase [Nilser	1996]	Vaccine	murine
528 5C2E	E5	Ab type C4 Dono References Lasky1 • 5C2E5: Blocks the	987, Cordell1991 gp120-CD4 interaction [La	Genentech, San Francisco	ordell1991]	Vaccine	murine
529 G3-2	211	gp160 (423–437) Vaccine Vector/Type	gp120 (423–437 IIIB) e: virus derived protein S	IINMWQKVGKAMYAP Strain: IIIB HIV componer	L at: gp120	Vaccine	murine (IgG1)

			Sequence	Neutralizing		Species(Isotype)
	• G3-211, 42, 299, 508	3, 519, 536, 537: Cross-rea	act with diverse strains by immuno	fluorescence – blocks H	IV binding to CD4+	cells – different neutralization
	Ab type C4 References Sun1989 G3-537, 211, 299, 50 efficiencies [Sun1989]	9, Ho1991b, McKeating19 08, 519, 536, 42: Cross-rea 9]	92b act with diverse strains by immuno	fluorescence – blocks H	_	murine (IgG1) cells – different neutralization
polyclonal	Ab type CD4BS References Bukawa • Polyclonal secretory	1995 IgA antibody raised by m	ucosal immunization is able to neu		Vaccine IN – HIV-1 neutraliz	murine (IgA) ation may be due to the V3,
1795	<b>Ab type</b> CD4BS <b>References</b> McKeati	ng1992b		L MYA, GKAM may be	Vaccine involved [McKeating	g1992b]
	Ab type C3, C4 References Cordell1 Kropelin1998, Vella ICR38.1a: Weakly n [McKeating1992b, C ICR38.1a: Unable to involved in CD4 bine ICR38.1a: Studied in ICR38.1a: Unreactiv MAbs, but are actual ICR38.1a: Called 38 ICR38.1a: The most	991, McKeating1992b, Mc2002 eutralizing – binds linear of Cordell1991] exert a synergistic effect ding [McKeating1992a] in the context of a neutralize with solid-phase decape ly subclones of the same 1.1a – 10 to 20 fold increas variable amino acids in the	cKeating1992a, McKeating1992c, determinant in the CD4 binding don in combination with V3 directed Mation escape mutant [McKeating19 ptide, competed in solution phase a MAb [Moore1993c] ed binding when V1/V2 or V1/V2 e V3 loop were replaced with sering	McKeating1993b, McK main – cross-competitio [Abs, in contrast to MAI 193a] assay – ICR 38.1a and IC and V3 were deleted from the sto make the immuno	n with MAbs G3-53 b 39.13g, that binds the CR 38.8f were initial om gp120 [Jeffs1996 dominant V3 loop le	6, 5C2E5, and ICR38.8f to a conformational epitope ly reported to be independent  ss immunogenic – these
	G3-537  polyclonal  1795  ICR38.1a (38.1a, 388/389, ARP388/389)	• G3-211, 42, 299, 508 efficiencies [Sun1989]  G3-537 gp160 (423–437) Vaccine Vector/Type Ab type C4 References Sun1989 • G3-537, 211, 299, 508 efficiencies [Sun1989] • G3-537: Weakly neuropolyclonal gp160 (425–436) Vaccine Vector/Type Ab type CD4BS References Bukawa • Polyclonal secretory CD4 or HPG30 compolyclonal gp160 (425–441) Vaccine Vector/Type Ab type CD4BS References McKeati • 1795: CD4 binding strength of the type CD4BS References Cordell In Kropelin 1998, Vellage ICR38.1a: Weakly neuropolyclonal secretory CD4 or HPG30 compolyclonal secretory CD4 or	gp160 (423–437) gp120 (423–437 IIIB)  Vaccine Vector/Type: virus derived protein S Ab type C4 References Sun1989, Ho1991b, McKeating19 G3-537, 211, 299, 508, 519, 536, 42: Cross-reactificiencies [Sun1989] G3-537: Weakly neutralizing – binds to a lineal polyclonal gp160 (425–436) gp120 Vaccine Vector/Type: peptide Strain: IIIB Ab type CD4BS References Bukawa1995 Polyclonal secretory IgA antibody raised by m CD4 or HPG30 component of the multicomponent of the multicomponent of the multicomponent of type: poliovirus HIV component National Polyclonal Secretor/Type: recombinant protein Strain: ICR38.1a (38.1a, BRU)  ICR38.1a gp160 (429–438) gp120 (dis 427–436 BRU)  Ab type C3, C4 References Cordell1991, McKeating1992b, McKropelin1998, Vella2002 ICR38.1a: Weakly neutralizing – binds linear of [McKeating1992b, Cordell1991] ICR38.1a: Weakly neutralizing – binds linear of [McKeating1992b, Cordell1991] ICR38.1a: Unable to exert a synergistic effect involved in CD4 binding [McKeating1992a] ICR38.1a: Studied in the context of a neutraliz ICR38.1a: Unreactive with solid-phase decape MAbs, but are actually subclones of the same Polyclonal Substance Sub	G3-537  G3-537  gp160 (423–437) gp120 (423–437 IIIB) IINMWQKVGKAMYAP  Vaccine Vector/Type: virus derived protein Strain: IIIB HIV component: gp12 Ab type C4  References Sun1989, Ho1991b, McKeating1992b  G3-537: Weakly neutralizing – binds to a linear binding domain of gp120, NMW  polyclonal  gp160 (425–436) gp120 NMWQEVGKAMYAP  Vaccine Vector/Type: peptide Strain: IIIB Adjuvant: cholera toxin adjuvant Ab type CD4BS  References Bukawa1995  Polyclonal secretory IgA antibody raised by mucosal immunization is able to neu CD4 or HPG30 component of the multicomponent peptide immunogen [Bukawa:  1795  gp160 (425–441) gp120 (425–441 IIIB) NMWQEVGKAMYAPPISG  Vaccine Vector/Type: poliovirus HIV component: Env Ab type CD4BS  References McKeating1992b  1795: CD4 binding site – weakly neutralizing – binding inhibited by WQEVGKA  ICR38.1a (38.1a, BRU)  388/389,  Vaccine Vector/Type: recombinant protein Strain: BH10 HIV component: gp Ab type C3, C4  References Cordell1991, McKeating1992b, McKeating1992a, McKeating1992c, Kropelin1998, Vella2002  ICR38.1a: Weakly neutralizing – binds linear determinant in the CD4 binding dor [McKeating1992b, Cordell1991]  ICR38.1a: Unable to exert a synergistic effect in combination with V3 directed M involved in CD4 binding [McKeating1992a]  ICR38.1a: Studied in the context of a neutralization escape mutant [McKeating198c]  ICR38.1a: Claled 38.1a – 10 to 20 fold increased binding when V1/V2 or V1/V2  ICR38.1a: The most variable amino acids in the V3 loop were replaced with seric changes did not affect the ability of sCD4 or MAbs to V1/V2, C1 and C4 to bind	G3-211, 42, 299, 508, 519, 536, 537: Cross-react with diverse strains by immunofluorescence – blocks Hefficiencies [Sun1989]  G3-537  gp160 (423-437) gp120 (423-437 IIIB) IINMWQKVGKAMYAP L Vaccine Vector/Type: virus derived protein Strain: IIIB HIV component: gp120 Ab type C4 References Sun1989, Ho1991b, McKeating1992b  G3-537: Weakly neutralizing – binds to a linear binding domain of gp120, NMWQEVGKAMYAPPISG  polyclonal  gp160 (425-436) gp120 NMWQEVGKAMYA L Vaccine Vector/Type: peptide Strain: IIIB Adjuvant: cholera toxin adjuvant Ab type CD4BS References Bukawa1995  Polyclonal secretory IgA antibody raised by mucosal immunization is able to neutralize IIIB, SF2, and M CD4 or HPG30 component of the multicomponent peptide immunogen [Bukawa1995]  1795  gp160 (425-441) gp120 (425-441 IIIB) NMWQEVGKAMYAPPISG L Vaccine Vector/Type: poliovirus HIV component: Env Ab type CD4BS References McKeating1992b  1795: CD4 binding site – weakly neutralizing – binding inhibited by WQEVGKAMYA, GKAM may be  ICR38.1a (38.1a, 388/389)  ARP388/389)  ARP388/389)  ARP388/389)  ARP388/389)  ARP388/389)  ARP388/389)  L CR38.1a: Weakly neutralizing – binds linear determinant in the CD4 binding domain – cross-competitio [McKeating1998, Vella2002]  ICR38.1a: Weakly neutralizing – binds linear determinant in the CD4 binding domain – cross-competitio [McKeating1998, Vella2002]  ICR38.1a: Studied in the context of a neutralization escape mutant [McKeating1993a]  ICR38.1a: Studied in the context of a neutralization escape mutant [McKeating1993a]  ICR38.1a: Called 38.1a – 10 to 20 fold increased binding when V1/V2 or V1/V2 and V3 were deleted fro ICR38.1a: Called 38.1a – 10 to 20 fold increased binding when V1/V2 or V1/V2 and V3 were deleted fro ICR38.1a: The most variable amino acids in the V3 loop were replaced with serines to make the immuno changes did not affect the ability of sCD4 or MAbs to V1/V2, Cl and C4 to bind – ICR38.1a was not affe	G3-211, 42, 299, 508, 519, 536, 537: Cross-react with diverse strains by immunofluorescence – blocks HIV binding to CD4+ efficiencies [Sun1989]  gp160 (423-437)  gp120 (423-437 IIIB)

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutr	ralizing Immunogen	Species(Isotype)
		<ul> <li>antibodies which bit</li> <li>ICR38.1a: Called A neutralization assay plasma/sera were sit</li> </ul>	nd in the C4 region of gp1 ARP388/ARP389: Herpesv s, and compared with a sta	20 (F105, 388/389, and irus saimiri-immortaliz andard PBMC protocol I-2 cells) and PBMCs –	l b12) [Kropelin1998] ted CD4+ T lymphocytes (H' – neutralization sensitivities lists epitope as WQEVGKA	VS T cells) were used to iso to a panel of MAbs and to	dditive when combined with blate virus and perform HIV-1 homologous or heterologous
534	G3-299	Ab type C4 Dono References Sun198 G3-299: Best neutra G3-299: C4 region and G3-536 – bound impaired binding, V G3-299: Binds with neutralization of lab G3-299: Discontinu anti-V3 MAbs – G3 G3-299: Epitope de for MAb 50-69 [Poi G3-299: Binds both G3-299: The MAb	alization of IIIB in panel o binds HXB2 20mer KQI d native gp120, not denatu 3 loop cleavage or insertion higher affinity to monomore strain [Sattentau1995b] hous V3-C4 epitope, binding 3-229 enhances the binding escribed as KQIINMWQK ignard1996a] high gp120 and soluble gp120 and Fab binding to the olig	HIV component: gp120 systems Inc and David 1995b, Moore1996, Po f 7 MAbs that bind ove INMWQKVGKAMYA red – poor peptide bind on abolished binding [Ner than to oligomer, slowg enhanced by a few a g of some anti-V2 MAbVGKAMYAPIS – bind-typ41 complex efficieng gomeric form of gp120	Ho, ADARC, NY ignard1996a, Binley1997a, I orlapping epitope [Sun1989] APPIS, and SF-2 and MN gpling, epitope spans V3-C4 regeometric Moore1993c] wassociation rate, although thi-C1, anti-CD4 binding sites [Moore1996]	120s – G3-42, G3-299 lowe gions – 433A/L, 435Y/H and faster than other C4 MAbs and e, and V2 MAbs – binding to dissociation from virus and tope is not blocked by gp41 ally correlated – authors sugg	er affinity than G3-508, G3-519, and 430V/S substitutions tested, with more potent reciprocally inhibited by d exposure of the gp41 epitope binding [Wyatt1997]
535	G3-42 (G3	Ab type C4 Dono References Sun198 Jagodzinski2000 G3-42: Neutralizati G3-42: C4 region – G3-519, and G3-536 substitutions impair G3-42: Inhibits bind G3-42: Binds with 1 G3-42: The sulfated binding – G3-42 epi G3-42: Inhibits bind G3-42: Epitope deser	on of IIIB but not RF [Sunbinds HXB2 20mer KQII 6 – bound native gp120, not be binding, V3 loop insert ding of CD4 inducible MA higher affinity to monomer a polysaccharide curdlan strategy of many anti-V3, -CE cribed as KQIINMWQKV ignard1996a] 12 – Does not inhibit gp126.	Strain: IIIB HIV com, and David Ho, ADARC, as, Sattentau1995b, Jago and Ballon	PPIS, and SF-2 and MN gp12 otide binding, epitope spans v Moore1993c] v association rate [Sattentau1 the Envelope of T-tropic viru 1996] region MAbs – enhances bi	20s – G3-42, G3-299 have I V3-C4 regions – 433A/L, 43 995b] uses and neutralizes virus – nding of some anti-V2 regional	lower affinity than G3-508, 35Y/H and 430V/S  CRDS potently inhibits G3-42 on MAbs [Moore1996] exposure of the gp41 epitope

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neut	tralizing Immunogen	Species(Isotype)
		raised in an immun created to mimic th CD4-IgG2, and also G3-519 – nor did it 17b and A32 were and 4D4, did not bi [Binley1999]  • 0.5beta: MAbs 0.51	e response to the oligomer to native conformation of E to by anti-V3 MAbs 19b and bind C11, 23A, and M90, very strongly induced by C and to SOSgp140, in contrasports and G3-42 were used to	on the virion surface rank and explore its pote d 83.1 – SOSgp140 is 1 MAbs that bind to gp1 dD4 in SOS gp140 – an st to 2F5, which binds to study synthesis of old	ather than dissociated subunntial as an immunogen – SC not recognized by C4 region 20 C1 and C5, where it interti-gp41 MAbs that bind in the to the only gp41 epitope that gomeric and monomeric for	affinity for the native trimer, its – a disulfide linked gp120-DS gp140 is recognized by NA MAbs that neutralize only T racts with gp41 – MAbs that he region that interacts with g at is well exposed in native gp rms of Env – inhibition of gly either MAb recognized non-g	-gp41 (SOS gp140) was Abs IgG1b12, 2G12, and CLA strains, G3-42 and bind CD4 inducible epitopes, p120, 7B2, 2.2B, T4, T15G1 120-gp41 complexes
536	G3-508 (G3 508)		gp120 (429–438 BRU)	Strain: IIIB HIV com		Vaccine	murine (IgG1)
		References Sun198	ation of IIIB and RF [Sun19] inding of CD4 inducible M — binds HXB2 20mer KQl 35Y/H and 430V/S substituted in higher affinity to monomending of some V3, C4 and assulted in slight gp120 diss 508 — inhibits gp120 internand Fab binding to the oligoraction of Ab sites occupied	c, Sattentau1995b, Mod 989] Ab 48d [Thali1993] INMWQKVGKAMYA attions impaired binding er than to oligomer, slo CD4 binding site MAb ociation from virus and action with CCR-5 in a gomeric form of gp120 ed on a virion irrespecti	APPIS, and SF-2 and MN gr [Moore1993c] w association rate [Sattental os, enhances binding of V2 r l exposure of the gp41 epito MIP-1beta-CCR-5 competi and neutralization were high ve of the epitope [Parren1993]	region MAbs [Moore1996] pe for MAb 50-69 [Poignard: ition study [Trkola1996a] hly correlated – authors sugge	10 fold greater affinity than  1996a]  est that neutralization is
537	G3-519	gp160 (429–438) Vaccine Vector/Typ Ab type C4 Done References Sun1989, Moore19 G3-519: Best neutr G3-519: Neutralize G3-519: C4 region native – 433A/L, 43 G3-519: Included i IINMWQKVGKAI G3-519: Binds with G3-519: Non-recip	gp120 (429–438 BRU)  e: virus derived protein  or Tanox Biosystems Inc a  93a, Moore1993c, D'Souz  alization of RF in panel of  es IIIB, is reactive with SF-  binds HXB2 20mer KQI  35Y/H, 438P/R and 430V/  n a multi-lab study for anti  MYAPP [D'Souza1994]  h higher affinity to monom	EVGKAMYAPP  Strain: IIIB HIV com, al 1994, Sattentau 1995b  7 MAbs that bind over 2 gp120, mild inhibition INMWQKVGKAMYAS substitutions impaired body characterization, er than to oligomer, slothe presence of the C5	L ponent: gp120 , NY , Moore1996, Poignard1996 lapping epitope [Sun1989] n of HIV-1+ sera binding to APPIS, and SF-2 and MN gp d binding [Moore1993c] and binding and neutralizati w association rate [Sattentat MAb 1C1 and the C1 MAb	o120s – bound denatured with ion assay comparison, also bin u1995b]	murine (IgG1)  Parren1998a, Binley1999  a 5 fold greater affinity than

No. N	MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizing Imm	unogen	Species(Isotype)
		for MAb 50-69 [Poi G3-519: Binds both G3-519: The MAb a determined by the fi G3-519: The MAbs raised in an immune created to mimic the CD4-IgG2, and also G3-519 – nor did it 17b and A32 were v	gnard1996a] gp120 and soluble gp120- and Fab binding to the oligoraction of Ab sites occupie with the broadest neutralize expense to the oligomer enative conformation of En by anti-V3 MAbs 19b and bind C11, 23A, and M90, very strongly induced by C	+gp41 complex efficient comeric form of gp120 a d on a virion irrespectiv zing activity, IgG1b12, 2 on the virion surface rat nv and explore its poten d 83.1 – SOSgp140 is no MAbs that bind to gp12 D4 in SOS gp140 – anti	elight gp120 dissociation from virus but not ly, suggesting its gp120 epitope is not block and neutralization were highly correlated—e of the epitope [Parren1998a] and 2F5, all have high affinity for the her than dissociated subunits—a disulfide tial as an immunogen—SOS gp140 is record recognized by C4 region MAbs that neu 0 C1 and C5, where it interacts with gp41—gp41 MAbs that bind in the region that in the only gp41 epitope that is well expose	cked by gp41 bind authors suggest t e native trimer, in- linked gp120-gp4 gnized by NAbs tralize only TCL/ – MAbs that bind tteracts with gp12	ding [Wyatt1997] hat neutralization is dicating that they were H (SOS gp140) was IgG1b12, 2G12, and A strains, G3-42 and I CD4 inducible epitopes, 0, 7B2, 2.2B, T4, T15G1
538 C	G3-536	Ab type C4 Dono References Sun1989, Ho1991b. G3-536: Weak neut epitope:IINMWQK G3-536: Cross-com G3-536: Weakly ne G3-536: Neutralize: G3-536: C4 region native – 433A/L, 43 G3-536: Enhances I G3-536: Binds with G3-536: Inhibits bin G3-536: Epitope de G3-536: The MAb	ralization of IIIB and RF – VGKAMYAP [Sun1989] petition with MAbs 5C2E3 utralizing – binds to a lineas IIIB, is reactive with SF-2 – binds HXB2 20mer KQI 5Y/H, 438P/R, and 430V/2 binding of anti-V2 MAb 69 higher affinity to monomending of some V3, C4 and scribed as KVGKAMYAP and Fab binding to the olig	Strain: IIIB HIV comp and David Ho, ADARC, 1992b, Moore1993a, Mo cross-react with diverse for ICR38.8f and ICR38. for determinant in the CD 2 gp120, mild inhibition INMWQKVGKAMYAI S substitutions impaired 197-D [Gorny1994] for than to oligomer, slow CD4 binding site MAbs P [Poignard1996a] fomeric form of gp120 a	ore1993c, Gorny1994, Sattentau1995b, Me strains by immunofluorescence – blocks in [Cordell1991] 4 binding domain of gp120 [McKeating19 of HIV-1+ sera binding to IIIB gp120 [McPPIS, and SF-2 and MN gp120s – bound decreases.]	Joore 1996, Poigna HIV binding to C 1992b] 1992b] 1993a] 1994 senatured with 15 1995 1996	D4+ cells –  fold greater affinity than
539 I	ICR38.8f	Ab type C4 References Cordell ICR38.8f: Weakly r [Cordell1991]	neutralizing – binds linear o	train: BH10 HIV com	L Vacci  ponent: gp120  binding domain – cross-competition with 1  endent MAbs, but are actually subclones o	ICR38.1a, 5C2E5	
540 N	MO86/C3	gp160 (429–443) <b>Ab type</b> C4	gp120 (429–443)	EVGKAMYAPPISG	<u> </u>	ro stimulation	human (IgM)

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizing	Immunogen	Species(Isotype)
		References Ohlin19  • MO86: Generated i		6-467 upon in vitro stimulatio	on of uninfected-donor lympho	cytes [Ohlin1992]	
541	13H8	Ab type C4 References Nakam  13H8: Cross blocks 13H8: Bound divers 13H8: Binds V3 and	se strains, neutralizing act d C4 peptides (J. P. Moore	Jeffs1996 SA – reactive with diverse strivity against MN [Nakamura e, per. comm.)	L ains in rgp120 ELISA [Nakam 993] re deleted from gp120, respecti	-	murine (IgG)
542	G45-60	Ab type C4 References Sun198 G45-60: C4 region denatured gp120 – 4 G45-60: Enhances I G45-60: Non-recipi inhibition with man	19, Moore1993c, Gorny19  — binds HXB2 20mer KQ 433A/L and 435Y/H (not binding of anti-V2 MAb 6 rocal enhancement of G45  y MAbs that bind to the V	Strain: IIIB HIV components 94, Moore1996, Jagodzinski I IINMWQKVGKAMYAPPI, 430V/S) substitutions impaire 697-D [Gorny1994] 6-60 binding by some C1 and 73, C4 and CD4 binding site r	996 decapeptide flanking peptides and binding [Moore1993c] C5 antibodies – reciprocal enhegions [Moore1996]	ancement of some	
543	polyclonal	Ab type C4 References Collado Vaccinia p14 can el noted when p14 or p domain, depending	icit NAbs and p39 tends to p39 was placed in the N-to on the construct – all chir	to be immunodominant, so the erm region of the fusion prote meric Env proteins: 14kEnv, 3	se two proteins were fused to r	he Env Ab respons strong Ab response	
544	1662	Ab type C4 References McKea	C	AMYAPPI onent: Env oot exposed [McKeating1992b	no	Vaccine	
545	1663	Ab type C4 References McKea		AMYAPPI onent: Env oot exposed [McKeating1992b	no o]	Vaccine	

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizing	Immunogen	Species(Isotype)
546	1664	Ab type C4 References McKeat		AMYAPPI  ment: Env  ot exposed [McKeating1992b]	no	Vaccine	
547	1697	Ab type C4 References McKeat	_	AMYAPPI  ment: Env  ot exposed [McKeating1992b]	no	Vaccine	
548	1794	Ab type C4 References McKeat	_	AMYAPPISGQ  ment: Env  ot exposed [McKeating1992b]	no	Vaccine	
549	1804	Ab type C4 References McKeat	_	AMYAPPISGQ  nnent: Env  ot exposed [McKeating1992b]	no	Vaccine	
550	1807	Ab type C4 References McKeat	•	AMYAPPISGQ  ment: Env  ot exposed [McKeating1992b]	no	Vaccine	
551	1808	Ab type C4 References McKeat	•	AMYAPPISGQ  ment: Env  ot exposed [McKeating1992b]	no	Vaccine	
552	polyclonal (VEI5)	positive subjects, inc	999 o the epitopes in a vaccine cluding sera from 6 non-su	LTRDGGNNNNESEIFRPGGGD c construct (VEI) containing peptides abtype B infections – serum samples a egions, but most consistently against	from San Francisco, C	anada and Puerto Rico	cohort showed presence of

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizing	Immunogen	Species(Isotype)
553	polyclonal	Ab type V5 References Loomis- HIV-1+ positive indi	-Price1997 ividuals were given a gp	NNNNGSEI  Strain: LAI HIV component:  160 vaccine as immunotherapy, ty – 4/14 showed vaccine-induc	and this region was the most		human asured by a modified
554	•	Ab type V5-C5 D References Moorel CRA1: Bound prefe CRA1: Some C5 mu CRA1: The relative 470 P/L impairs bind CRA1: C5 region lin non-reciprocal bindi CRA1: Does not net CRA1: A combinati trimers (gp140-GNC F91) and CD4i (17b gp140-GNC4 glycop and M91) bound effi	onor M. Page, NIBSC, U993a, Moore1994d, Mooretentially to denatured III utations abrogate binding affinity for denatured [Moore denatured] adding to denatured [Moore denatured] may be enhancement some Courtalize JR-FL nor block ion of gp41 fusion with the C4) that preserve and experience and 48d) recognized gp	Strain: LAI HIV component: UK ore1994c, Moore1996, Trkola19 IB and SF2 gp120 [Moore1993a g 470 P/L or G, 475 M/S, some tive gp120 is 24 – C5 mutations re1994c] cl to nondenatured monomeric cl and V2 antibodies – non-reci gp120 interaction with CCR-5 the GNC4 trimeric sequences an pose some neutralizing epitopes 140-GNC4 as well as gp120 or compared to gp120 – MAbs din [Yang2000]	96a, Yang2000  ] C2 mutations enhance bindin 470 P/L or G, 475 M/S important of the second binding in the second binding in a MIP-1 beta-CCR-5 completed disruption of the YU2 gp12 while occluding some non-negp140 – non-neutralizing MA	airs binding to the native gp ahibition with anti-C5 antibo ome CD4 binding site antib- etition study [Trkola1996a] 20-gp41 cleavage site resulte eutralizing epitopes – CD4E Abs C11, A32, 522-149, M90	odies 1C1 and M91 – odies [Moore1996] ed in stable gp140 eS MAbs (F105 and 0, and #45 bound to the
555	•	Ab type V5-C5 D References diMarzo M91: Immunoblot re [diMarzo Veronese1] M91: The relative and M91: 470 P/L impai M91: C5 region line M91 – non-reciproca M91: A panel of MA gp120 protein ( Delt M91: A combination trimers (gp140-GNC F91) and CD4i (17b	eactive, RIP negative, bu 992] ffinity for denatured/natiins binding, but not 475 I ear epitope, binds weakly all binding enhancement Abs were shown to bind ta V1, V2, and V3), thus nof gp41 fusion with the C4) that preserve and expended and 48d) recognized gp protein at reduced levels	ent: Env	120 – reacts with strains IIIE sition 470 P/L impairs binding to C2 mutations can enhance to 120 – M91 binding was enharceiprocal binding inhibition and similar competition profil structure closely approximated disruption of the YU2 gp120 while occluding some non-negp140 – non-neutralizing MA	g [Moore1994c] pinding [Moore1994d] anced by 1C1, but 1C1 bind of CD4 binding site antibodes to a deglycosylated or varing full length folded monority for the state of the st	lies [Moore1996] riable loop deleted core her [Binley1998] in stable gp140 sS MAbs (F105 and 0, and #45 bound to the

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizing	Immunogen	Species(Isotype)
556	9201	gp160 (471–482) <b>Ab type</b> C5 <b>Dono References</b> McDou  • 9201: Does not neur		GGGDMRDNWRSE	no		murine
557	1C1	Ab type C5 Dono References Moore1  1C1: The relative af  1C1: C2 and V3 reg  1C1: Linear epitope  1C1: C5 region line	r Repligen Inc, Cambridge, 994c, Moore1994d, VanCoofinity for denatured/native gions substitutions can influent exposed on conformatian epitope, binds weakly to	tt1995, Moore1996	M91 binding was enha	-	-
558	3F5	Ab type C5 Dono References Moore1	gp120 (471–490 LAI) I HIV component: Env r S. Nigida, NCI, USA 994c finity for denatured/native g	GGGDMRDNWRSELYKYKVVK  p120 is 100 [Moore1994c]		Vaccine	murine (IgG)
559	5F4/1	Ab type C5 Dono References Moore1		GGGDMRDNWRSELYKYKVVK ROD S-DTT denatured gp120 (>10 fold)	) – mutation 485 K/V in	Vaccine  npairs binding [Moo	murine ore1994c]
560	660-178	gp160 (471–490) Vaccine Vector/Type Ab type C5 Dono References Moore1  • 660-178: The relative	gp120 (471–490 LAI) e: recombinant protein Str r G. Robey, Abbott Labs 994c, Moore1994d e affinity for denatured/nat	GGGDMRDNWRSELYKYKVVK rain: LAI HIV component: Envive gp120 is >100 [Moore1994c] ace binding – C2 and C5 mutations		Vaccine	murine (IgG)
561	9301	Ab type C5 Dono References Skinner  9301: Bound prefere 9301: The relative a	r Dupont, commercial 1988b, Moore1993a, Moore entially to denatured IIIB gr ffinity for denatured/native			Vaccine	murine (IgG)

No. MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizing	Immunogen	Species(Isotype)
562 B221 (221	Vaccine Vector/Typ Ab type C5 Done References Moore  B221: Called 221 - B221: MAb genera B221: The relative B221: Called 221 -	or Rod Daniels 1993a, Bristow1994, Moon bound preferentially to do ted in a study of the humo affinity for denatured/nativ	Strain: NL43 HIV component: gp160 re1994c enatured IIIB gp120 [Moore1993a] oral immune response to Baculovirus-exve gp120 is 12 – mutation 477 D/V impinfluence binding [Moore1994d]	kpressed mis-folded r		murine (IgG1ĸ) icroGenSys [Bristow1994
563 8C6/1	References Moore 8C6/1: V5-C5 region	<b>Donor</b> S. Ranjbar, NIBSC, 1994c	UK DS-DTT denatured gp120 (>30 fold) –	- mutation 485 K/V ir	Vaccine npairs binding [Moon	murine (IgG) re1994c]
564 H11	gp160 (472–477) Ab type C5 References Pincus • H11: Binds to gp12 [Pincus1993a, Pinc	20 but not to infected cells	(2) GGDMRD  - when linked to ricin A, the immunot	oxin did not mediate	cell killing – sCD4 h	murine as no effect
565 W2	Ab type C5 Done References Moore			irs binding [Moore19	Vaccine  94c]	murine (IgG)
566 M38	Ab type C5 References Beretta  M38: Binds to gp12  M38: Binds to the company of the M38: Infected individuals of M38: This epitope	20 and to a 80 kd human p carboxy terminus of gp120 viduals have HLA class I-g is similar to a fragment of	KYKVVKEIPLGVAPTKAKRR  IIV component: virus  o1993, DeSantis1994, Beretta1994, Ma protein expressed on a small fraction of 0, in a gp41 binding region, and also to gp120 cross-reactive antibodies [DeSan the human protein mast/stem cell grow ein, ARTKARSRVRDKRA [Maksiuto	mononuclear cells in denatured human HL atis1994] th factor receptor pre	As (antigenic homole	ogy) [Lopalco1993]
		nated if RD2 (I C I B) prot	em, mem more reprincipalities			

**References** Pincus1993a, Pincus1996

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutraliz	zing Immunogen	Species(Isotype)
		• Chim 1: Binds to gp [Pincus1993a, Pincu		s – when linked to ricin A, the	immunotoxin did not n	nediate cell killing – sCD4	has no effect
568	polyclonal		gp120 (495–516 BRU) dez2000, Maksiutov2002 mbining two peptides gp16	KIEPLGVAPTKAKRRVVQR 0(495-516 and 584-612) served		HIV-1 infection dly reactive antigen for dia	human gnostic detection of HIV-1
		• This epitope is simil	_	an protein mast/stem cell grow SRVRDKRA [Maksiutov2002]		ursor, VVPTKADKRRSV,	as well as to a fragment of
569	1331A	<ul><li>References Nyambi</li><li>1331A: Using a who anti-C5 Abs 670-D a</li><li>1331A: Core epitopo</li></ul>	1998, Gorny2000a, Hochle ble virion-ELISA method, 1 and 1331A bound to 3/4 B c e dwVVQREKR maps to gr	dwVVQREKR as01@mcrcr6.med.nyu) (NYU itner2000b, Nyambi2000, Gorn 8 human MAbs were tested for clade viruses (they don't bind to b120(510-516) – binding of par though anti-V3 and CD4BS M	ny2002, Edwards2002 their ability to bind to o IIIB), and to subtype nel of 21 MAbs to solu	D MAL [Nyambi1998] ble oligomeric gp140 versu	us gp41 or gp120 monomers
		<ul> <li>1331A: The Ab bind enzymes) and extract E-507 and I-487, wh</li> <li>1331A: 26 HIV-1 gr</li> </ul>	ling site was studied with eption (protein is digested the hich are thought to be locate oup M isolates (clades A to	bound with a 5-10 fold prefer bitope excision (protein is bour n allowed to react with Ab), fo d on opposite sides of hydroph H) were tested for binding to 4 tested, while MAb 1331A, wh	nd in native conformation of the conformation	on to immobilized MAb, the oscopy – two non-contiguon gp120/gp41 interaction [ICS MAbs, 2 bound well, 2 t	us aa in C5 were protected, Hochleitner2000b] bound weakly – MAb 858-I
		<ul> <li>1331A: Conformation of the V3 loop and conformation and the strength bind as controls: anti-V3 1331A (anti-C5 used disulfide bonds), and 1331A: Truncation of the external Envelop MAb 2G12 and the bearing the truncation</li> </ul>	cross-compete with the MAI ding was highly correlated v 447-52D (anti-V3 MAb for d as a linear binding site MAI d MAb 246 (anti-gp41 MAb of the gp41 cytoplasmic don he, enhancing binding of CD anti-gp41 MAb 246D – in c	Abs may be more cross-reactive 447-52D and are conformation with percent neutralization using competition and neutralization Ab control as binding was not contain of X4, R5, and X4R5 virual MAbs 17b and 48d and of Contrast, binding of the anti-V2 putralization by MAbs 48d, b12071	onally sensitive – MAbig the ghost cell or PHA in studies), 654 (anti-CI liminished by treating good of all clades) [Gorny2 is sessiones a conformatic CD4BS MAbs F105, big MAb 697D and the and	s showed cross-clade binding blast assay – five well-chad blast assay – five well-chad blast used as a conformation of the property of the pro	ng to native, intact virions aracterized MAbs were use on-sensitive MAb control), a metaperiodate to reduce ables the CD4 bound state of cosylation site dependent not affected – viruses
570	110.1	gp160 (491–500) Vaccine Vector/Type Ab type C5 Dono References Gosting1987, Linsle	gp120 (491–500 LAI)  gr: infected-cell lysate Stra  Genetic Systems Corp, Se  gy1988, Thomas 1988, Pincu	IEPLGVAPTK  in: BRU HIV component: vi attle WA, E. Kinney-Thomas  s1991, Moore1994c, Cook199 at binds to gp120, but at aa 200	4, McDougal1996, Bin	Vaccine Vaccine lley1997a, Valenzuela1998.	murine (IgG1 $\kappa$ ), Maksiutov2002

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• 110.1: Referred to as 110-1 – does not inhibit CD4-gp120 binding or neutralize HIV-1 strains [Linsley1988]

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizing	Immunogen	Species(Isotype)
		<ul> <li>[Pincus1991]</li> <li>110.1: The relative :</li> <li>110.1: MAbs agains against the carboxy-MAb binding [Cook</li> <li>110.1: Does not new</li> <li>110.1: Does effect I</li> </ul>	affinity for denatured/nativest the glycosphingolipid Gaterminus of gp120 inhibit (1994) attralize HIV-1 LAI [McDot LAI viral binding or entry in	e gp120 is 0.7 [Moore199 llCer block HIV infection gp120 binding to GalCer ngal1996] nto CEM cells [Valenzuel	of normally susceptible CD4 negout not as potently as anti-V3 MA	gative cells from the babs – binding of GalC	orain and colon – MAbs Cer to gp120 does not inhibit
571	42F	<ul> <li>42F: 42F and 43F w stained diverse strai absorbed gp120 [Al</li> <li>42F: A study of 6 an lysis against strains</li> </ul>	ns of infected cells and diresmadi 1997] nti-Env MAbs and their abi IIIB, MN, SF-2, and RF, b	siutov2002 rm non-progressor by EB ected ADCC – were more lity to bind or direct ADC ut not a clone of MN [Als	no V transformation of PBMC – san potent for ADCC if the cell was C against target cells infected wi madi 1998] n cell growth factor receptor prec	infected with HIV-1, th IIIB, MN, SF-2, an	rather than just presenting and RF – bound and directed
572	43F	<ul> <li>43F: 42F and 43F w stained diverse strai absorbed gp120 [Al</li> </ul>	ns of infected cells and dires	rm non-progressor by EB ected ADCC – were more	no V transformation of PBMC – san potent for ADCC if the cell was m cell growth factor receptor precent and the contract of the cell was more than the contract of the cell growth factor receptor precent of the cell growth factor receptor growth factor receptor growth growth factor receptor growth g	infected with HIV-1,	rather than just presenting
573	RV110026	gp160 (491–500) Vaccine Vector/Type Ab type C5 Dono References Moore1 • RV110026: Preferen	gp120 (491–500 LAI) e: peptide Strain: LAI or Commercial, Olympus In 994c, Moore1994d, Maksi ntially binds SDS-DTT der	IEPLGVAPTK  nc utov2002 natured gp120 (15 fold usi	ng R1/87 as capture reagent) [Mo ast/stem cell growth factor recep	Vaccine oore1994c]	human
574	105-306	gp160 (492–500)  Vaccine Vector/Type Ab type C-term	gp120 (498–505 HAM112, O group) e: recombinant protein Si	KPFSVAPTP	) HIV component: gp160	Vaccine	murine (IgG1 κ)

**HIV Antibodies Tables** 

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizing	Immunogen	Species(Isotype)
575	GV1G2	gp160 (494–499)	gp120 (494–499 IIIB)	LGVAPT		Vaccine	murine
		**	: protein-Ab complex HIV	Component: gp120 complexed with MA	Ab M77		
		Ab type C5					
		References Denisova					
				gp120 and used as an immunogen, it sti		IAbs to linear epitopes – MA	Abs GV12F6 and
		GV3H1 are homolog	gous to GV1G2 and were ge	nerated in the same experiment [Denisov	/a1996]		
576	750-D	gp160 (498–504)	gp120 (503-509)	PTKAKRR	no	HIV-1 infection	human (IgG3λ)
		Ab type C-term					
		References Forthal1	995, Hioe2000				
		• 750-D: Not neutraliz	ing, positive ADCC activity	, and no viral enhancing activity [Fortha	11995]		
		• 750-D: Ab responses	s, because of their capacity t	o alter antigen uptake and processing, ca	in influence help	er T cell responses – CD4BS	MAbs or serum Ig
				sponses of gp120 specific T cells – C5 M			
577	450-D	gp160 (498-504)	gp120 (475–486 BH10)	PTKAKRR(orRRVVQRE,orMRDNW-	no	HIV-1 infection	human (IgG1λ)
	(450-D-3,			RSELYKYdependingonreferen-			
	450D)			ce)			

Ab type C5 Donor Susan Zolla-Pazner (Zollas01@mcrcr6.med.nyu), NYU Med Center, NY, NY References Durda1988, Karwowska1992a, Karwowska1992b, Spear1993, Laal1994, Gorny1994, Cook1994, Forthal1995, Manca1995a, Li1997, Hioe1997b, Hioe2000, Hioe2001, Verrier2001

- 450-D: Bound to MN, SF-2 and IIIB, but was not neutralizing [Karwowska1992a]
- 450-D: Did not mediate deposition of complement component C3 on HIV infected cells [Spear1993]
- 450-D: Not neutralizing alone, could synergize anti-CD4 binding site antibody neutralization [Laal1994]
- 450-D: Epitope is defined as PTKAKRR [Gorny1994]
- 450-D: MAbs against the glycosphingolipid GalCer block HIV infection of normally susceptible CD4 negative cells from the brain and colon MAbs against the carboxy-terminus of gp120 do not inhibit gp120 binding to GalCer binding of GalCer to gp120 does not inhibit MAb binding [Cook1994]
- 450-D: No neutralizing activity, no ADCC activity, and no viral enhancing activity [Forthal1995]
- 450-D: Virions complexed to gp120 Ab facilitate presentation of p66 RT epitopes to Th cells [Manca1995a]
- 450-D: One of 14 human MAbs tested for ability to neutralize a chimeric SHIV-vpu+, which expressed HIV-1 IIIB env 50% neutralization could not be achieved at a maximal concentration of 6 mug/ml [Li1997]
- 450-D: Four primary isolates showed distinct patterns of sensitivity to neutralization by polyclonal sera or plasma and MAbs BZ167 was the only isolate inhibited by all polyclonal sera and plasma tested, and was also neutralized by 8/17 MAbs, in particular anti-V3 loop (419-D, 447-52D, 782-D, and 838-D), anti-CD4bd (559/64-D, 654-D and 830-D and a cluster II of gp41 directed MAb (98-6) isolates 92HT593 and 91US056 were neutralized by V3 loop (419-D, and 447-52D)and cluster II gp41 (98-6) MAbs at higher concentrations US4 was neutralized by some of the polyclonal sera/plasma tested and not at all by MAbs individually or by a cocktail of ten MAbs consisting of 419-D, 447-52D, 782-D, 838-D, 559/64-D, 654-D, 450-D, 670-D, 1281-D and 98-6 [Hioe1997b]
- 450-D: Ab responses, because of their capacity to alter antigen uptake and processing, can influence helper T cell responses CD4BS MAbs or serum Ig from HIV+ individuals inhibited proliferative responses of gp120 specific T cells C5 MAbs 450-D and 750-D did not effect proliferation [Hioe2000]
- 450-D: CD4BS MAbs when complexed with gp120, inhibit proliferation of gp120-specific CD4 T-cells and IFN gamma production 450-D does not have this effect and was used as a control in this study [Hioe2001]

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutraliz	ing Immunogen	Species(Isotype)
		at 2 to 10 ug/ml: 2F:	5, 50-69, IgG1b12, 447-52 we effects were seen for pair	D, 2G12, and 670-D six	alize the dual-tropic primary is did not have neutralizing activ (Abs, and antagonism was note	ity: 654-D, 4.8D, 450-D, 2	246-D, 98-6, and 1281 – no
578	670-D (670)	References Zolla-Pazner1995a, 670-D: Group specif 670-D: Not neutraliz 670-D: gp120 can in 447, 257, 1027 – Ma 670-D: Four primary inhibited by all polyanti-CD4bd (559/64 (419-D, and 447-52I at all by MAbs indiv [Hioe1997b] 670-D: Using a who anti-C5 Abs 670-D a A[Nyambi1998] 670-D: A Semliki Forecognized by the an and 694/98D and no antibodies and not by 670-D: A gp120 C5 670-D: 26 HIV-1 gro bound 21/26, and wa 670-D: A panel of 15 at 2 to 10 ug/ml: 2F5	fic cross-clade binding in string, positive ADCC activithibit MIP-1alpha from bir Ab 670 which binds in the visolates showed distinct pelonal sera and plasma test-D, 654-D and 830-D and D) and cluster II gp41 (98-6 ridually or by a cocktail of le virion-ELISA method, 1 and 1331A bound to 3/4 B are stringly and by a man by an and by an an angative of the coup M isolates (clades A to as the most cross-reactive of 2 MAbs was used to identify, 50-69, IgG1b12, 447-52 are effects were seen for pair	orny 1997, Hioe 1997b, Goerotyping study using floty, and no viral enhancing ading to CCR5, but this in C5 region had no effect [batterns of sensitivity to need, and was also neutralia a cluster II of gp41 directs. MAbs at higher concerten MAbs consisting of 48 human MAbs were test clade viruses (they didn't on system carrying BX08 5, while gp120 at the plasm rat brain also showed the eyer 1999] ontrol in a study of anti-good H) were tested for bindicts MAb [Nyambi 2000] of H) were that could neutral D, 2G12, and 670-D six and consisting flow of the end of the extension of the end of the	rny1998, Nyambi1998, Altme w-cytometry [Zolla-Pazner1998 g activity, numbering provided shibitory effect is blocked by p Hill1997] eutralization by polyclonal ser zed by 8/17 MAbs, in particul fed MAb (98-6) – isolates 92H strations – US4 was neutralized 419-D, 447-52D, 782-D, 838-I ted for their ability to bind to at bind to IIIB), and to subtype env was used to study the comma membrane was detected on at surface-expressed Env was	suggests epitope is RRVV re-incubation of gp120 with a or plasma and MAbs – I ar anti-V3 loop (419-D, 44 T593 and 91US056 were at by some of the polyclona D, 559/64-D, 654-D, 450-I apanel of 9 viruses from a panel of 9 viruses	VQRE [Forthal1995] ith three anti-V3 MAbs: BZ167 was the only isolate 47-52D, 782-D, and 838-D), neutralized by V3 loop al sera/plasma tested and not D, 670-D, 1281-D and 98-6 lades A, B, D, F, G, and H – eted with subtype acytoplasmic gp120 was adent MAbs 2G12, 670-D information-dependent  ye significant neutralization 246-D, 98-6, and 1281 – no
579	polyclonal	References Jeyaraja  • Mice were immunize	ed with peptide APTKAK	RRVVQREKR – epitope	excision and extraction combi		
580	722-D	gp160 (503–509) <b>Ab type</b> C-term <b>References</b> Laal199	gp120 (503–509) 4, Forthal1995	RRVVQRE	no	HIV-1 infection	human (IgG1κ)

No.	MAb ID	<b>HXB2</b> Location	Author's Location	Sequence	Neutralizing	Immunogen	Species(Isotype)
				anti-CD4 binding site antibody rity, and no viral enhancing act			
581	polyclonal	• Most HIV-1+ individ	gp120 (508–516) 987, Loomis-Price1997 duals have an antibody resp ients [Loomis-Price1997]	RRVVQREKR  onse to this epitope – in this str	udy, reactivity to RRVVQR	HIV-1 infection  EKR was used as a pos	human sitive control for HIV-1+
582	1131-A			VVQREKR tudies that demonstrate that CΣ lation [Bandres1998]	no CCR4 can bind to gp120 in	HIV-1 infection the absence of CD4-gp	human (IgG3 $\lambda$ ) o120 interactions, and that
583	858-D	<ul> <li>References Zolla-Pa</li> <li>858-D: Group specif</li> <li>858-D: No neutraliz</li> <li>858-D: Binding of p anti-V3 and CD4BS a 5-10 fold preference</li> <li>858-D: 26 HIV-1 group</li> </ul>	azner1995a, Forthal1995, G fic cross-clade binding in se ing activity, no ADCC activanel of 21 MAbs to soluble MAbs reacted better with the for the monomer[Gorny2] oup M isolates (clades A to	rotyping study using flow-cyto rity, and no viral enhancing act oligomeric gp140 versus gp41 he oligomer and V2 and C5 ter	metry [Zolla-Pazner1995a] ivity [Forthal1995] or gp120 monomers was conded to favor the monomer	compared – no MAb wa – C5 MAbs 858-D, 98 (Abs, 2 bound well, 2 b	9-D and 1331A bound with bound weakly – MAb 858-D
584	989-D	<ul> <li>References Zolla-Pa</li> <li>989-D: In serotyping</li> <li>989-D: Binding of p anti-V3 and CD4BS a 5-10 fold preference</li> </ul>	azner1995a, Gorny2000a, N g study using flow-cytometr anel of 21 MAbs to soluble MAbs reacted better with t ce for the monomer[Gorny2 oup M isolates (clades A to	y, showed B clade specificity, l oligomeric gp140 versus gp41 he oligomer and V2 and C5 ter	out only reacted with 7/11 l or gp120 monomers was conded to favor the monomer	compared – no MAb wa – C5 MAbs 858-D, 98	as oligomer specific, though 9-D and 1331A bound with
585	1A1	References Buchach • 1A1: Human MAb g		AAGSTMGAASMTLTVQARQ nna, Austria ormation of PBL from HIV-1+ e HLA class II histocompatibil	volunteers [Buchacher199-		human (IgG1κ)
586	24G3	gp160 (525–543) <b>Donor</b> H. Katinger,	gp41 (526–543 BH10)	AAGSTMGAASMTLTVQARQ	no	HIV-1 infection	human (IgG1κ)

No.	MAb ID	HXB2 Location	<b>Author's Location</b>	Sequence	Neutralizing	Immunogen	Species(Isotype)
		• 24G3: Human MAb	•	Maksiutov2002 n of PBL from HIV-1+ volunte the HLA class II histocompatil	_	_	002]
587	25C2 (IAM 41-25C2)	References Buchacl  25C2: Human MAb [Buchacher1994]  25C2: Called IAM 4 defined as: gp41(21-	ner1992, Buchacher1994, S generated by electrofusion 41-25C2 – Binding domain 38 BH10) [Sattentau19956	AAGSTMGAASMTLTVQARGENNA, Austria and Viral Testing Sattentau1995c, Maksiutov200 of PBL from HIV-1+ volunted overlaps sites that are critical class II histocompatible.	Systems, Houston, TX 2 ers with CB-F7 cells – binds for gp120-gp41 association	<ul> <li>binding is enhanced !</li> </ul>	by sCD4 – binding region
588	5F3	References Buchacl • 5F3: Human MAb g		AAGSTMGAASMTLTVQARGENNA, Austria of PBL from HIV-1+ volunteeree HLA class II histocompatibil	s with CB-F7 cells [Buchac		human (IgG1 $\kappa$ )
589	α(566-586)	gp160 (561–581) <b>References</b> Poumbo	gp41 (566–586 BRU) purios1992	AQQHLLQLTVWGIKQLQA	RIL	HIV-1 infection	human
590	PC5009	References Poumbo	gp41 (577–596 BRU) e: recombinant protein Hourios1992 d only monomeric gp41 [P	. 0.	20	Vaccine	murine
591	polyclonal α577-596	gp160 (572–591) <b>References</b> Poumbo  • alpha(577-596): Aff		GIKQLQARILAVERYLKDo		HIV-1 infection	human
592	polyclonal		ıman sera were tested agai	LQARILAVERYLKDQQL  nst wildtype peptide, and pepti even more weakly with substi		HIV-1 infection	human ngly with wildtype, weakl
593		was observed with to	002a xposed uninfected individuotal IgA from both EU and	QARILAV  tals(EU), HIV-infected individ  HIV+ – the EU IgA exclusive - sera of QAFILAV-immunized	ly bound to a distinctive epi	tope within gp41, QAR	RILAV, in the coiled coil

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizing	Immunogen	Species(Isotype)
594		Ab type Leucine zip References Clerici2 Six sera from HIV-e was observed with to	oper motif 002a xposed uninfected individua otal IgA from both EU and	QARILAV  gp41 Adjuvant: keyhole limp  als(EU), HIV-infected individuals  HIV+ – the EU IgA exclusively balizing with the dose-dependent b	and healthy controls we	tope within gp41, QA	
595	1F11	References Buchach	gp41 (579–613 BH10) Inst. Appl. Microbiol., Viener1992, Buchacher1994 electrofusion of PBL from	ARILAVERYLKDQQLLGIWGO ICTTAVPWNA nna, Austria HIV-1 positive volunteers with C		HIV-1 infection	human (IgG1κ)
596	1H5		gp41 (579–613 BH10) her1992, Buchacher1994 electrofusion of PBL from F	ARILAVERYLKDQQLLGIWGG ICTTAVPWNA HIV-1 positive volunteers with CF		HIV-1 infection	human (IgG1 $\kappa$ )
597	3D9	References Buchach	gp41 (579–613 BH10)  Inst. Appl. Microbiol., Viewher1992, Buchacher1994 electrofusion of PBL from F	ARILAVERYLKDQQLLGIWGO ICTTAVPWNA nna, Austria HIV-1 positive volunteers with CF		HIV-1 infection	human (IgG1κ)
598	4B3	gp160 (578–612) <b>Donor</b> H. Katinger, <b>References</b> Buchacl	gp41 (579–613 BH10) Inst. Appl. Microbiol., Viether1992, Buchacher1994, C	ARILAVERYLKDQQLLGIWGO ICTTAVPWNA nna, Austria	CSGKL- no	HIV-1 infection	human (IgG1λ)
599	4D4	<ul> <li>References Buchacl</li> <li>4D4: Generated by 6</li> <li>4D4: The MAbs with in an immune responsible to the native contained by anti-V3 MA bind C11, 23A, and very strongly induced</li> </ul>	her1992, Buchacher1994, Chelectrofusion of PBL from In the broadest neutralizing has to the oligomer on the value of the formation of Env and exploses 19b and 83.1 – SOSgp14 M90, MAbs that bind to gp and by CD4 in SOS gp140 – and solve of the solve of	ARILAVERYLKDQQLLGIWGO ICTTAVPWNA nna, Austria and Viral Testing Synhen1994b, Sattentau1995c, Binled IV-1 positive volunteers with CF activity, IgG1b12, 2G12 and 2F5 irion surface rather than dissociatore its potential as an immunogen 0 is not recognized by C4 region 120 C1 and C5, where it interacts anti-gp41 MAbs that bind in the rads to the only gp41 epitope that	stems, Houston, TX sy1999 3-F7 cells [Buchacher199, all have high affinity for sed subunits – a disulfide a – SOS gp140 is recogni MAbs that neutralize on s with gp41 – MAbs that region that interacts with	r the native trimer, ind linked gp120-gp41 (S zed by NAbs IgG1b12 ly TCLA strains, G3-4 bind CD4 inducible e gp120, 7B2, 2.2B, T4	OS gp140) was created to 2, 2G12, and CD4-IgG2, and 42 and G3-519 – nor did it pitopes, 17b and A32 were, T15G1 and 4D4, did not

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizing	Immunogen	Species(Isotype)
600	4G2	gp160 (578–612)	gp41 (579–613 BH10)	ARILAVERYLKDQQLLGIWGCSGKL- ICTTAVPWNA	no	HIV-1 infection	human (IgG1 $\kappa$ )
			Inst. Appl. Microbiol., View	nna, Austria			
			her1992, Buchacher1994 electrofusion of PBL from I	HIV-1 positive volunteers with CB-F7 cells	s [Buchacher19	941	
601	polyclonal	gp160 (579–589)	gp41 (586–596 IIIB)	RILAVERYLKD	, [Bueilleileilei	Vaccine	murine, rabbit
001	porycionar	C1 .	e: peptide HIV component			vacenie	marine, racore
		References Xiao200					
		Strong epitope-spec:	ific neutralizing antibody re	sponses were induced using the peptide C	(RILAVERYLK	(D)_2-BSA, but not ful	l gp160 [Xiao2000b]
602	polyclonal	gp160 (579–589)	gp41 (586–596)	RILAVERYLKD		Vaccine	rabbit (Ig)
		Ab type N-term	e: polyepitope, protein HI	V component: gp160 Adjuvant: BSA			
		References Lu2000	c, Lu2000b				
		• High titer response t	to ELDKWA and RILAVER	RYLKD was observed upon vaccination wi			
				KD conjugated to BSA, a weak response to			
				d, yielding a strong Ab response to both E	LDKWA and G	PGRAFY – gp160 vac	cination yielded strong Ab
			any of the peptides studied h				
603	polyclonal	gp160 (579–599)	gp41 (583–604) e: protein HIV component	RILAVERYLKDQQLLGIWGCS	no	Vaccine	rabbit
		References Benjoua	-	desiarylated gp160			
		3		cross-react with HIV-2 gp140 due to immu	unodominant co	onserved epitope in gp4	1 [Benjouad1993]
604	2A2/26	gp160 (579–601)	gp41 (584–606 BRU)	RILAVERYLKDQQLLGIWGCSGK		Vaccine	murine (IgG)
			e: protein HIV component				
			ourios1992, Poumbourios19		1		
				ligomer and monomer [Poumbourios 1992 LL), a region important for oligomer forms		s hinding Delta (550-5	61 +571-581) abrogates
		binding [Poumbouri		3D), a region important for ongoiner forme	tton ummines	omanig, Dena (330 3)	01 1371 301) abiogaics
605	50-69	gp160 (579–603)	gp41 (579–603 BH10)	RILAVERYLKDQQLLGIWGCSGKLI	no	HIV-1 infection	human (IgG2κ)
	(SZ-50.69)	C1 .		(Zollas01@mcrcr6.med.nyu), NYU, NY			(8- )
				Xu1991, Robinson1991, Sattentau1991, Ed			
				Binley1996, Klasse1996, Stamatatos1997,	Boots1997, Hi	oe1997b, Mitchell1998	3, Gorny2000b,
			bi2000, Zwick2001b, Verrie	er2001 of ricin is toxic to lines of HIV-infected T	calls (H0) and r	managutas (I 1027) [Till	10001
				ter, compared to gp41 monomer [Pinter198]		nonocytes (0937) [1111	1909]
				o deglycosylated ricin A chain [Gorny1989]			
		• 50-69: The epitope	is affected by the conformat	tion conferred by the two cysteines at amir	no acids 598 and		
				ergizes with huMAb 120-16 in vitro to enh	nance HIV-1 info	ection to level approach	ning that found in
		polyclonal anti-HIV	serum [Robinson1991]				

No. MAb ID HXB2 Location Author's Location Sequence Neutralizing Immunogen Species(Isotype)

- 50-69: Two fold increase in binding to gp120 in the presence of bound sCD4 [Sattentau1991]
- 50-69: Called SZ-50.69 binds to an epitope within aa 579-613 [Eddleston1993]
- 50-69: Did not mediate deposition of complement component C3 on HIV infected cells unless cells were pre-incubated with sCD4 complement mediated virolysis of MN and IIIB in the presence of sCD4 [Spear1993]
- 50-69: Epitope described as cluster I, 601-604, conformational does not neutralize IIIB or synergize neutralization by anti-V3 MAb 447-52D or by CD4 BS MAbs [Laal1994]
- 50-69: One of several anti-gp41 MAbs that bind to a gp41-maltose binding fusion protein designed to study the leucine zipper domain of gp41, showing that the construct has retained aspects of normal gp41 conformation [Chen1995]
- 50-69: Preferentially binds oligomer binding increased after pretreatment of infected cells with sCD4 binding domain overlaps site that is critical for gp120-gp41 association [Sattentau1995c]
- 50-69: Virions complexed to gp41 Ab facilitate presentation of p66 RT epitopes to Th cells [Manca1995a]
- 50-69: Does not neutralize HIV-1 LAI [McDougal1996]
- 50-69: Prebinding of anti-V3, and CD4i MAbs 48d and 17b, but not anti-V2 neutralizing MAbs, expose the 50-69 epitope [Poignard1996a]
- 50-69: Binds to a linear epitope located in the cluster I region binding of 50-69 and 240-D inhibited by Fabs A1, A4, M8B, M26B, M12B and T2 [Binley1996]
- 50-69: Used to test exposure of gp41 upon sCD4 binding [Klasse1996]
- 50-69: Binding of anti-gp120 MAbs IgG1b12 or 654-30D does not mediate significant exposure of the gp41 epitopes for MAbs 2F5 and 50-69 [Stamatatos1997]
- 50-69: Abs that recognize discontinuous epitopes can identify mimotopes from a phage peptide display library 50-69 maps to an immunodominant domain in gp41 three groups of peptides were selected, one which seems most closely related to gp41 sequence peptide consensus is WGCxx(RK)(x n)LxC the analogous gp41 sequence WGCSGKLIC is present in most M group clades, except D with a common L to H substitution [Boots 1997]
- 50-69: Mutations in BH10 gp160, W596Y and T605A, as well as deletions of 605-609 (TTAVP) and 597-609 (GCSGKLICTTAVP), abrogate binding of enhancing MAbs 86, 240D, 50-69, and 246-D 5/6 enhancing MAbs identified to date bind to the immunodominant region 579-613 identifies non-contiguous W596-G597-C598 and C604-T605 as minimal epitope [Mitchell1998]
- 50-69: A cluster I epitope that binds to rgp41 567-647, recognizes a peptide N51-C43 complex trimer of heterodimers that approximates the core of the fusogenic form of gp41 this MAb doesn't react with either of the peptides N51 or C43 individually MAbs 50-69 and 1367 had similar properties MAb 50-69 bound the fusogenic form of the protein in liquid phase [Gorny2000b]
- 50-69: Binding of panel of 21 MAbs to soluble oligomeric gp140 versus gp41 or gp120 monomers was compared no MAb was oligomer specific, but gp41 MAb 50-69 bound with a 5 fold preference for the oligomer, while other gp41 MAbs (1367, 98-6, 167-D, 1281, 1342, and 1379) did not show a preference [Gorny2000a]
- 50-69: 26 HIV-1 group M isolates (clades A to H) were tested for binding to 47 MAbs, including 5 cluster I anti-gp41 MAbs which showed good cross clade reactivity 50-69 bound the majority of isolates although binding was moderate to weak specifies discontinuous binding site range as aa 579-613 [Nyambi2000]
- 50-69: This paper primarily concerns 4E10 and Z13, MAbs that both bind proximally to the 2F5 binding site to a conserved epitope, and that neutralize some primary isolates from clades B, C, and E MAb 50-69 binding to infected cells is enhanced by sCD4, while 4E10 and Z13 binding is essentially unaltered [Zwick2001b]
- 50-69: A panel of 12 MAbs was used to identify those that could neutralize the dual-tropic primary isolate HIV-1 89.6 six gave significant neutralization at 2 to 10 ug/ml: 2F5, 50-69, IgG1b12, 447-52D, 2G12, and 670-D six did not have neutralizing activity: 654-D, 4.8D, 450-D, 246-D, 98-6, and 1281 no synergy, only additive effects were seen for pairwise combinations of MAbs, and antagonism was noted between gp41 MAbs 50-69 and 98-6, as well as 98-6 and 2F5 [Verrier2001]
- 50-69: NIH AIDS Research and Reference Reagent Program: 531

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizing	Immunogen	Species(Isotype)
606	9-11	References Mani19			41.1 D.K. :100	Vaccine	murine (IgG1)
		• 9-11: required the C	-C disulfide bridge and loo	p formation, can bind simultaneously with	41-1 [Man1199	4]	
607	98-43	<ul><li>98-43: Reacts equal</li><li>98-43: Poor ADCC</li><li>98-43: 579-604 bind</li></ul>	gp41 (579–604 HXB2) 989, Gorny1989, Tyler1990 ly well with oligomer and r (in contrast to MAb 120-16 Is in the immunodominant r esearch and Reference Rea	, Xu1991 monomer [Pinter1989] 6, gp41(644-663)) [Tyler1990] region [Xu1991]	no	HIV-1 infection	human (IgG2κ)
608	41-1 (41.1)	gp160 (579–608)	gp41 (584–609)	RILAVERYLKDQQLLGIWGCSGKLI- CTTAV		Vaccine	murine (IgG1κ)
		<ul> <li>41-1: Efficacious as</li> <li>41-1: Called 41.1, at coupled to ricin A cl</li> <li>41-1: Did not requir</li> <li>41-1: Called 41.1, at</li> </ul>	ve [Gosting1987] seems to have been named an immunotoxin when cou nd described as a human M hain (RAC) [Pincus1993a] e the C-C disulfide bridge a nd described as a human M	the same as a different MAb to gp41(735-1) pled to RAC – gave linear epitope as gp16(Ab – cross-competes with 41.4 – sCD4 enland loop formation, can bind simultaneousl (Ab, binding 579-604 – a panel of immunot was not directly proportional to binding [F	0 579-603 [Pinch nances the effich y with 9-11 [M oxins was gene	cus1991] acy of immunotoxins i ani1994]	
609	41.4	gp160 (579–608)	gp41 (584–609)	RILAVERYLKDQQLLGIWGCSGKLI- CTTAV			
		References Pincus 1 • 41.4: Binds to peption	993a de weakly, but to gp160 wi	armaceutical Res Inst, Seattle, WA th higher affinity than 41.1, and cross-compacy of immunotoxins in vitro 30-fold [Pinc		– probably conformati	onal – MAb was coupled to
610	Fab A1	gp160 (579–608)	gp41 (584–609 LAI)	RILAVERYLKDQQLLGIWGCSGKLI- CTTAV	no	HIV-1 infection	human (IgG1κ)
		References Binley1	996				
				rith MAbs 240-D and 50-69 - conformation	sensitive – var	iable regions sequence	ed [Binley1996]
611	Fab A4	gp160 (579–608)	gp41 (584–609 LAI)	RILAVERYLKDQQLLGIWGCSGKLI- CTTAV	no	HIV-1 infection	human (IgG1 $\kappa$ )
		References Binley1	996				

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizing	Immunogen	Species(Isotype)		
		• Fab A4: Binds to clu	ıster I region – competes w	vith MAbs 240-D and 50-69 – conformation	n sensitive – var	iable regions sequence	d [Binley1996]		
612	Fab M12B	gp160 (579–608)	gp41 (584–609 LAI)	RILAVERYLKDQQLLGIWGCSGKLI- CTTAV	no	HIV-1 infection	human (IgG1 $\kappa$ )		
		References Binley1	996						
		• Fab M12B: Binds to	cluster I region - compete	es with MAbs 240-D and 50-69 – conforma	tion sensitive -	variable regions sequer	iced [Binley1996]		
613	Fab M26B	gp160 (579–608)	gp41 (584–609 LAI)	RILAVERYLKDQQLLGIWGCSGKLI- CTTAV	no	HIV-1 infection	human (IgG1κ)		
		References Binley1							
		• Fab M26B: Binds to	cluster I region – compete	es with MAbs 240-D and 50-69 – conforma	tion sensitive –	variable regions sequer	iced [Binley1996]		
614	Fab M8B	gp160 (579–608)	gp41 (584–609 LAI)	RILAVERYLKDQQLLGIWGCSGKLI- CTTAV	no	HIV-1 infection	human (IgG1 $\kappa$ )		
		References Binley1							
		• Fab M8B: Binds to	cluster I region – competes	with MAbs 240-D and 50-69 – conformati	ion sensitive – v	ariable regions sequenc	ed [Binley1996]		
515	Fab T2	gp160 (579–608)	gp41 (584–609 LAI)	RILAVERYLKDQQLLGIWGCSGKLI- CTTAV	no	HIV-1 infection	human (IgG1 $\kappa$ )		
		References Binley1996							
		Fab T2: Binds to clu	ister I region – competes w	rith MAbs 240-D and 50-69 – conformation	n sensitive – var	iable regions sequenced	l [Binley1996]		
516	86 (No. 86)	gp160 (579–613)	gp41 (586–620 IIIB)	RILAVERYLKDQQLLGIWGCSGKLI- CTTAVPWNAS	no	HIV-1 infection	human (IgG1 $\kappa$ )		
			and Yoh-Ichi Matsumoto						
				oinson1990c, Pincus1991, Moran1993, Wis	newski 1996, M	itchell1998			
			1 and also reacted weakly	of HIV-1 IIIB infectivity in the presence of	complement [R	ohinson1990hl			
				ated ADE [Robinson1990c]	complement [K	oomson19900j			
				o RAC – peptide binding stated to be aa 57	9-603 [Pincus19	991]			
		• 86: Heavy (V HI) ar	nd light (V kappaI) chain so	equenced – enhancing activity – similar ger	rmline sequence	to MAb S1-1, but very	different activity		
		[Moran1993]							
				vas examined and a bias of enhanced V H1	and V H4, and	reduced V H3, was note	ed among HIV infected		
		individuals [Wisnew	-	05A, as well as deletions of 605-609 (TTA	VP) and 597-60	9 (GCSGKI ICTTAVP)	abrogate hinding of		
			-	- 5/6 enhancing MAbs identified to date bit					
		_	arch and Reference Reage	<del>-</del>		C	,		
617	polyclonal	gp160 (580–597) <b>References</b> Petrov1	gp41 (584–602)	ILAVERYLKDQQLLGIWG	no	HIV-1 infection	human		
			nd broadly reactive peptide	[Petrov1990]					
618	V10-9	gp160 (580–613)	gp41 (586–620 IIIB)	ILAVERYLKDQQLLGIWGCSGKLIC-	no	HIV-1 infection	human (IgG1 K)		
				TTAVPWNAS					

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizing	Immunogen	Species(Isotype)
				E) of HIV-1 IIIB infectivity, synergistically diated ADE [Robinson1990c]	y enhanced by N	- ИАЬ 120-16 [Robinson199	0b]
619	polyclonal	gp160 (582–589) <b>References</b> Klasse1	gp41 (589–596) 991	AVERYLKD		HIV-1 infection	human
		• Substitutions and de 14 human sera [Klas		were systematically studied – alterations in	n AVERYLKD a	abrogated the antigenicity of	of peptides with most of
620	polyclonal	gp160 (584–604) <b>References</b> Shaffern  • Immunogenic doma	gp41 (74–94) man1989 in useful for diagnostics [Sh	ERYLKDQLLGIWGCSGKLIC afferman1989]		HIV-1 infection	human
621	polyclonal	gp160 (584–612)	gp41 (587–617 BRU)	ERYLKDQQLLGIWGCSGKLICTTAV- PWNA	no	HIV-1 infection	human
		• Chimeric peptide co [Hernandez2000]		0(495-516 and 584-612) served as a speci	fic and broadly	reactive antigen for diagno	stic detection of HIV-1
622	2F11	<ul><li>2F11: Enhances info</li><li>2F11: Monoclonal a</li></ul>		DQQLLGIWGCSG of complement – does not mediate ADCC ve distinct phenotypes—41-7 and 1B8.env		_	human (IgG1)
623	246-D (SZ-246.D, 246, 246D)	References Xu1991 Nyambi2000, Verrie 246-D: Fine mappin 246-D: Did not med 246-D: No neutraliz 246-D: Called SZ-2 246-D: No neutraliz 246-D: Virions com 246-D: Ab-mediated results in part from 1 246-D: Mutations ir enhancing MAbs 86 246-D: Four primarinhibited by all polyanti-CD4bd (559/64 (419-D, and 447-52) polyclonal sera/plas	, Robinson1991, Spear1993 ar 2001, Gorny2002, Edwards indicates core is LLGI [Xi iate deposition of compleme ing activity, some enhancing 46.D [Eddleston1993] ing activity, both ADCC and plexed to gp41 Ab facilitate di activation of complement of IgM in normal human serum BH10 gp160, W596Y and Si, 240D, 50-69, and 246-D—y isolates showed distinct parclonal sera and plasma tester-D, 654-D and 830-D and a D) and cluster II gp41 (98-6)	Zollas01@mcrcr6.med.nyu), NYU Med G, Eddleston1993, Forthal1995, Manca199 s2002 u1991] ent component C3 on HIV infected cells ug activity [Robinson1991] d viral enhancing activity [Forthal1995] presentation of p66 RT epitopes to Th cells in HIV+ cells is higher than Ab independent that is HIV-cross-reactive [Saarloos1995] T605A, as well as deletions of 605-609 (Tollo 5/6 enhancing MAbs identified to date bitterns of sensitivity to neutralization by ped, and was also neutralized by 8/17 MAbs cluster II of gp41 directed MAb (98-6) — MAbs at higher concentrations and 246-IMAbs individually or by a cocktail of ten MAbs individually or by a cocktail of ten MAbs.	Is [Manca1995] ent activation— i] TTAVP) and 597 nd to the immurolyclonal sera o s, in particular a isolates 92HT59 D neutralized 91	a] -what has been termed "Ab 7-609 (GCSGKLICTTAVP nodominant region 579-613 or plasma and MAbs – BZI anti-V3 loop (419-D, 447-5 93 and 91US056 were neut 1US056 – US4 was neutral	independent" in fact ), abrogate binding of 3 [Mitchell1998] 67 was the only isolate 2D, 782-D, and 838-D), ralized by V3 loop ized by some of the

No.	MAb ID	HXB2 Location	Author's Location	Sequence		Neutralizing	Immunogen	Species(Isotype)
		T35) [Earl1997]  • 246-D: Core epitopogp41 or the individue  • 246-D: 26 HIV-1 grelade reactivity – 24 tested, including the [Nyambi2000]  • 246-D: A panel of 1 at 2 to 10 ug/ml: 2F synergy, only additi 98-6 and 2F5 [Verries 246-D: Called 246-bind to the tip of the intact virions and the MAbs were used as conformation-sensities isolates of all clades 246-D: Called 246-D bound state of the esite dependent MAB viruses bearing the surface expression of	al peptides N51 and C43 oup M isolates (clades A 6-D bound strongly or me V3 and C5 region MAbs 2 MAbs was used to iden 5, 50-69, IgG1b12, 447-5 we effects were seen for per 2001] - Conformation-dependent V3 loop and cross-compe strength binding was high controls: anti-V3 447-52 ive MAb control), 1331A tested, A, B, C, D, F and D - Truncation of the gp41 sternal Envelope, enhancing 2G12 and the anti-gp41.	I epitope that does at that form this structo H) were tested for oderately to all 26 H – notes core epitopetify those that could 2D, 2G12, and 670 airwise combination at anti-V3 loop Absorbet with the MAb 4 ghly correlated with D (anti-C5 used as a CRF01 (clade E) [ cytoplasmic domaing binding of CD4 MAb 246D – in consitive to neutralizatid dwards 2002]	not bind to either a peptid ture – MAbs 181-D and 2 or binding to 47 MAbs, in HIV-1 group M clades virue as LLGI – no neutralized d neutralize the dual-tropid D six did not have neutralized so of MAbs, and antagonismay be more cross-reactive 47-52D and are conformant percent neutralization used competition and neutral linear binding site MAb of Gorny 2002 in of X4, R5, and X4R5 virus MAbs 17b and 48d and antrast, binding of the antion by MAbs 48d, b12, and	de complex that 246-D had siminal activities a clusting activity was described in a cluding activity: is a cluding activity activity.	approximates the core of the fusogenic form of alar properties [Gorny2000b] ter I anti-gp41 MAbs which showed good cross showed the strongest binding of all anti-Env MA is observed when 246-D was tested with five isolated at the HIV-1 89.6 – six gave significant neutralizations: 654-D, 4.8D, 450-D, 246-D, 98-6, and 1281 – no between gp41 MAbs 50-69 and 98-6, as well as V3 MAbs were generated – the six new MAbs allowed in the MAbs showed cross-clade binding to native cell or PHA blast assay – five well-characterized phab 246 (anti-gp41 MAb that bound to primary conformation that more closely resembles the CI also F105, b12, and in most cases of glycosylation pand the anti-V3 MAb 694/98D were not affected anti-C5 MAb 1331A was used to track levels of central conformation and the asset of contracts of the conformation of the conformation of the conformation that more closely resembles the CI and the anti-V3 MAb 694/98D were not affected anti-C5 MAb 1331A was used to track levels of central conformation of the conformation that more closely resembles the CI and the anti-V3 MAb 694/98D were not affected anti-C5 MAb 1331A was used to track levels of central conformation that more closely resembles the CI and the anti-V3 MAb 694/98D were not affected anti-C5 MAb 1331A was used to track levels of central conformation that more closely resembles the CI and the anti-V3 MAb 694/98D were not affected anti-C5 MAb 1331A was used to track levels of central conformation that more closely resembles the CI and the conformation that more closely resembles the CI and the conformation that more closely resembles the CI and the conformation that more closely resembles the CI and the conformation that more closely resembles the CI and the conformation that more closely resembles the CI and the conformation that more closely resembles the CI and the conformation that more closely resembles the CI and the conformation that more closely resembles the CI and the conformation that more closely resembles the CI and the conformation that mo	
624	9G5A	gp160 (591–594) <b>References</b> Lopalco • 9G5A: Anti-idiotyp	gp41 (596–599 IIIB) o1993, Beretta1994 e to gp120 C terminus (C.	QLLG 5 region) MAb M3	8 [Lopalco1993]		anti-idiotype	murine (IgM)
625	181-D (SZ-181.D)	gp160 (591–597) <b>Ab type</b> cluster I <b>References</b> Xu1991  • 181-D: Fine mappir  • 181-D: No enhancir  • 181-D: Called SZ-1  • 181-D: No neutraliz  • 181-D: Core epitopogp41 or the individu  • 181-D: 26 HIV-1 gr	gp41 (591–597 HXB2 Donor Susan Zolla-Pazne , Robinson1991, Eddleste g indicates core is LLGIV g or neutralization activit	qLLGIWg er (Zollas01@mcrei on1993, Forthal199 W [Xu1991] ry [Robinson1991] ral enhancing activit I epitope that does in that form this structor to H) were tested for	r6.med.nyu), NYU, NY 5, Fontenot1995, Gorny2 http://example.com/sity.examp	le complex that 246-D had simi acluding 5 clust	approximates the core lar properties [Gorny20 er I anti-gp41 MAbs w	000b]
626	polyclonal	gp160 (591–608) <b>References</b> Parekh2	gp41 2002	QQLLGIWGCS	GGKLICTTA	no	HIV-1 infection	human (IgG)

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizing	Immunogen	Species(Isotype)
		longitudinal specime	- · · · · · · · · · · · · · · · · · · ·	tions in the US and Thail	nti-HIV IgG after seroconversion and were used in the study – the		~
627	240-D (F240	Ab type cluster I References Xu1991  240-D: Fine mappin  240-D: No neutraliz  240-D: Did not med  240-D: Binds to a li [Binley1996]  240-D: Called F240 among HIV infected  240-D: Mutations ir enhancing MAbs 86  240-D: 26 HIV-1 graclade reactivity – 24	g indicates core is IWG [X ing activity, some enhancin iate deposition of complem near epitope located in the complement of the complement	3, Binley1996, Wisnewsk u1991] g activity [Robinson1991] ent component C3 on HI cluster I region – binding heavy chain usage was 6 96] T605A, as well as deleti -5/6 enhancing MAbs id H) were tested for bindin lerately to 24/26 HIV-1 g	i1995, Wisnewski1996, Mitchell	Fabs A1, A4, M8B, NV H1 and V H4, and Cooper GCSGKLICTT and common tregion 57 or I anti-gp41 MAbs v	reduced V H3, was noted CAVP), abrogate binding of 9-613 [Mitchell1998]
628	F240	<ul> <li>References Cavacin</li> <li>F240: Seems to be of HIV isolates RF, SF F240 is enhanced by homology to hu MA</li> <li>F240: Abs against the showed similar bind 320SI-C3.3), but the</li> </ul>	ii 1998a, York 2001 listinct from MAb 240-D, a 2, IIIB, and MN was observ preincubation of cells with ab 3D6 was observed, as 3D ne V3 loop (50.1, 58.2, 59.1) ing efficiency to Env derive	n antibody with a similar wed – F240 had no neutra n sCD4 or anti-CD4BS M 66 binds to the same epito 1, 257-D, 268-D, 447-52I and from related pairs of proore susceptible to neutral	no vard Med. School, Boston MA, Usepitope in the immunodominant lizing activity and enhances infect IAb F105 – heavy and light chain ppe, these MAbs may define a hur D), CD4BS (IgG1b12, 559-64D, Isimary and TCLA lines (primary: ization suggesting that the change	region of gp41 – dose tion in the presence of variable domains we man Ab clonotype [Ca F105), CD4i (17b), an 168P and 320SI, and	f complement – reactivity of re sequenced, and a strong avacini1998a] d to gp41 (2F5, F240) each TCLA: 168C and
629	D49	gp160 (592–608)  Vaccine Vector/Type Ab type cluster I References Earl199  D49: Generated dur	gp41 (597–613)  e: protein HIV component  4, Earl1997  ing a study of the influence	LLGIWGCSGKLICTT  :: dimeric Env  of the oligomeric structu	AV re of Env in determining the repension	-	
630	D61	<b>Ab type</b> cluster I References Earl199	gp41 (592–608 HXB2) e: protein HIV component Donor Patricia Earl and Ch 4, Richardson1996, Weisse ing a study of the influence	t: dimeric Env ristopher Broder, NIH nhorn1996, Earl1997, Go		Vaccine rtoire of the Ab respo	murine onse [Earl1994]

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizing Immunogen	Species(Isotype)
		<ul> <li>D61, and T4 [Richa</li> <li>D61: Does not precthis region may cha</li> <li>D61: Binding maps human MAb 246-D competition group a</li> <li>D61: The fusion prediction bundles form prior to the present th</li></ul>	irdson1996] ipitate gp41(21-166), but nge conformation during to to region 597-613: WGC to, can be blocked by any or the blocked by sera from Forcess was slowed by using the blocked by the column of E/T cells at 31.5 to fusion – the preincubation	due to a structural difference the activation of the memodification of the memodificatio	binding in oligomeric ELISA assay to a similar extent in the disulfide bonding region near the two cystein brane fusion state of the HIV-1 glycoprotein [Weissenheimmunodominant region containing two Cys residues – onal MAbs (M10, D41, D54, T4, T6, T9, T10 and T35) 997] re (31.5 C) to re-evaluate the potential of Abs targeting in ti-N-HR Ab and anti-six-helix bundle Abs to inhibit furter the inhibitory activity of neutralizing Abs anti-gp41 inability to inhibit fusion [Golding2002b]	es – the authors propose that orn1996] this antibody, along with – members of this fusion intermediates to block sion, indicating six-helix
631	T32	Ab type cluster I References Earl199 T32: Generated dur	ing a study of the influence	Christopher Broder, NIH te of the oligomeric struc	TTAV Vaccine  ture of Env in determining the repertoire of the Ab respectiment of the Ab respective containing two Cys residues [I	
632	T34	Ab type cluster I References Earl199 T34: Generated dur gp120/gp41 cleavag	ing a study of the influence site was used as the imr	Christopher Broder, NIH te of the oligomeric struc munogen [Earl1994]	TTAV Vaccine  ture of Env in determining the repertoire of the Ab responsible immunodominant region containing two Cys residues [I	-
633	115.8	References Oldstor • 115.8: Stimulated b	y immunization with the p	peptide: LGLIWGCSGK	Vaccine  LIC (aa 598-609) – poor reactivity with CSGKLIC – reween cysteines required [Oldstone1991]	murine (IgM) acts well with longer HIV-2
634	M-1	gp160 (593–604)  Vaccine Vector/Typ References Yamada	gp41 (598–609)  e: peptide HIV compone a1991	LGIWGCSGKLIC	Vaccine  vaccine  nan astrocytes [Yamada1991]	murine (IgG1, IgG2b)
635	M-11	References Yamada			Vaccine  Numan astrocytes as well as with gp41 [Yamada1991]	murine (IgG1)

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizing	Immunogen	Species(Isotype)
636	M-13	References Yamada				Vaccine	murine (IgG2b)
		M-13: Reacted with		and in rat and human astrocy	es as well as with gp41 [Yam	lada 1991]	
637	M-2	References Yamada		LGIWGCSGKLIC  t: gp41  tein found in rat and human	strocytes as well as with on4	Vaccine	murine (IgG2b)
638	M-22	gp160 (593–604) Vaccine Vector/Type References Yamada	gp41 (598–609) 2: peptide HIV component	LGIWGCSGKLIC		Vaccine	murine (IgG2b)
639	M-24	References Yamada		LGIWGCSGKLIC  t: gp41  otein found in rat and human	astrocytes as well as with gp	Vaccine 41 [Yamada1991]	murine (IgG1)
640	M-25	References Yamada		LGIWGCSGKLIC  t: gp41  und in rat and human astrocy	es as well as with gp41 [Yam	Vaccine ada1991]	murine (IgG1)
541	M-28	References Yamada		LGIWGCSGKLIC  t: gp41  otein found in rat and human	astrocytes as well as with gp	Vaccine 41 [Yamada1991]	murine (IgG1)
542	M-29	References Yamada		LGIWGCSGKLIC  t: gp41  ein found in rat and human a	strocytes [Yamada1991]	Vaccine	murine (IgG1)
643	M-36	References Yamada		LGIWGCSGKLIC  t: gp41  ein found in rat and human a	strocytes [Yamada1991]	Vaccine	murine (IgG1)
644	M-4	References Yamada		LGIWGCSGKLIC  t: gp41 in found in rat and human as	rocytes [Yamada1991]	Vaccine	murine (IgG2b)

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizing	Immunogen	Species(Isotype)
645	M-6	References Yamada				Vaccine	murine (IgG2b)
		• M-6: Unlike M-22, o	did not react to 43-kd protei	n found in rat and human astrocytes [Ya	amada1991]		
646	polyclonal α598-609	gp160 (594–601)	gp41 (598–609)	GIWGCSGK		HIV-1 infection	human
		<ul><li>References Poumbo</li><li>alpha(598-609): Affi</li></ul>		plasma – immunodominant region, bind	ls oligomer and m	onomer [Poumbourios1992]	
647	1B8.env	gp160 (594–604) <b>References</b> Banapou	gp41 (594–605 HXB2) ur1987, Enshell-Seijffers200	GIWGCSGKLIC D1	no	HIV-1 infection	human (IgG2 $\lambda$ )
		• 1B8.env: Monoclona		by the majority of HIV-1 infected people have distinct phenotypes—41-7 and 1B			possibly enhancing,
648	polyclonal	gp160 (594–609) <b>References</b> Petrov19  • Immunodominant ar	gp41 (601–616) 990 ad broadly reactive peptide	GIWGCSGKLICTTAVP [Petrov1990]	no	HIV-1 infection	human
649	clone 3	<ul><li>clone 3: Core bindin [Cotropia1992]</li><li>clone 3: Inhibits rep</li><li>clone 3: Monoclonal</li></ul>	g domain gcsgkLIC – lack lication of three diverse HIV	GCSGKLICTT pia1996, Enshell-Seijffers2001 of serological activity to this region corn 7-1 laboratory strains, as well as an AZT nave distinct phenotypes—41-7 and 1B8	Γ-resistant isolate	[Cotropia1996]	
650	4	<ul><li>References Oldstone</li><li>There is another MA</li><li>4: Stimulated by improved</li></ul>		ith integrase [Oldstone1991, Bizub-Ben : LGLIWGCSGKLIC (aa 598-609) – po	_	Vaccine y with HIV-2 peptide CAFF	murine (IgG2b)  RQVC – slightly more
651	41-6	References Oldstone • 41-6: Stimulated by	immunization with the pept	CSGKLIC : gp41 :ide: LGLIWGCSGKLIC (aa 598-609) V-2 form NSWGCAFRQVC – disulfide			
652	41-7		gp41 (605–611) 990, Enshell-Seijffers2001 HIV-1 positive, but no HIV-	CSGKLIC  2 positive individuals, interfered with 4	no 11-7 binding – Ab	HIV-1 infection does not neutralize [Bugge	human (IgG1κ)

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizir	g Immunogen	Species(Isotype)
			ntibodies to this epitope ha Enshell-Seijffers2001].	ve distinct phenoty	pes—41-7 and 1B8.env were found to	be not neutralizing, 2F1	1 possibly enhancing, and
653	68.1	References Oldston • 68.1: Stimulated by	immunization with the per	otide: LGLIWGCS0	GKLIC (aa 598-609) – cross-reactive WGCAFRQVC [Oldstone1991]	Vaccine with HIV-2 peptide CAFI	murine (IgM)  RQVC – more reactive with
654	68.11	gp160 (598–604) Vaccine Vector/Type References Oldston • 68.11: Stimulated b	gp41 (598–609)  e: peptide HIV component e1991  y immunization with the pe	CSGKLIC  at: gp41  eptide: LGLIWGCS	GGKLIC (aa 598-609) – cross-reactive NSWGCAFRQVC [Oldstone1991]	Vaccine e with HIV-2 peptide CA	murine (IgM) FRQVC – more reactive
655	75	gp160 (598–604)  Vaccine Vector/Type References Oldston  75: Stimulated by in	gp41 (598–609) e: peptide HIV componente	CSGKLIC  at: gp41  de: LGLIWGCSGF	KLIC (aa 598-609) – poor cross-react	Vaccine ivity with HIV-2 peptide (	rat (IgG) CAFRQVC – more reactive
656	polyclonal	beneficial – isolated	ies to this epitope have dismimotope-presenting phass in 30 HIV+ sera, and all I	ges corresponding to	41-7 and 1B8.env were found to be no to the immunodominant gp41 epitope ats reacted showing distinctive variab	CSGKLIC were used to s	study the diversity of
657	105-732	References Scheffe	11999	_	oup O) HIV component: gp160 were tested for MAb reactivity – MAb	Vaccine 105-732 bound to two or	murine (IgG2b $\kappa$ ) verlapping peptides
658	3D6 (IAM 41-3D6)	References Felgenhauer 1990, F	le1992, Chen1994b, Satten DNA encoding V- regions crystal structure [He1992] ds to HIV gp41, and to a 4. 1-3D6: binding increased a	tau1995c, Stigler19 [Felgenhauer1990] 3 kd protein found i fter pretreatment of	1. Microbiol., Vienna, Austria and Vi 195, Wisnewski 1996, Kunert 1998, Ca In human T, B and monocyte cell line infected cells with sCD4 – binding of	vacini1998b, Cavacini199ss, proposed molecular mi	98a, Cavacini1999 micry [Chen1994b]

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutraliz	ing Immunogen	Species(Isotype)
		<ul> <li>individuals [Wisnew</li> <li>3D6: The complete homologies of 97-90</li> <li>3D6: Binds to the in these MAbs may de</li> </ul>	vski1996] V, J and D(H) domain was 8% relative to germline ge nmunodominant region of fine a human Ab clonotyp note that both MAbs F22	s sequenced – in contras nes [Kunert1998] gp41 – a strong homolo e [Cavacini1998a]	bias of enhanced V H1 and V H the sequences of five neutralizi gy between heavy variable dom 1 Env MAbs that have an autoir	ing MAbs, 3D6 had very lains of hu MAb 3D6 and	ittle somatic mutation, with MAb F20 was observed,
659	F172-D8 (F172-D8, scFvD8)	directed at a loop in	proach to intercellular imm	otad repeat regions – inti	-chain variable fragment, scFvD acellular scFvD8 expression dec Legastelois2000]		
660	D50	Ab type cluster II References Earl199  D50: Generated dur  D50: Thought to be S10 block binding [  D50: Richardson su  D50: Found to bind D37, D40, D44, D5  ADA, in which the O50: A combination (gp140-GNC4) – gg gp140-GNC4 timer  D50: Oligomeric gg	a discontinuous epitope re Binley1996] ggests this is a linear gp41 to a linear peptide, betwee 5, D59, T37, and T45 – the change E659D and E662A n of gp41 fusion with the C 41 MAbs T4, D12, T3, an equivalently to gp140(-), a o140 (o-gp140) derived fro	Christopher Broder, NIH n1996, Earl1997, Yang2 e of the oligomeric structerognizing residues between the properties of the epitope [Richardson19] en Env amino acids 642-e region is in the immunation may result in the loss of GNC4 trimeric sequence and D50 bound less efficient T3 and D50 recognition R5 primary isolate U	000, Srivastava2002 sture of Env in determining the r yeen 649-668 – designated cluster	nformation dependent MA tive with 9/10 HIV-1 stra rl1997] 20-gp41 cleavage site res ooled sera, but T4 and D1 han gp140(-) [Yang2000] a vaccine reagent – D50 v	T3, M12, M15, S6, S8, S9, abs D16, D17, D31, D36, ans tested, all except HIV-1 ulted in stable gp140 trimers 2 recognized the
661	5-21-3	References Hunt19 • 5-21-3: Recognizes	e: recombinant protein <i>H</i> 90, Scheffel 1999	on-dependent epitope in	a hydrophilic region [Hunt1990]	Vaccine	murine
662	120-16 (SZ-120.16)	<ul><li>120-16: Antibody d</li><li>120-16: Potent ADO</li><li>120-16: Less reactive</li></ul>	992, Robinson1990b, Tylo ependent enhancement (A CC (in contrast to MAb 98	DE) of HIV-1 IIIB infect -43, gp41(579-604)) [Ty ion – most Abs involvin	on1991, Eddleston1993, Forthal tivity, synergistically enhanced ler1990] g this region bound conformation	by MAb V10-9 [Robinson	

No. MAb ID

**HXB2** Location

[Hioe1997b]

**Author's Location** 

HIV Antibodies Tables gp160 Antibodies

Sequence

Neutralizing Immunogen

Species(Isotype)

	<ul> <li>120-16: Called SZ-120.16 [Eddleston1993]</li> <li>120-16: No neutralizing activity, both ADCC and viral enhancing activity [Forthal1995]</li> <li>120-16: 120-16 is V H4 – V-region heavy chain usage was examined and a bias of enhanced V H1 and V H4, and reduced V H3, was noted among HIV infected individuals [Wisnewski1996]</li> </ul>
663	98-6 (SZ-98.6, gp160 (644–663) gp41 (644–663 HXB2) SLIEESONOQEKNEQELLEL no HIV-1 infection human (IgG2κ) 98.6) Ab type alpha-helical C-HR, hairpin intermediate Donor Susan Zolla-Pazner (Zollasol @mcrer6.med.nyu), NYU, NY References Pinter1989, Gorny1989, Till1989, Robinson1990b, Tyler1990, Andris1992, Sattentau1991, Robinson1991, Xu1991, Eddleston1993, Spear1993, Tani1994, Laal1994, Chen1995, Forthal1995, Manca1995a, Sattentau1995c, Wisnewski1996, Hioe1997b, Nyambi1998, Gorny2000b, Gorny2000a, Nyambi2000, Taniguchi2000, Verrier2001, Golding2002b  98-6: Reacts preferentially with gp160 oligomer, compared to gp41 monomer [Pinter1989]  98-6: Kills HIV-infected T cells (H9) and monocytes (U937) when coupled to deglycosylated A chain of ricin [Till1989]  98-6: No neutralizing or enhancing activity for HIV-1 IIIB [Robinson1990b]  98-6: Serves as target for antibody-dependent cellular cytotoxicity, ADCC [Tyler1990]  98-6: No neutralizing or enhancing activity [Robinson1991]  98-6: No neutralizing or enhancing activity [Robinson1991]  98-6: Appeared to be specific for a conformational or discontinuous epitope [Xu1991]  98-6: Called SZ-98.6 – binds to a conformational domain within aa 644-663 of gp41, and reacts with astrocytes, as do 167-7 and ND-15G1 [Eddleston1993]  98-6: This MAb was expressed as a surface anti-gp41 monoclonal antibody receptor for gp41 on a CD4-negative B-cell line. Transfected cells could bind HIV Envelope, but could not be infected by HIV-1. When CD4 delivered by retroviral constructs was expressed on these cells, they acquired the ability to replicate HIV-1, and slg/gp41 specifically enhanced viral replication [Tani1994]  98-6: Cone of several anti-gp41 MAbs that bind to a gp41-maltose binding fusion protein designed to study the leucine zipper domain of gp41, showing that
	the construct has retained aspects of normal gp41 conformation [Chen1995]  • 98-6: No neutralizing activity, positive ADCC activity, and no viral enhancing activity [Forthal1995]  • 98-6: Virions complexed to gp41 Ab facilitate presentation of p66 RT epitopes to Th cells [Manca1995a]  • 98-6: Preferentially recognizes oligomeric form of gp41 – enhanced binding to HIV-1 infected cells at 37 degrees relative to 4 degrees – addition of sCD4
	<ul> <li>enhances binding [Sattentau1995c]</li> <li>98-6: 98-6 is V H4 – V-region heavy chain usage was examined and a bias of enhanced V H1 and V H4, and reduced V H3, was noted among HIV infected individuals [Wisnewski1996]</li> <li>98-6: Four primary isolates showed distinct patterns of sensitivity to neutralization by polyclonal sera or plasma and MAbs – BZ167 was the only isolate inhibited by all polyclonal sera and plasma tested, and was also neutralized by 8/17 MAbs, in particular anti-V3 loop (419-D, 447-52D, 782-D, and 838-D) anti-CD4bd (559/64-D, 654-D and 830-D and a cluster II of gp41 directed MAb (98-6) – isolates 92HT593 and 91US056 were neutralized by V3 loop</li> </ul>

anti-gp41 Abs 98-6, 1367 and 1342 were not able to bind detectably with any of the viruses from any clade [Nyambi1998]

at all by MAbs individually or by a cocktail of ten MAbs consisting of 419-D, 447-52D, 782-D, 838-D, 559/64-D, 654-D, 450-D, 670-D, 1281-D and 98-6

• 98-6: Using a whole virion-ELISA method, 18 human MAbs were tested for their ability to bind to a panel of 9 viruses from clades A, B, D, F, G, and H -

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutra	lizing Immunogen	Species(Isotype)
		<ul> <li>98-6: 98-6 and 2F5 alone but not to N51 inhibited by N51 [G</li> <li>98-6: Binding of pa MAb 50-69 bound v [Gorny2000a]</li> <li>98-6: 26 HIV-1 ground and 1281 bound acrom MAbs – no neutralized sheet which form an alpha</li> <li>98-6: A panel of 12 2 to 10 ug/ml: 2F5, no synergy, only add</li> </ul>	both bind to a peptide N51 alone – 98-6 and 2F5 hav orny2000b] nel of 21 MAbs to soluble with a 5 fold preference for ap M isolates (clades A to oss clades, but usually weaking activity was observed form of gp41 is recognized the lical bundle [Taniguch MAbs was used to identify 50-69, IgG1b12, 447-52D litive effects were seen for	d-C43 complex trimer re comparable affinitie oligomeric gp140 ver re the oligomer, while of the oligomer of the olig	of heterodimers that approximas for C43, but 98-6 has a higher sus gp41 or gp120 monomers wither gp41 MAbs (1367, 98-6, 1342 had poor cross reactivity—isolates, but 98-6 did not bind tope is a conformational epitoparalize the dual-tropic primary in the six did not have neutralizing of MAbs, and antagonism was	ates the core of the fusogenic r affinity for the complex and was compared – no MAb was 167-D, 1281, 1342, and 1379 cluster II anti-gp41 MAbs – o Clade D isolates bound most to these isolates [Nyambi200 pe formed by the interaction of isolate HIV-1 89.6—six gave g activity: 654-D, 4.8D, 450-	form of gp41, and to C43 I the binding of 98-6 is not oligomer specific, but gp41 olid not show a preference of these 2F5, 167-D, 126-6, occonsistently to cluster II olion of two regions of gp41 significant neutralization at -D, 246-D, 98-6, and 1281
		HIV entry – preincu bundles form prior t after 1 hour, doesn't incubation [Golding	bation of E/T cells at 31.5 of fusion – 98-6 binds to a inhibit – this is in contrast	C enabled polyclonal C-HR hairpin epitope t to six-helix bundle A	ture (31.5 C) to re-evaluate the anti-N-HR Ab and anti-six-hel and blocks fusion when added bs 167-D and 1281 that inhibit	ix bundle Abs to inhibit fusion to a 2 hour E/T preincubation	on, indicating six-helix n at 31.5 C, but if added
664	167-7 (SZ-167.7)	gp160 (644–663) <b>Ab type</b> cluster II <b>References</b> Xu1991 • 167-7: Specific for a	gp41 (644–663) , Eddleston1993 a conformational epitope [3	SLIEESQNQQEK Xu1991]	NEQELLEL  na 644-663 of gp41, and reacts	HIV-1 infection with astrocytes, as do 98-6 as	human (IgG2λ) nd ND-15G1
665	ND-15G1	gp160 (644–663) <b>Ab type</b> cluster II <b>References</b> Eddleste  • ND-15G1: Mapped			NEQELLEL , and reacts with astrocytes, as	HIV-1 infection do 98-6 and 167-7 [Eddlesto	human (IgG1κ) on1993]
666	167-D	<ul><li>References Spear 19</li><li>167-D: Did not med sCD4 [Spear 1993]</li><li>167-D: No neutraliz</li></ul>	93, Forthal 1995, Gorny 20 iate deposition of complening activity, no ADCC acti	Susan Zolla-Pazner (Zo 1000b, Gorny2000a, Ny ment component C3 or ivity, and no viral enha	ollas01@mcrcr6.med.nyu), NY	ent mediated virolysis of MN	human ( $IgG1\lambda$ )  N and IIIB in the presence of

HIV Antibodies Tables gp160 Antibodies

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutraliz	zing Immunogen	Species(Isotype)
		reacted similarly) it nor to N51 alone [G  167-D: Binding of pgp41 MAb 50-69 bc preference [Gorny2]  167-D: 26 HIV-1 gr and 1281 bound acr MAbs [Nyambi200]  167-D: The fusion pblock HIV entry – psix-helix bundles fo	binds to a peptide N51-Ca forny2000b] banel of 21 MAbs to solub bound with a 5 fold preferer 000a] oup M isolates (clades A to oss clades, but usually we. 0] brocess was slowed by using oreincubation of E/T cells a rm prior to fusion – 98-6 to doesn't inhibit – this is in o	43 complex trimer of half oligomeric gp140 value for the oligomer, value for the oligomer, value for half of the h	region 644-663 – like most clust eterodimers that approximates the ersus gp41 or gp120 monomers withile other gp41 MAbs (1367, 98-14) and good cross reactivity – Corature (31.5 C) to re-evaluate the clonal anti-N-HR Ab and anti-six in epitope and blocks fusion when guide Abs 167-D and 1281 that in	e core of the fusogenic for vas compared – no MAb -6, 167-D, 1281, 1342, ar luster II anti-gp41 MAbs lade D isolates bound mo potential of Abs targeting t-helix bundle Abs to inhall added to a 2 hour E/T pr	orm of gp41, but not to C43 was oligomer specific, but nd 1379) did not show a  – of these 2F5, 167-D, 126-6, est consistently to cluster II g fusion intermediates to ibit fusion, indicating reincubation at 31.5 C, but if
667		gp160 (656–671)  Ab type adjacent to Testing Systems Co References Buchac Chen1994b, Muster McKeating1996a, P Mo1997, Li1997, K Mondor1998, Conn Kunert1998, Franke Robert-Guroff2000, Yang2000, Si2001, Zeder-Lutz2001, Pa Golding2002b, Schr Kunert2002, Zhang.  2F5: DKWA define 2F5: Synergy with 6 2F5: Synergy with 6 2F5: Roadly reactive 2F5: Failed to show 2F5: MAb generate 2F5: Included in a resistant isolate had 2F5: gp41 mutation	gp41 (662–667 BH10) cluster II <b>Donor</b> Hermarp., Houson TX her1992, Muster1993, All 1994, Beretta1994, D'Sou loignard1996b, Sattentaul' essler II1997, Moore1997 or1998, Parren1998a, Yan 1998, Montefiori1999, Pot. Gorny2000b, Kunert2000 Dong2001, Kolchinsky200 rker2001, Spenlehauer200 alke2002, Ferrantelli2002, Liu das the core sequence – he combinations of CD4-base 1-2F5 – reports MAb to be ance to conformationally size neutralizing activity, EI synergy with anti-CD4 bid by electrofusion of PBL multi-lab study for antibod 1-2F5 – neutralized lab an the sequence KLDNWA [(582 A/T) that reduces neutralized lab and the sequence KLDNWA	amn Katinger, Institute away1993, Klasse199 uza1995, Trkola1995, 1996, Conley1996, Pine Mascola1997, Stama g1998, Trkola1998, Foignard1999, Beddow D, Liao2000, Lu2000c, U1, Tumanova2001, Yo D1, Verrier2001, Stiegl D02, Xu2002, Chakrab u2002 ighly conserved epitop ed molecules in inhibit e IgG1 – the gp41 mut sensitive neutralizing I LDKWA is relatively of inding site IIIB neutra from HIV-1 positive of y characterization bin d primary isolates – t [Conley1994b] eutralization of anti-Cl	SLWN L P of Applied Microbiology, Vienna Ba, Purtscher1994, Laal1994, Buc Battentau1995c, Moore1995b, Ne Bus1996, McKeating1996b, Stoib Butatos1997, Turbica1997, Ugolini1 Buts1998, Ernst1998, Takefman19 Buts1998, Muhlbacher1999, Parren19 Lu2000b, Nyambi2000, Park200 Bork2001, Zwick2001b, Zwick200 Ber2001, Hofmann-Lehmann2001, Barti2002, Joyce2002, Clerici2002 Be neutralizing MAb [Buchacher1 Bion of HIV-1 Env mediated cell for Bution 582(Ala to Thr) results in co MAbs – neutralization efficiency of Buttons of Miv-1 Environmentalized 2 primary Buttons of Envir	chacher 1994, D'Souza 1999; urath 1995, Kessler 1996, Ser 1996, Purtscher 1996, Ser 1997, Burton 1997, Earl 1998, Li 1998, Jiang 1998, Li 1998, Jiang 1998, Mascola 1999, Mascolo, Pai 2002, Sanhadji 2000 1c, Mascola 2001, Barnet Xu 2001, Root 2001, Arna, Xiang 2002b, Grundne 1992, Muster 1993 1 1991, Ission [Allaway 1993] 1992, Insion [Allaway 1993] 1993, Ission [Allaway 1993] 1994, Ission [Purtscher 1994] 1994, Ission [D'Souza 1994] 1994, Ission	94, Conley 1994b, Thali 1994, Calarota 1996, Schutten 1997, D'Souza 1997, 2997, Gorny 1997, Andrus 1998, Parren 1998b, Geffin 1998, ola 2000, Baba 2000, 0, Coeffier 2000, Xiao 2000c, t 2001, Moore 2001, nbruster 2002, Srivastava 2002, r 2002, Mascola 2002, a gp 120 that confer asse 1993a]

- 2F5: Found to neutralize MN, JRCSF, and two B subtype primary isolates, but not a D subtype primary isolate, by most labs in a multi-laboratory study involving 11 labs [D'Souza1995]
- 2F5: Cross-clade primary virus neutralizing activity LDKW defined as the core epitope [Trkola1995]
- 2F5: Called IAM 41-2F5 exposed in the presence of gp120 on the cell surface, while most of gp41 is masked binds proximal to transmembrane region [Sattentau1995c]
- 2F5: Review: binds to the only generally accepted strong neutralizing epitope outside of gp120, one of only 3 MAbs with strong broad activity against primary viruses, the others are 2G12 and IgG1b12 unique member of epitope cluster [Moore1995b] and John Moore, per comm 1996
- 2F5: MAb binding decreases the accessibility or alters the conformation of the gp41 fusion domain and of gp120 domains, including the binding site for the CD4 cell receptor [Neurath1995]
- 2F5: Broad cross-clade neutralization of primary isolates additive neutralization in combination with anti-CD4BS MAb IgG1b12 (Called BM12) [Kessler1995]
- 2F5: Only 4/20 Argentinian and 3/43 Swedish HIV+ sera reacted with LLELDKWASL sera reacting with peptides that contained ELDKWA tended to have high neutralization titers the region carboxyl terminal to EDLKWA was found to be more important for polyclonal sera AB binding, 670-675 WNWFDI 2F5 bound most strongly to the peptide QELLELDKWA [Calarota1996]
- 2F5: ELDKWAS is in a gp41 binding region for the negative regulator of complement factor H (CFH) Abs to HIV generally do not cause efficient complement-mediated lysis, but binding of 2F5 can interfere with CHF binding, facilitating HIV destruction by complement [Stoiber1996]
- 2F5: Primary isolates from clade A, B, and E are neutralized by 2F5 neutralization requires the LDKW motif neutralization resistant isolates or 2F5 selected variants all had substitutions in the D or K [Purtscher1996]
- 2F5: Neutralizes HXB2, primary isolates, and chimeric virus with gp120 from primary isolates in an HXB2 background [McKeating1996b]
- 2F5: Review: one of three MAbs (IgG1b12, 2G12, and 2F5) generally accepted as having significant potency against primary isolates [Poignard1996b]
- 2F5: Review: only four epitopes have been described which can stimulate a useful neutralizing response to a broad spectrum of primary isolates, represented by the binding sites of MAbs: 447-52-D, 2G12, Fab b12, and 2F5 [Sattentau1996]
- 2F5: 2F5 was infused into two chimpanzees which were then given an intravenous challenge with a primary HIV-1 isolate both became infected, but with delayed detection and prolonged decrease in viral load relative to controls, indicating that preexisting, neutralizing antibodies (passively administered or actively elicited) affect the course of acute-phase virus replication and can be influential after the Ab can no longer be detected in the peripheral circulation [Conley1996]
- 2F5: A panel of immunotoxins were generated by linking Env MAbs to ricin A immunotoxins mediated cell killing, but killing was not directly proportional to binding [Pincus1996]
- 2F5: Called IAM 2F5 antibody mediated enhancement or inhibition seemed to be determined by isolate rather than antibody specificity in this study, only 2F5 inhibited the entry of all the viruses studied, irrespective of their phenotype, and directly proportional to its affinity to monomeric HIV-1 gp160 [Schutten1997]
- 2F5: Of three neutralizing MAbs (257-D, IgG1b12, and 2F5), 2F5 was the only one to inhibit the entry of all viruses studied, both SI and NSI, with a potency proportional to its affinity for monomeric gp126 [Schutten1997]
- 2F5: In a multilab evaluation of monoclonal antibodies, only IgG1b12, 2G12, and 2F5 could neutralize at least half of the 9 primary test isolates at a concentration of < 25 mug per ml for 90% viral inhibition the isolates with no 2F5 neutralizing susceptibility had the sequences ALGQWA or ELDTWA instead of EDLKWA 7/9 primary isolates were neutralized, and ALDKWQ and ALDKWA were susceptible to neutralization [D'Souza1997]
- 2F5: A JRCSF variant that was selected for IgG1b12 resistance remained sensitive to MAbs 2G12 and 2F5, for combination therapy [Mo1997]
- 2F5: One of 14 human MAbs tested for ability to neutralize a chimeric SHIV-vpu+, which expressed HIV-1 IIIB Env strong neutralizer of SHIV-vpu+ all Ab combinations tested showed synergistic neutralization 2F5 has synergistic response with MAbs 694/98-D (anti-V3), 2G12, b12, and F105 [Li1997]
- 2F5: IgG1b12 was more potent with greater breadth than MAb 2F5 in an infection reduction assay including 35 primary isolates [Kessler II1997]

- 2F5: Review: MAbs 2F5, 2G12 and IgG1b12 have potential for use in combination with CD4-IgG2 as an immunotherapeutic or immunoprophylactic –
  homologous MAbs to these are rare in humans and vaccine strategies should consider including constructs that may enhance exposure of these MAbs'
  epitopes [Moore1997]
- 2F5: Binding of anti-gp120 MAbs IgG1b12 or 654-30D does not mediate significant exposure of the gp41 epitopes for MAbs 2F5 and 50-69 [Stamatatos1997]
- 2F5: Using concentrations of Abs achievable in vivo, the triple combination of 2F5, 2G12 and HIVIG was found to be synergistic to have the greatest breadth and magnitude of response against 15 clade B primary isolates [Mascola1997]
- 2F5: Used to standardize polyclonal response to CD4 BS [Turbica1997]
- 2F5: The only MAb out of a large panel to show no correlation between Viral binding inhibition and neutralization [Ugolini1997]
- 2F5: This review summarizes results about 2F5: it binds extracellularly, near the transmembrane domain, it is the only gp41 MAb that is neutralizing, it reacts with many non-B clade viruses and has a paradoxically weak binding to virus, given the neutralizing titers [Burton1997]
- 2F5: Post-exposure prophylaxis was effective when MAb 694/98-D was delivered 15 min post-exposure to HIV-1 LAI in hu-PBL-SCID mice, but declined to 50% if delivered 60 min post-exposure, and similar time constraints have been observed for HIVIG, 2F5 and 2G12, in contrast to MAb BAT123 that could protect delivered 4 hours post infection [Andrus1998]
- 2F5: This MAb and the results of [Ugolini1997] are discussed the authors propose that an Ab bound to gp41 would typically project less from the surface of the virion and so be unable to interfere with attachment [Parren1998a]
- 2F5: Ab from gp120 vaccinated individuals prior to infection, who subsequently became HIV infected, could not achieve 90% neutralization of the primary virus by which the individuals were ultimately infected these viruses were not particularly refractive to neutralization, as determined by their susceptibility to neutralization by MAbs 2G12, IgG1b12, 2F5 and 447-52D [Connor1998]
- 2F5: A neutralization assay was developed based on hemi-nested PCR amplification of the LTR (HNPCR) LTR-HNPCR consistently revealed HIV DNA and was shown to be a rapid, specific and reliable neutralization assay based on tests with 6 MAbs and 5 isolates [Yang1998]
- 2F5: A wide range of neutralizing titers was observed that was independent of co-receptor usage 2F5 was the most potent of the MAbs tested [Trkola1998]
- 2F5: Points out that 2G12 and 2F5, potent neutralizing antibodies, were identified by screening for cell surface (oligomeric Envelope) reactivity [Fouts1998]
- 2F5: The ELDKWA epitope was inserted into the antigenic site B of influenza hemagglutinin and expressed on baculovirus infected insect cells, flanked by 3 additional random amino acids, xELDKWAxx FACS was used to isolate the clone that displayed the epitope with the most markedly increased binding capacity for 2F5, to identify particularly specific immunogenic constructs PELDKWAPP was a high affinity form selected by FACS [Ernst1998]
- 2F5: Induces complement-mediated lysis in MN but not primary isolates primary isolates are refractive to CML [Takefman1998]
- 2F5: Neutralization synergy was observed when the MAbs 694/98-D (V3), 2F5 (gp41), and 2G12 (gp120 discontinuous) were used in combination, and even greater neutralizing potential was seen with the addition of a fourth MAb, F105 (CD4 BS) [Li1998]
- 2F5: Used as a control in the study of anti-gp41 MAb NC-1 2F5 does not react with HIV-2 gp41 or gp160 [Jiang1998]
- 2F5: MAbs 2G12, 2F5 and b12 are broadly neutralizing, as are some human polyconal sera, but this paper describes a set of primary isolates that are resistant to all three MAbs and 2 broadly neutralizing sera results indicate that resistance levels of pediatric isolates might be higher than adult isolates resistance in general did not seem to be conferred by a loss of binding affinity for gp120 or gp41, rather by a more global perturbation of oligomeric Envelope [Parren1998b]
- 2F5: The natural immune response to the epitope of 2F5, ELDKWA, was studied in perinatally infected children and levels of reactivity to this epitope were correlated with absolute CD4 numbers over time and health status 3/10 children who had no antibody reactivity to ELDKWA had substitutions in the epitope (ALDKWA, ELDQWA, and KLDKWA) 2F5 competed with the ELDKWA-reactive sera depending on the serum titer [Geffin1998]

- 2F5: The complete V, J and D(H) domain was sequenced unlike non-neutralizing anti-gp41 MAb 3D6, five neutralizing MAbs (2F5, 2G12, 1B1, 1F7, and 3D5) showed extensive somatic mutations giving evidence of persistent antigenic pressure over long periods in contrast to Geffin98, where multiple pediatric sera were found to compete with 2F5, cross-competition was noted to be very rare in sera from HIV+ adults Kunert et al. propose that because there is a binding site of human complement factor H which overlaps the 2F5 binding site, it may generally be masked from the immune system 2F5 also has a remarkably long CDR3 loop of 22 amino acids, and this region could not be readily assigned to any described D(H) fragment, leading to the suggestion of recombination of two fragments from novel regions [Kunert1998]
- 2F5: Infection of dendritic cells cultured from CD14+ blood cells or from cadaveric human skin was blocked by neutralizing MAbs IgG1b12, or 2F5 and 2G12 delivered together, but not by control non-neutralizing anti-gp120 MAb 4.8D, indicating that NAbs could interrupt early mucosal transmission events [Frankel1998]
- 2F5: rgp120 derived from a R5X4 subtype B virus was used to vaccinate healthy volunteers and the resulting sera were compared with sera from HIV-1 positive subjects and neutralizing MAbs [Beddows1999]
- 2F5: A meeting summary presented results regarding neutralization –MAbs 2G12 and 2F5 tested for their ability to neutralize primary isolate infection of genetically engineered cell lines (cMAGI and others, presented by T. Matthews, A. Trkola, J. Bradac) an advantage of such cells lines over PBMCs is that markers (X-Gal) can be added for staining to simplify the assay the consensus of the meeting was that these engineered cell lines did not improve the sensitivity of detection of primary isolate neutralization D. Burton and J. Mascola presented results concerning passive immunization and protection of hu-PBL-SCID mice and macaques, respectively, and both found combinations of MAbs that were able to achieve 99% neutralization in vitro corresponded to efficacy in vivo [Montefiori1999]
- 2F5: Hu-PBL-SCID mice were infected with HIV-1s JRCSF and SF162 to study the effect of NAbs on an established infection no significant differences in the initial rate of decrease in viral load or the plateau levels of viral RNA between the b12 treated and control mice were seen in most of the Ab treated mice b12 escape mutants were observed with varying patterns of mutations a combination of b12, 2G12 and 2F5 protected 1/3 mice, and an isolate from one of the other two was resistant to neutralization by all three MAbs [Poignard1999]
- 2F5: In a study of 116 HIV-1+ individuals, Ab reactivity to a peptide encompassing the ELDKWA peptide decreased in CDC stage C patients compared with stage A patients, and longitudinal studies showed a decline in 6/8 patients, while overall Ab reactivity to rec soluble gp160 stayed constant [Muhlbacher1999]
- 2F5: Review of the neutralizing Ab response to HIV-1 [Parren1999]
- 2F5: Combinations of HIVIG, 2F5, 2G12 were administered in passive-transfer experiments 24 hours prior to challenge with pathogenic SHIV 89.6PD 3/6 animals given HIVIG/2F5/2G12 were completely protected, the others had reduced viremia and normal CD4 counts 1/3 monkeys given 2F5/2G12 showed transient infection, the other two had reduced viral load all monkeys that received HIVIG, 2F5, or 2G12 alone became infected and developed high-level plasma viremia, although animals that got HIVIG or 2G12 had a less profound CD4 T cell decline [Mascola1999]
- 2F5: Because HIV-1 is most often transmitted across mucosal surfaces, the ability of passive transfer of infused HIVIG/2F5/2G12 to protect against mucosal exposure of macaques to pathogenic SHIV 89.6PD was studied HIVIG/2F5/2G12 protected 4/5 animals against vaginal challenge, 2F5/2G12 combined protected 2/5 animals, and 2G12 alone protected 2/4 animals in contrast, Mascola and co-workers had previously shown single MAbs could not protect against intervenous challenge Ab treated animals that got infected through vaginal innoculation had low viral loads and only modest declines in CD4 counts the infused Abs were detected in the nasal, vaginal, and oral mucosa [Mascola2000]
- 2F5: Paper uses IgG1 form of 2F5 a triple combination of 2F5, F105 and 2G12 effectively neutralized perinatal infection of macaque infants when challenged with SHIV-vpu+ the plasma half-life was 4.2 +/- 0.8 days [Baba2000]
- 2F5: A mini-review of observations of passive administration of IgG NAbs conferring protection against intervenous or vaginal SHIV challenge, that considers why IgG MAbs might protect against mucosal challenge [Robert-Guroff2000]
- 2F5: MAbs 98-6 and 2F5 both bind to a peptide N51-C43 complex trimer of heterodimers that approximates the core of the fusogenic form of gp41, and to C43 alone but not to N51 alone 98-6 and 2F5 have comparable affinities for C43, but 98-6 has a higher affinity for the complex and 2F5 may bind to an epitope of C43 that is directly involved with complex formation –and IgG1 rec form of the Ab was used in this study [Gorny2000b]

No. MAb ID

HIV Antibodies Tables gp160 Antibodies

• 2F5: 2F5 is a candidate for immunotherapy, but generally IgG1 has a longer half life in humans than IgG3, so the isotype was switched – rec CHO-derived MAb 2F5 IgG1kappa and hybridoma-derived MAb 2F5 IgG3kappa displayed identical specificity, in vitro function, and epitope (ELDKWA) – it remains to

Sequence

• 2F5: Low levels of anti-ELDKWA antibodies are observed in HIV-1+ individuals, so a C-domain P2 peptide linked to a carrier was used to immunize mice and rabbits, and stimulated a high-level anti-ELDKWA response [Liao2000]

**Neutralizing Immunogen** 

Species(Isotype)

- 2F5: A rare mutation in the neutralization sensitive R2-strain in the proximal limb of the V3 region caused Env to become sensitive to neutralization by MAbs directed against the CD4 binding site (CD4BS), CD4-induced (CD4i) epitopes, soluble CD4 (sCD4), and HNS2, a broadly neutralizing sera 2/12 anti-V3 MAbs tested (19b and 694/98-D) neutralized R2, as did 2/3 anti-CD4BS MAbs (15e and IgG1b12), 2/2 CD4i MAbs (17b and 4.8D), and 2G12 and 2F5 thus multiple epitopes on R2 are functional targets for neutralization and the neutralization sensitivity profile of R2 is intermediate between the highly sensitive MN-TCLA strain and the typically resistant MN-primary strain [Zhang2002]
- 2F5: ELDKWA peptide vaccine study [Lu2000c]

**Author's Location** 

be determined if isotype switching will prolongs beta-clearance [Kunert2000]

**HXB2** Location

- 2F5: ELDKWA peptide vaccine study [Lu2000b]
- 2F5: 26 HIV-1 group M isolates (clades A to H) were tested for binding to 47 MAbs, including 6 cluster II anti-gp41 MAbs of these 2F5, 167-D, 126-6, and 1281 bound across clades, but usually weakly, while 98-6 and 1342 had poor cross reactivity Clade D isolates bound most consistently to cluster II MAbs [Nyambi2000]
- 2F5: Six mutations in MN change the virus from a high-infectivity neutralization resistant phenotype to low-infectivity neutralization sensitive V3, CD4BS, and CD4i gp120 specific MAbs are 20-100 fold more efficient at neutralizing the sensitive form gp41 MAbs bind less, and 2F5 behaves the opposite of gp120 MAbs in that it neutralizes the "sensitive" form less efficiently [Park2000]
- 2F5: ELDKWAS co-crystallized bound to the Fab' 2F5 fragment showed the epitope peptide in a type I beta-turn conformation [Pai2002]
- 2F5: 2F5 or sCD4-IgG chimeric immunoadhesin were transferred into 3T3 cells, incorporated into a collagen structure called the neo-organ, and transplanted into SCIDhu mice that were then challenged with MN or LAI the continuous production of the therapeutic molecules in this context resulted in dramatic reduction of viral load [Sanhadji2000]
- 2F5: A combination of gp41 fusion with the GNC4 trimeric sequences and disruption of the YU2 gp120-gp41 cleavage site resulted in stable gp140 trimers (gp140-GNC4) gp41 MAbs T4, D12, T3, and D50 bound less efficiently to gp140-GNC4 than did pooled sera, but T4 and D12 recognized the gp140-GNC4 timer equivalently to gp140(-), and T3 and D50 recognized the trimer at greater levels than gp140(-) 2F5 did not bind efficiently to these constructs, presumably because of the YU2 strain has a substitution in the 2F5 epitope (ALDKWA instead of ELDKWA) [Yang2000]
- 2F5: SHIV-HXBc2 is a neutralization sensitive non-pathogenic virus, and several in vivo passages through monkey's yielded highly pathogenic SHIV KU-1 HXBc2 and the KU-1 clone HXBc2P3.2 differ in 12 amino acids in gp160 substitutions in both gp120 and gp41 reduced the ability of sCD4, IgG1b12, F105 and AG1121 to Env achieve saturation and full occupancy, and neutralize KU-1 17b and 2F5 also bound less efficiently to HXBc2P3.2, although 2G12 was able to bind both comparably [Si2001]
- 2F5: ELNKWA is an escape variant not recognized by the broadly neutralizing MAb 2F5, which recognizes the core epitope ELDKWA Abs were raised
  against the peptide escape variant CGELNKWAGELNKWA linked to KLH carrier these polyclonal antibodies, like the monoclonal antibody TH-Ab1
  also raised to ELNKWA, could recognize ELDKWA and escape mutant peptide epitopes ELEKWA and ELDEWA [Dong2001]
- 2F5: Mutations in two glcosylation sites in the V2 region of HIV-1 ADA at positions 190 and 197 (187 DNTSYRLINCNTS 199) cause the virus to become CD4-independent and able to enter cells through CCR5 alone these same mutations tended to increase the neutralization sensitivity of the virus, including to antibody 2F5 [Kolchinsky2001]
- 2F5: A peptide called 5-Helix was designed that binds to the C-peptide region of gp41 5-Helix is a potent inhibitor of HIV-1 entry that binds immediately COOH-terminal to the C-peptide region targeted by 5-Helix the conformation of the bound 2F5 epitope is a hairpin turn [Root2001]
- 2F5: A phage peptide library was screened with MAb 2F5, and from the peptides that bound the amino acids DKW were found to be most critical for binding the mimetic peptide RDWSFDRWSLSEFWL elicited a cross-reactive Ab response to gp41 when used to immunize rabbits [Tumanova2001]

 No.
 MAb ID
 HXB2 Location
 Author's Location
 Sequence
 Neutralizing
 Immunogen
 Species(Isotype)

 • 2F5: Abs against the V3 loop (50.1, 58.2, 59.1, 257-D, 268-D, 447-52D), CD4BS (IgG1b12, 559-64D, F105), CD4i (17b), and to gp41 (2F5, F240) each

- 2F5: Abs against the V3 loop (50.1, 58.2, 59.1, 257-D, 268-D, 447-52D), CD4BS (IgG1b12, 559-64D, F105), CD4i (17b), and to gp41 (2F5, F240) each showed similar binding efficiency to Env derived from related pairs of primary and TCLA lines (primary: 168P and 320SI, and TCLA: 168C and 320SI-C3.3), but the TCLA lines were much more susceptible to neutralization suggesting that the change in TCLA lines that make them more susceptible to NAbs alters some step after binding [York2001]
- 2F5: This paper primarily concerns 4E10 and Z13, MAbs that both bind proximally to the 2F5 binding site to a conserved epitope, and that neutralize some primary isolates from clades B, C, and E the minimal 2F5 epitope is determined to be EQELLELDKWASLW, based on screening a gp160 fragment expression library, longer than previous studies broadly neutralizing MAbs 2F5, IgG1b12, and 4E10 and Z13 fail to neutralize different subsets of viruses [Zwick2001b]
- 2F5: Neutralization synergy between anti-HIV NAbs b12, 2G12, 2F5, and 4E10 was studied a classic fixed-ratio method was used, as well as a method where one Ab was fixed at a low neutralization titer and the other was varied using primary isolates, a two-four fold enhancement of neutralization was observed with MAb pairs, and a ten-fold enhancement with a quadruple Ab combination no synergy was observed with any MAb pair in the neutralization of TCLA strain HXB2 [Zwick2001c]
- 2F5: Review of studies in macaques that have shown immune control of pathogenic SHIV viremia, improved clinical outcome, and protection, and the implications of the observations for HIV vaccines [Mascola2001]
- 2F5: SF162DeltaV2 is a virus that has a 30 amino acids deletion in the V2 loop that does not abrogate its infectivity but renders it highly susceptible to neutralization when incorporated into a codon-optimized DNA vaccine with a CMV promoter and delivered by gene gun, SF162DeltaV2 gave higher neutralizing Ab titers against SF162 than did SF162 itself, and Abs that cross-neutralized non-homologous primary isolates were obtained only when SF162DeltaV2, but not intact SF162, was used as the immunogen Control MAbs 2F5 and 2G12 could neutralize all of the following primary isolates: 91US056(R5), 92US714(R5), 92US660(R5), 92HT593(R5X4), and BZ167(R5X4), while after the first protein boost, the sera from two SF162DeltaV2 immunized macaques could neutralize 91US056(R5), 92US714(R5), 92US660(R5) and ADA(R5), but not 92HT593(R5X4) or 92US657(R5) the pattern of cross-recognition shifted after the second boost [Barnett2001]
- 2F5: Moore and colleagues review the data concerning the lack of a clear relationship between genetic subtype and serotype 2F5 is considered in some detail, as it represents a rare vulnerability from the neutralizing antibody perspective, although while it is apparently linear, attempts to present the peptide to the immune system have failed to elicit neutralizing Abs [Moore2001]
- 2F5: Neutralizing synergy between MAbs 1b12, 2G12 and 2F5 was studied using surface plasmon resonance to determine the binding kinetics for these three mAbs with respect to monomeric and oligomeric env protein gp160 IIIB the 2G12 epitope is highly accessible on both monomeric and oligomeric Envs, 1b12 is highly accessible on monomers but not oligomers, and 2F5 on neither form binding of 2G12 exposes the 2F5 epitope on gp160 oligomers [Zeder-Lutz2001]
- 2F5: Matrix-assisted laser desorption ionization mass spectrometry (MALDI-MS) in combination with proteolytic protection was used to identify the
  functional epitope for MAb 2F5, NEQELLELDKWASLWN, in the disulfide bond associated gp120/gp41 protein SOS-gp140 (JRFL) this minimal
  epitope is much larger than the ELDKWA core epitope previously defined by peptide ELISA, and this could help explain why ELDKWA-peptides are poor
  immunogens in terms of eliciting a 2F5-like antibody response [Parker2001]
- 2F5: A luciferase-reporter gene-expressing T-cell line was developed to facilitate neutralization and drug-sensitivity assays luciferase and p24 antigen neutralization titer end points were found comparable using NAb from sera from HIV+ donors, and MAbs 2F5, 2G12 and IgG1b12 [Spenlehauer2001]
- 2F5: A panel of 12 MAbs was used to identify those that could neutralize the dual-tropic primary isolate HIV-1 89.6 six gave significant neutralization at 2 to 10 ug/ml: 2F5, 50-69, IgG1b12, 447-52D, 2G12, and 670-D six did not have neutralizing activity: 654-D, 4.8D, 450-D, 246-D, 98-6, and 1281 no synergy, only additive effects were seen for pairwise combinations of MAbs, and antagonism was noted between gp41 MAbs 50-69 and 98-6, as well as 98-6 and 2F5 [Verrier2001]
- 2F5: 4E10 binds proximal to 2F5 and neutralizes primary isolates of clades A, B, C, D, and E viruses that were resistant to 2F5 were neutralized by 4E10 and vice versa [Stiegler2001]

- 2F5: A combination of MAbs IgG1b12, 2F5, and 2G12 was given postnatally to four neonates macaques that were then challenged with highly pathogenic SHIV89.6P one of the four infants remained uninfected after oral challenge, two infants had no or a delayed CD4(+) T-cell decline [Hofmann-Lehmann2001]
- 2F5: Twenty HIV clade C isolates from five different countries were susceptible to neutralization by anti-clade B MAbs in a synergistic quadruple combination of mAbs IgG1b12, 2G12, 2F5, and 4E10 [Xu2001]
- 2F5: Oligomeric gp140 (o-gp140) derived from R5 primary isolate US4 was characterized for use as a vaccine reagent antigen capture ELISA was used to compare the antigenicity of gp120 and o-gp140 using a panel of well characterized MAbs 2F5 recognized o-gp140 [Srivastava2002]
- 2F5: The fusion process was slowed by using a suboptimal temperature (31.5 C) to re-evaluate the potential of Abs targeting fusion intermediates to block HIV entry preincubation of E/T cells at 31.5 C enabled polyclonal anti-N-HR Ab and anti-six-helix bundle Abs to inhibit fusion, indicating six-helix bundles form prior to fusion the preincubation 31.5 C step did not alter the inhibitory activity of neutralizing Abs anti-gp41 2F5, or anti-gp120 2G12, IG1b12, 48d, and 17b [Golding2002b]
- 2F5: Ab binding characteristics of SOS gp140 were tested using SPR and RIPA SOS gp140 is gp120-gp41 bound by a disulfide bond NAbs 2G12, 2F5, IgG1b12, CD4 inducible 17b, and 19b bound to SOS gp140 better than uncleaved gp140 (gp140unc) and gp120 non-neutralizing MAbs 2.2B (binds to gp41 in gp140unc) and 23A (binds gp120) did not bind SOS gp140 SOS gp140-2F5-IgG1b12 formed multiple ring structures composed of two SOS gp140 proteins bridged by two Ab molecules, while 2F5 and 2G12 formed extended chains rather than closed rings [Schulke2002]
- 2F5: Expanding the minimal epitope ELDKWA to an end-capped, linear nonapeptide, Ac-LELDKWASL-amide attained maximal affinity within a set of native gp41-sequence peptides scanning single residue substitutions confirmed that essential recognition requirements were the central DKW core sequence and the importance of the terminal Leu residues for high-affinity binding high specificity binding pockets at central Lys and Trp side-chains and an absolute requirement for the carboxylate group of the Asp side chain were found the nine residue fragment flanked by pairs of Ser and constrained by a disulfide bridge had high affinity for 2F5 [Tian2002]
- 2F5: ELDKWAS was embedded into a beta-turn-like conformational site on a framework of an antibody specific for human leukocyte antigen HLA-DR this construct was recognized by 2F5, and is suggested as an adjuvant-independent vaccine candidate [Ho2002]
- 2F5: Passive immunization of neonate macaques with a combination of F105+2G12+2F5 conferred complete protection against oral challenge with SHIV-vpu+ or the combination b12+2G12+2F5 conferred partial protection against SHIV89.6 such combinations may be useful for prophylaxis at birth and against milk born transmission the synergistic combination of IgG1b12, 2G12, 2F5, and 4E10 neutralized a collection of HIV clade C primary isolates [Xu2002]
- 2F5: A modified gp140 (gp140deltaCFI), with C-term mutations intended to mimic a fusion intermediate and stabilize trimer formation, retained antigenic conformational determinants as defined by binding to CD4 and to MAbs 2F5, 2G12, F105, and b12, and enhanced humoral immunity without diminishing the CTL response in mice injected with a DNA vaccine [Chakrabarti2002]
- 2F5: DP178 is a peptide derived from the C-term heptad repeat of gp41 that is a potent inhibitor of viral-mediated fusion—it contains the 2F5 epitope but fails to stimulate 2F5-like NAbs upon immunization—the peptide was extended to force an increase in helicity, and the modified peptide had a increase in affinity for 2F5, but upon guinea pig immunization although high peptide-specific Ab titers were achieved the sera were incapable of viral neutralization—the authors propose that 2F5 may bind with low affinity to a maturation intermediate, which may account for its breadth and why it is hard to recreate the epitope, but also suggests that the high concentrations required for neutralization are not relevant *in vivo* [Joyce2002].
- 2F5: Six sera from HIV-exposed uninfected individuals(EU) had IgA neutralizing activity dominated by recognition of a distinctive epitope within gp41, QARILAV sera of QAFILAV-immunized BALB/c mice was neutralizing with the dose-dependent behavior similar to 2F5 [Clerici2002a]
- 2F5: A combination of MAbs 2F5 and 2G12 given in multiple infusions was found to be safe and well tolerated even in high doses in a phase I study of seven HIV-1 infected healthy volunteers—the median elimination half-life was 7.94 days for 2F5, and 16.48 for 2G12—no anti-2F5 or anti-2G12 IgM or IgG responses were detected—although there was some transient increases, overall plasma viral RNA levels decreased in 6/7 volunteers, by a median of 0.62 log\_10 [Armbruster2002].

No.	MAb ID	HXB2 Location	<b>Author's Location</b>	Sequence	Neutralizing	g Immunogen	Species(Isotype)
		gp120 closer to the 15e, IgG1b12, 21h a neutralize either W7 different conformati • 2F5: HIV-1 gp160Δ and X4 strain HXBo reconstituted membres F105, A32 (C1-C4), [Grundner2002]. • 2F5: Rhesus macaquinfected) than from vaginal challenge af 2F5: A 2F5 anti-idic competition assay – 2F5-epitope specific 2F5: Review of NAI well tolerated in hur [Ferrantelli2002] • 2F5: Review of NAI [Liu2002] • 2F5: UK Medical R	CD4-bound state, and is read F91 was markedly red on and did not bind CD4, CT (cytoplasmic tail-delegate), were made in a physio rane ten-fold better than the C11 (C1-C5), and 39F (1) was were better protected intravenous challenge (Mater Ab infusion had low of type murine MAb Ab2/3 Ab2/3H6 diminished the responses in immunized by that notes that 2F5 along mans, and that illustrates gother than the control of the control o	eadily bound by sCD2 luced – IgG1b12 faile to polymorphism in t CCR5, or CD4i antib ted) proteoliposomes logic membrane settir he same protein on be V3) MAbs bound gp10 from vaginal challeng Ab 2G12, 0/3; MAbs r undetectable viral R H6 was developed that neutralizing potency of B6D2F1 mice [Kuner he or in combination v gp41's conformational	gp120 that favored different conformer and CD4i MAbs (17b, 48d, 49e, 21c) and CD4i MAbs (17b, 48d, 49e, 21c) at to neutralize this mutant, while neurone YU2 epitope – another mutant, 42 odies, but did bind to CD4BS MAbs (PLs) containing native, trimeric enverge as candidate immunogens for HIV ads (except for the YU2 form that does 60\(\Delta\text{CT PLs}\) indistinguishably from grewith SHIV89.6D (MAb 2G12, 2/4; 2F5/2G12, 1/3; and HIVIG/2F5/2G12, NA levels and modest CD4 T-cell dect to blocks 2F5 binding to a synthetic epof 2F5 – Ab2/3H6 Fab fragments were table 2D did to the MAbs can protect some marchange and exposure of the 2F5 epit passive transfer of NAbs and protections.	e and 23e) but bind tralization by 2G12 3 I/P, disrupted the [Xiang2002b] elope glycoproteins vaccines—2F5 boresn't bind 2F5)—a b160\(\Delta\)CT expressed MAbs 2F5/2G12, 2, 3/6 infected)—th cline [Mascola2002 bitope peptide and re capable of induction caques against SH ope in the transient	ing of anti-CD4BS MAbs (F105, 2 was enhanced – 2F5 did not gp120 bridging sheet, favored a strom R5 strains YU2 and JRFL, and to gp160ΔCT with a nti-CD4BS MAbs IgG1b12 and d on the cell surface  2/5; and HIVIG/2F5/2G12, 4/5 e animals that were infected by 2] to gp160 in an ELISA ing neutralizing Abs and IV infection, that it is safe and a pre-hairpin form
668	polyclonal	gp160 (662–667)  Vaccine HIV compos  References Joyce20  2F5: DP178 is a perstimulate 2F5-like N for 2F5, but upon guauthors propose that	002  otide derived from the C-t  JAbs upon immunization  linea pig immunization al  2F5 may be a low affinit	ELDKWA  erm heptad repeat of g  the peptide was extered though high peptide-s y maturation intermed	no  1941 that is a potent inhibitor of viral- nded to force an increase in helicity, pecific Ab titers were achieved the se iate, which may account for its bread ation are not relevant in vivo [Joyce20]	and the modified p ora were incapable th and why it is ha	eptide had a increase in affinity of viral neutralization – the
669	5B2	<ul> <li>Ab type C-domain</li> <li>References Tian200</li> <li>5B2: There is an RT</li> <li>5B2: Peptides GPG</li> </ul>	01 Specific Ab [Szilvay1992 RAFY and ELDKWA we	2] and a gp41 specific re conjugated to keyho	onjugate Strain: IIIB HIV compose  Ab [Tian2001] both called 5B2  ble limpet hemocyanin and used to rade and to rgp41 [Tian2001]		murine (IgG)  MAb hybridomas were
670	9G11	gp160 (662–667) Vaccine Vector/Type	Env (669–674 IIIB)	ELDKWA hemocyanin (KLH) c	onjugate Strain: IIIB HIV compor	Vaccine nent: gp41	murine (IgG)

No.	MAb ID	HXB2 Location	<b>Author's Location</b>	Sequence	Neutralizing	Immunogen	Species(Isotype)
			RAFY and ELDKWA wer	re conjugated to KLH and uso	ed to raise mouse monoclonal	l Ab—MAb hybridomas v	were generated with
671	TH-Ab1	adjuvant Ab type C-domain References Xiao200 TH-Ab1: ELNKWA raised against the pel	0a, Dong2001 is an escape variant not re otide escape variant CGEL	cognized by the broadly neut NKWAGELNKWA linked to	L P Strain: B clade TH936705  ralizing MAb 2F5, which rec KLH carrier—these polycloi ELEKWA and ELDEWA [Do	ognizes the core epitope l nal antibodies, like the M.	ELDKWA—Abs were
672	polyclonal	Ab type C-domain References Liao200 Low levels of anti-El rabbits, and stimulate	LDKWA antibodies are ob	served in HIV-1+ individuals WA response in mice and rab	L P , so a C-domain P2 peptide li bits – vaccine was C-TSLIHS		
673	polyclonal	<b>Ab type</b> C-domain <b>References</b> Xiao200		•	a Env peptide bound to BSA,	Vaccine C(ELDKWAG)_4-BSA,	murine, rabbit but not full gp160
674	polyclonal	<b>Ab type</b> C-domain <b>References</b> Muster 1	994, Muster1995	ELDKWA  ) HIV component: gp41 per  nucosa of immunized mice [1]		Vaccine	murine (IgG, IgA)
675	polyclonal	Ab type C-domain References Lu2000c • High titer response to CG-GPGRAFY-G-E CG-(ELDKWA-GPC	e, Lu2000b o ELDKWA and RILAVEI LDKWA-G-RILAVERYL	KD conjugated to BSA, with d., yielding a strong Ab response	vant: BSA vaccination with multiple-epit a weak response to GPGRAF onse to both ELDKWA and G	FY – immunization with	rabbit (Ig) ation yielded strong Ab

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizing	Immunogen	Species(Isotype)
676	4E10	References Buchac  4E10: MAbs general proteins – anti-class Zwick et al. study in 4E10: Included in a 4E10: 4E10 binds publication 4E10: 4E10 binds publication 4E10: MAbs 4E10: Weakly to infected depitope to NWFDIT 4E10 [Zwick2001b]  4E10: Neutralization where one Ab was an observed with MAb of TCLA strain HX  4E10: Twenty HIV combination of mA  4E10: Passive immoderation of the control of the	her1992, Buchacher1994, I ated by hybridoma, electrofic II Abs are only found in H in 2001 revised the epitope I multi-lab study for antibodoroximal to 2F5 and neutralia [Stiegler2001] and Z13 both bind proximal tells in a manner that is not a contrary to an earlier report in synergy between anti-HIV fixed at a low neutralization in pairs, and a ten-fold enhanced at Europe 1 [Stiegler2001c] clade C isolates from five dots IgG1b12, 2G12, 2F5, and a ten-fold enhanced in the synergy between the synergy combination b12+2G12+2F5 and transmission—the synergy for the synergy	O'Souza1994, Stiegler20 usion of PBL from HIV- IV-1 positive people – the ocation [Buchacher1994 y characterization, bind zes primary isolates of of ly to 2F5 to a conserved disrupted by sCD4 and rt – different strains were IV-NAbs b12, 2G12, 2F5 titer and the other was a cement with a quadruple different countries were sell 4E10 [Xu2001] uses with a combination of conferred partial protect gistic combination of Ign	Pural Science, Vienna, Austria 01, Zwick2001b, Zwick2001c, Xi 1+ volunteers with CB-F7 heteroris paper maps 4E10's binding site.] Ing and neutralization assay compelades A, B, C, D, and E – viruses linear epitope that has some confineutralize some primary isolates for erefractive to neutralization by broad 4E10 was studied – a classic raied – using primary isolates, a total Ab combination – no synergy was susceptible to neutralization by and of F105+2G12+2F5 conferred contion against SHIV89.6—such confib12, 2G12, 2F5, and 4E10 neutralization of the 4E10/Z13 epitope	myeloma cells – also bile to AEGTDRV, gp160 arison [D'Souza1994] that were resistant to 2 formational aspects – birom clades B, C, and Eroadly neutralizing Abirocella fixed-ratio method wa wo-four fold enhancem as observed with any Miti-clade B MAbs in a symplete protection again inbinations may be usel ralized a collection of	inds to MHC class II (823-829), but the later (823-829), but the later (875) were neutralized by oth bind to MN virions, bind (875) and (875) and (875) and (875) and (875) and (875) are sused, as well as a method nent of neutralization was (875) and in the neutralization was (975) are in the neutralization of the pair in the neutralization of t
677	Z13	<ul> <li>Z13: MAb 4E10 an virions, bind weakly selected using a pha broad NAb response here is by analogy t</li> <li>Z13: Review of NA</li> </ul>	y to infected cells in a mann tige display library with the leteroide – different strains were refused to MAb 4E10 [Zwick2001b] bs that notes Z13 is a phage	er that is not disrupted by MN gp41 peptide LLEL ractive to neutralization by display generated FAb	P ely conserved linear epitope that h by sCD4 and can neutralize some p DKWASLWNWFDITNWSW fro by broadly neutralizing Abs IgG1 fragment from a B clade infected nsient pre-hairpin form [Ferrantel	primary isolates from c m an HIV infected don lb12, 2F5, Z13 and 4E individual and that illu	clades B, C, and E – Z13 was nor who had an exceptionally 10 – epitope location noted
678	B30	gp160 (720–734)  Vaccine Vector/Typ  Donor George Lew  References Abacio	gp41 (720–734 BH10) e: recombinant protein Statis	HLPIPRGPDRPEGI rain: LAI HIV compo	E gp160	Vaccine	murine (IgG1)

HIV Antibodies Tables gp160 Antibodies

HXB2 Location	<b>Author's Location</b>	Sequence	Neutraliz	zing Immunogen	Species(Isotype)
References Durrani	1998	Strain: IIIB HIV compo	onent: gp41 peptide	Vaccine	murine (IgA, IgG2a)
gp160 (725–745)  Vaccine Vector/Type References Hifumi2  41S-2: BALBc mice proteolytic activity t	gp160 (732–750) e: peptide keyhole limper 2000 e were immunized with g toward the peptide epitop	RGPDRPEGIEEEGGI t hemocyanin (KLH) conju gp41 peptide and a MAb spoe which may be due to a ca	ERDRDRS yes gate HIV component: gp41 ecific for the peptide was gene	Vaccine erated – isolated MAb light	murine (IgG2b $\kappa$ ) chains displayed
References Gorny 19 Gorny 1994, Moore 1 Jagodzinski 1996, Tr Gorny 1997, Inouye 1 Hioe 1999, Beddows Sharon 2002, Gorny 2 447-52D: Requires 0 447-52D: Reacts wi 447-52D: Neutralize 447-52D: Peptide pl [Keller 1993] 447-52D: Additive r 447-52D: Compleme 447-52D: Requires 0	992, Buchbinder1992, K 1994a, Sattentau1995a, F rkola1996a, Sattentau199 1998, Mondor1998, Smit s1999, Gorny2000a, Grov 2002, He2002, Ferrantell GPXR at the tip of the V acrease in neutralization p th MN, NY5, CDC4, SF, es MN and IIIB: GPGR, chage library showed that neutralization of MN and tent mediated virolysis of GPxR at the tip of the V3	arwowska1992b, Gorny1995 ontenot1995, Saarloos1995 of, D'Souza1997, Binley1996 th1998, Parren1998a, Zolla vit-Ferbas2000, Hioe2000, li2002, Poignard2003 ontency when combined 1:12, RF, WM52, and HXB2 [and binds SF2: GPGR [Go any of the residues ADGL] and SF2 when combined with f IIIB, but not in the present loop, common in B clade	23, Keller1993, Cavacini1993a 5, Zolla-Pazner1995a, Zolla-Pa 97a, Fouts1997, Hioe1997a, F -Pazner1999a, Zolla-Pazner19 Ly2000, Nyambi2000, Park20 d array of B clade lab isolates with human MAb 588-D [Bu Karwowska1992b] rny1993] MNQRS in the X position tole CD4 binding site MAb F105- ce of sCD4 [Spear1993]	a, Spear1993, Conley1994a azner1995b, Moore1995a, 1 Hioe1997b, Boots1997, Par 999b, Connor1998, Gorny1 000, York2001, Verrier2001 [Gorny1992] achbinder1992] erated in peptides that react – supra-additive neutralizat	Moore 1995b, Forthal 1995, ren 1997c, Hill 1997, 998, Nyambi 1998, ., Srivastava 2002, well with the antibody
	gp160 (724–745) Vaccine Vector/Type References Durrani Comparison of intra gp160 (725–745) Vaccine Vector/Type References Hifumi2 41S-2: BALBc mice proteolytic activity t observed for the who gp160 (726–729) Ab type V3 Dono References Gorny19 Gorny1994, Moore1 Jagodzinski1996, Tr Gorny1997, Inouyel Hioe1999, Beddows Sharon2002, Gorny2 447-52D: Requires 6 447-52D: Neutralize 447-52D: Neutralize 447-52D: Additive r 447-52D: Compleme 447-52D: Compleme 447-52D: Requires 6	gp160 (724–745) gp41 (731–752)  Vaccine Vector/Type: Cowpea mosaic virus  References Durrani1998  Comparison of intranasal and oral immunizat  gp160 (725–745) gp160 (732–750)  Vaccine Vector/Type: peptide keyhole limpe  References Hifumi2000  41S-2: BALBc mice were immunized with g  proteolytic activity toward the peptide epitop  observed for the whole antibody [Hifumi200]  gp160 (726–729) gp120 (MN)  Ab type V3 Donor Dr. Susan Zolla-Pazne  References Gorny1992, Buchbinder1992, K  Gorny1994, Moore1994a, Sattentau1995a, F  Jagodzinski1996, Trkola1996a, Sattentau1995  Gorny1997, Inouye1998, Mondor1998, Smit  Hioe1999, Beddows1999, Gorny2000a, Gror  Sharon2002, Gorny2002, He2002, Ferrantell  447-52D: Requires GPXR at the tip of the V  447-52D: Reacts with MN, NY5, CDC4, SF  447-52D: Neutralizes MN and IIIB: GPGR,  447-52D: Peptide phage library showed that  [Keller1993]  447-52D: Complement mediated virolysis of  447-52D: Requires GPXR at the tip of the V  447-52D: Requires GPXR at the tip of the V	gp160 (724–745) gp41 (731–752) PRGPDRPEGIEEEGG Vaccine Vector/Type: Cowpea mosaic virus Strain: IIIB HIV compose References Durrani1998  Comparison of intranasal and oral immunization of HIV-1 peptide expres gp160 (725–745) gp160 (732–750) RGPDRPEGIEEEGGE Vaccine Vector/Type: peptide keyhole limpet hemocyanin (KLH) conjut References Hifumi2000  41S-2: BALBc mice were immunized with gp41 peptide and a MAb speproteolytic activity toward the peptide epitope which may be due to a car observed for the whole antibody [Hifumi2000]  gp160 (726–729) gp120 (MN) GPXR Ab type V3 Donor Dr. Susan Zolla-Pazner, NYU Med Center NY, N References Gorny1992, Buchbinder1992, Karwowska1992b, Gorny1995 Gorny1994, Moore1994a, Sattentau1995a, Fontenot1995, Saarloos1995 Jagodzinski1996, Trkola1996a, Sattentau1996, D'Souza1997, Binley19 Gorny1997, Inouye1998, Mondor1998, Smith1998, Parren1998a, Zolla Hioe1999, Beddows1999, Gorny2000a, Grovit-Ferbas2000, Hioe2000, Sharon2002, Gorny2002, He2002, Ferrantelli2002, Poignard2003  447-52D: Requires GPXR at the tip of the V3 loop – neutralizes a broad 447-52D: Reacts with MN, NY5, CDC4, SF2, RF, WM52, and HXB2 [ 447-52D: Neutralizes MN and IIIB: GPGR, and binds SF2: GPGR [Go. 447-52D: Peptide phage library showed that any of the residues ADGLI [Keller1993]  447-52D: Complement mediated virolysis of IIIB, but not in the presence	gp160 (724–745) gp41 (731–752) PRGPDRPEGIEEEGGERDRDRS  Vaccine Vector/Type: Cowpea mosaic virus Strain: IIIB HIV component: gp41 peptide  References Durrani1998  Comparison of intranasal and oral immunization of HIV-1 peptide expressed in a plant viral vector –  gp160 (725–745) gp160 (732–750) RGPDRPEGIEEEGGERDRDRS yes  Vaccine Vector/Type: peptide keyhole limpet hemocyanin (KLH) conjugate HIV component: gp41  References Hifumi2000  41S-2: BALBc mice were immunized with gp41 peptide and a MAb specific for the peptide was gene proteolytic activity toward the peptide epitope which may be due to a catalytic triad on light chain (A observed for the whole antibody [Hifumi2000]  gp160 (726–729) gp120 (MN) GPXR L  Ab type V3 Donor Dr. Susan Zolla-Pazner, NYU Med Center NY, NY, or Cellular Products Inc, B  References Gorny1992, Buchbinder1992, Karwowska1992b, Gorny1993, Keller1993, Cavacini1993, Gorny1994, Moore1994a, Sattentau1995a, Fontenot1995, Saarloos1995, Zolla-Pazner1995a, Zolla-P  Jagodzinski1996, Trkola1996a, Sattentau1996, D'Souza1997, Binley1997a, Fouts1997, Hioe1997a, If Gorny1997, Inouye1998, Mondor1998, Smith1998, Parren1998a, Zolla-Pazner1999a, Zolla-Pazner1999, Beddows1999, Gorny2000a, Grovit-Ferbas2000, Hioe2000, Ly2000, Nyambi2000, Park20  Sharon2002, Gorny2002, He2002, Ferrantelli2002, Poignard2003  447-52D: Requires GPXR at the tip of the V3 loop – neutralizes a broad array of B clade lab isolates  447-52D: Requires GPXR at the tip of the V3 loop – neutralizes a broad array of B clade lab isolates  447-52D: Reacts with MN, NY5, CDC4, SF2, RF, WM52, and HXB2 [Karwowska1992b]  447-52D: Peptide phage library showed that any of the residues ADGLMNQRS in the X position tole [Keller1993]  447-52D: Additive neutralization of MN and SF2 when combined with CD4 binding site MAb F105  447-52D: Complement mediated virolysis of IIIB, but not in the presence of sCD4 [Spear1993]	pp160 (724–745) gp41 (731–752) PRGPDRPEGIEEEGGERDRDRS Vaccine  Vaccine Vector/Type: Cowpea mosaic virus Strain: IIIB HIV component: gp41 peptide  References Durrani1998  Comparison of intranasal and oral immunization of HIV-1 peptide expressed in a plant viral vector – intranasal gave the better re  gp160 (725–745) gp160 (732–750) RGPDRPEGIEEEGGERDRDRS yes Vaccine  Vaccine Vector/Type: peptide keyhole limpet hemocyanin (KLH) conjugate HIV component: gp41  References Hifumi2000  41S-2: BALBc mice were immunized with gp41 peptide and a MAb specific for the peptide was generated – isolated MAb light proteolytic activity toward the peptide epitope which may be due to a catalytic triad on light chain (Asp73, Ser76, and His79) – 1 observed for the whole antibody [Hifumi2000]  gp160 (726–729) gp120 (MN) GPXR  References Gorny1992, Buchbinder1992, Karwowska1992b, Gorny1993, Keller1993, Cavacini1993a, Spear1993, Conley1994a Gorny1994, Moore1994a, Sattentau1995a, Fontenot1995, Saarloos1995, Zolla-Pazner1995b, Moore1995a, Jagodzinski1996, Trkola1996a, Sattentau1996, D'Souza1997, Binley1997a, Fouts1997, Hioe1997a, Hioe1997b, Boots1997, Par Gorny1997, Inouye1998, Mondor1998, Smith1998, Parren1998a, Zolla-Pazner1999b, Connor1998, Gorny1 Hioe1999, Beddows1999, Gorny2000a, Grovit-Ferbas2000, Hioe2000, Ly2000, Nyambi2000, Park2000, York2001, Verrier2001 Sharon2002, Gorny2002, He2002, Ferrantelli2002, Poignard2003  447-52D: Requires GPXR at the tip of the V3 loop – neutralizes a broad array of B clade lab isolates [Gorny1992]  447-52D: Reacts with MN, NY5, CDC4, SF2, RF, WM52, and HXB2 [Karwowska1992b]  447-52D: Reacts with MN, NY5, CDC4, SF2, RF, WM52, and HXB2 [Karwowska1992b]  447-52D: Peptide phage library showed that any of the residues ADGLMNQRS in the X position tolerated in peptides that react [Keller1993]  447-52D: Complement mediated virolysis of IIIB, but not in the presence of sCD4 [Spear1993]

- 447-52D: Competition studies with human sera from seroconverting individuals showed that anti-CD4 BS antibodies can arise very early in infection, comparable or prior to anti-V3 antibodies [Moore1994a]
- 447-52D: Called 447d Formalin inactivation of virus at 0.1% formalin for 10 hours at 4 degrees was optimal for inactivation of virus while maintaining epitope integrity [Sattentau1995c]
- 447-52D: Called 447 The tip of the V3 loop was presented in a mucin backbone higher valency correlates with stronger affinity constant [Fontenot1995]
- 447-52D: Ab-mediated activation of complement on HIV+ cells is higher than Ab independent activation—what has been termed "Ab independent" in fact results in part from IgM in normal human serum that is HIV-cross-reactive [Saarloos1995]
- 447-52D: Serotyping study using flow-cytometry bound only to GPGR V3 loop tips [Zolla-Pazner1995a]
- 447-52D: Neutralization of primary and prototype laboratory HIV-1 isolates using a resting cell assay enhances sensitivity [Zolla-Pazner1995b]

- 447-52D: Binding affected by identity of amino acids flanking GPGR core poor breadth of primary virus neutralization [Moore1995a]
- 447-52D: Review: the V3 loop motif GPGR is not common outside subtype B isolates, MAb 19b is more cross-reactive [Moore1995b]
- 447-52D: Neutralizing (- complement), no ADCC activity, and no viral enhancing activity [Forthal1995]
- 447-52D: Called 447-52-D The sulfated polysaccharide curdlan sulfate (CRDS) binds to the Envelope of T-tropic viruses and neutralizes virus CRDS inhibits binding [Jagodzinski1996]
- 447-52D: Neutralizes JR-FL strongly inhibits gp120 interaction with CCR-5 in a MIP-1beta-CCR-5 competition study [Trkola1996a]
- 447-52D: Review: called 447-52-D only four epitopes have been described which can stimulate a useful neutralizing response to a broad spectrum of primary isolates, represented by the binding sites of MAbs: 447-52-D, 2G12, Fab b12, and 2F5 [Sattentau1996]
- 447-52D: In a multilaboratory blinded study, failed to consistently neutralize any of nine B clade primary isolates many of these isolates had the GPGR motif at the apex of the V3 loop [D'Souza1997]
- 447-52D: Study shows neutralization is not predicted by MAb binding to JRFL monomeric gp120, but is associated with oligomeric Env binding 447-52D bound monomer, oligomer, and neutralized JRFL [Fouts1997]
- 447-52D: Tested using a resting cell neutralization assay [Hioe1997a]
- 447-52D: Four primary isolates showed distinct patterns of sensitivity to neutralization by polyclonal sera or plasma and MAbs BZ167 was the only isolate inhibited by all polyclonal sera and plasma tested, and was also neutralized by 8/17 MAbs, in particular anti-V3 loop (419-D, 447-52D, 782-D, and 838-D), anti-CD4bd (559/64-D, 654-D and 830-D and a cluster II of gp41 directed MAb (98-6) isolates 92HT593 and 91US056 were neutralized by V3 loop (419-D, and 447-52D)and cluster II gp41 (98-6) MAbs at higher concentrations US4 was neutralized by some of the polyclonal sera/plasma tested and not at all by MAbs individually or by a cocktail of ten MAbs consisting of 419-D, 447-52D, 782-D, 838-D, 559/64-D, 654-D, 450-D, 670-D, 1281-D and 98-6 [Hioe1997b]
- 447-52D: Viral binding inhibition by 447-D was correlated with neutralization (all other neutralizing MAbs tested showed some correlation except 2F5) [Ugolini1997]
- 447-52D: Neutralizes TCLA strains but not primary isolates [Parren1997c]
- 447-52D: Called 447 gp120 can inhibit MIP-1alpha from binding to CCR5, but this inhibitory effect is blocked by pre-incubation of gp120 with three anti-V3 MAbs: 447, 257, 1027 MAb 670 which binds in the C5 region had no effect [Hill1997]
- 447-52D: Abs that recognize discontinuous epitopes can identify mimotopes from a phage peptide display library 447-52D has an epitope involving the tip of the V3 loop, that was previously studied with this method [Keller1993] in Keller et al., with no competition, LxGPxR was the most common six-mer, 38% of the peptides after competition with a gp120 IIIB ligand (QRGPGR)i, RGPxR was the most common and one peptide had the sequence QRGPGR, showing type specific mimotopes can be enriched by strain specific ligand competition protocols [Boots1997]
- 447-52D: Used as a control for comparison to five V3 RF selected antibodies 447-52D was reactive with A, B, and C clade peptides, but not E [Gorny1997]
- 447-52D: Called 447-D 447-D resistance took longer to acquire in virus with the M184V substituted RT, and had the form (AAC N to TAC Y) at position 5 of the V3 loop, rather than the GPGR to GPGR resistance found with wildtype RT [Inouye1998]
- 447-52D: Inhibits binding of Hx10 to both CD4 positive and negative HeLa cells [Mondor1998]
- 447-52D: Called 447-52-D The tip of the MN V3 loop was inserted into cold causing human rhinovirus 14 (HRV14) chimeras were immunoselected, and chimeric viruses were neutralized by anti-V3 loop antibodies, and 447-52D was among the Abs used chimeric viruses elicited potent NAbs in guinea pigs against ALA-1 and MN [Smith1998]
- 447-52D: The MAb and Fab binding to the oligomeric form of gp120 and neutralization were highly correlated authors suggest that neutralization is determined by the fraction of Ab sites occupied on a virion irrespective of the epitope [Parren1998a]
- 447-52D: Ab from gp120 vaccinated individuals prior to infection, who subsequently became HIV infected, could not achieve 90% neutralization of the
  primary virus by which the individuals were ultimately infected these viruses were not particularly refractive to neutralization, as determined by their
  susceptibility to neutralization by MAbs 2G12, IgG1b12, 2F5 and 447-52D [Connor1998]

No.	MAb ID	<b>HXB2</b> Location	<b>Author's Location</b>	Sequence	Neutralizing Immunogen	Species(Isotype)
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• 447-52D: Kinetic parameters were measured, and the association rates were similar, but dissociation rate constants were quite variable for V3 MAbs, 1324E was comparable to 447-52D [Gorny1998]

- 447-52D: Using a whole virion-ELISA method, 18 human MAbs were tested for their ability to bind to a panel of 9 viruses from clades A, B, D, F, G, and H 447-52D was the most potent and cross-reactive of 18 human MAbs tested and was the only MAb which bound to virions from isolates CA20 (subtype F), CA13 (subtype H), and VI526 (subtype G) [Nyambi1998]
- 447-52D: Review of clade specificity and anti-V3 HIV-1-Abs [Zolla-Pazner1999a]
- 447-52D: MAb peptide-reactivity pattern clustered with the immunological related MAbs: 1334, 419, 504, 447, 453 and 537 the core amino acids GP tended to be critical for reactivity in this group 447 reacted with peptides containing GPGR, but also with many lacking this sequence (GPGQ, for example), and it failed to react with 2/14 peptides containing GPGR, illustrating the importance of context [Zolla-Pazner1999b]
- 447-52D: The presence of leukocyte function-associated molecule 1 (LFA-1) promotes virus infectivity and hinders neutralization, and anti-LFA-1 MAbs can enhance the neutralizing effect of anti-HIV V3 MAb 447-52D and anti-HIV CD4BS MAb IgG1b12 non-neutralizing anti-HIV CD4BS MAb 654-D did not become neutralizing in the presence of anti-LFA-1 MAbs [Hioe1999]
- 447-52D: rgp120 derived from a R5X4 subtype B virus, HIV-1 W61D, was used to vaccinate healthy volunteers and the resulting sera were compared with sera from HIV-1 positive subjects and neutralizing MAbs TCLA strains showed enhanced 447-52D neutralization sensitivity relative to PBMC-adapted lines (32X increase between HIV-1(M2424/PBMC(p0)) and HIV-1(M2424/H9(p9)) and a >128X increase between HIV-1(W61D/PBMC) and HIV-1(W61D/SupT1) isolates) [Beddows1999]
- 447-52D: Binding of panel of 21 MAbs to soluble oligomeric gp140 versus gp41 or gp120 monomers was compared no MAb was oligomer specific, though anti-V3 and CD4BS MAbs reacted better with the oligomer and V2 and C5 tended to favor the monomer V3 MAbs 447-52D, 838-D, and 1334 bound with a 7-10 fold preference for the oligomer [Gorny2000a]
- 447-52D: To determine the antigenicity of virus killed by thermal and chemical inactivation, retention of conformation-dependent neutralization epitopes was examined, and exposure of CD4BS epitopes was found to be enhanced (MAbs IgG1b12, 205-46-9, and 205-43-1) binding to 2G12 and 447-52D epitopes was essentially unaltered the 17b CD4i epitope was also exposed [Grovit-Ferbas2000]
- 447-52D: Ab responses, because of their capacity to alter antigen uptake and processing, can influence helper T cell responses CD4BS MAbs or serum Ig
  from HIV+ individuals inhibited proliferative responses of gp120 specific T cells V3 MAbs 447-52-D and 268-10-D did not effect proliferation
  [Hioe2000]
- 447-52D: Called 447D SF162 is a neutralization-resistant HIV-1 isolate N-linked glycosylation modifications in the V2 loop of the SF162 gp120 revealed that these sites prevent neutralization by CD4BS MAbs (IgG1b12 and IgGCD4), and protect against neutralization by V3 MAbs (447D and 391-95D) V2-region glycosylation site mutations did not alter neutralization resistance to V2 MAbs (G3.4 and G3.136) or CD4i MAbs (17b and 48d) V2 glycosylation site modification allows infection of macrophages, probably due to glycosylated forms requiring fewer CCR5 molecules for viral entry [Ly2000]
- 447-52D: A panel of 47 human MAbs was tested against 26 HIV-1 group M primary isolates from clades A through H 19 V3 MAbs were tested, and of 494 combinations, 44% displayed some viral binding V3 MAbs tended to have the most cross-reactive binding to clade A, B, C, and D isolates, less to E, F, G, and H 447-52D showed the highest cross-reactivity, bound to 24/26 viruses tested, but achieved 90% neutralization only against MN, 50% against CA5, and no neutralization was observed for 3 other isolates tested [Nyambi2000]
- 447-52D: Six mutations in MN change the virus from a high-infectivity neutralization resistant phenotype to low-infectivity neutralization sensitive V3, CD4BS, and CD4i MAbs are 20-100 fold more efficient at neutralizing the sensitive form the mutation L544P reduced binding of all MAbs against gp120 by causing conformational changes [Park2000]
- 447-52D: Abs against the V3 loop (50.1, 58.2, 59.1, 257-D, 268-D, 447-52D), CD4BS (IgG1b12, 559-64D, F105), CD4i (17b), and to gp41 (2F5, F240) each showed similar binding efficiency to Env derived from related pairs of primary and TCLA lines (primary: 168P and 320SI, and TCLA: 168C and 320SI-C3.3), but the TCLA lines were much more susceptible to neutralization suggesting that the change in TCLA lines that make them more susceptible to NAbs alters some step after binding the dissociation constant, Kd of 447-52D for the cell associated primary and TCLA Envs was equal, 3nM [York2001]

No. N	MAb ID	HXB2 Location	Author's Location	Sequence		Neutralizing Immunogen	Species(Isotype)
		neutralization at 2 trand 1281 – no syne as well as 98-6 and 447-52D: Oligomer used to compare the readily than o-gp14 447-52D: The feasi for obtaining NMR was obtained [Share 447-52D: Conformatip of the V3 loop a virions of clades A( was highly correlate 447-52D (anti-V3 Mas a linear binding sclades except CRFC 447-52D: Transgen producing hybridom 697D (and SC258, 447-52D: Review of 447-52D: Virion ca functional Enveloped did not inhibit b12 transports and support to the support of the support o	o 10 ug/ml: 2F5, 50-69, Igrgy, only additive effects of 2F5 [Verrier2001] ric gp140 (o-gp140) derive e antigenicity of gp120 and 0, suggesting the V3 loop bility of determining the 1 structures of V3 peptide-ion2002] ation-dependent anti-V3 Indicross-compete with the (N=2), B(N=4), and F(N=2) de with percent neutralizade MAb for competition and issite MAb control), MAb 201 (E), was conformational ic mice carrying human genes by immunization with V2) were used as controls of NAbs [Ferrantelli2002] pture assays are not a good espikes on primary isolate neutralization — Ab 447-5 tent at neutralizing the thr	gG1b12, 447-52D, 2 were seen for pairwis ed from R5 primary d o-gp140 using a pa is less exposed on o NMR structure of the Fab fragments develo oop Abs may be more e MAb 447-52D and 2), limited binding to tion using the ghost encutralization studies 46 (anti-gp41 MAb ally sensitive and sho enes allowing product HIV SF162 gp120 - E [He2002]  d preditor of neutrali- es – F105 and b6 cou 2D was able to poter ee primary virions II	G12, and 670-D six did the combinations of MAB assolate US4 was characterized and of well and it is on the eV3(MN) peptide bound oped – preliminary NMI are cross-reactive, so six are conformationally set of C(N=3) and D(N=3), and cell or PHA blast assay as of C4 (anti-CD4BS used that bound to primary is swed the some of the most tion of fully human MAB are the previously described at the previously described at the previously block the atty neutralize 89.6 and R-CSF, ADA, and 89.6,	ropic primary isolate HIV-1 89.6 – size not have neutralizing activity: 654-Eps, and antagonism was noted between the terized for use as a vaccine reagent—ed MAbs—447-D recognized the gp1 intact virions [Srivastava2002]. do to the 447-52D Fab fragment was to the Respect of the terized for 447-52D complexed to new V3 MAbs were generated – the ensitive – MAbs showed cross-clade and did not bind to CRF01(subtype Epsilon of the terized MAbs were ed as a conformation-sensitive MAbs solates of all clades) – 447-52D bound on the terized matter a panel of the terized matter and the terized matter a	antigen capture ELISA was 20 monomer much more ested and a general strategy a 23 amino acid V3 peptide six new MAbs all bind to the binding to native, intact E, N=2) – the strength binding used as controls: anti-V3 control), 1331A (anti-C5 used d to primary isolates from all /2002] tel of anti-HIV gp120 MAb 117C (plus others, V3) and ms to be different from that of irions in a virus capture, but intration but poorly neutralized which did not neutralize
682 C	C8	References Pincus:  C8: Immunotoxin c  C8: Ab response in was to this mid-gp4 immunotoxins [Pincus C8: Epitope boundate C8: The substitution call the call t	IIIB lab workers was con 11 region, but not among t cus1993b] aries mapped by peptide s n 725 RG (P[R->G]GPDI	Strain: LAI HIV concioglu 1994, McLain: oes not mediate cells appared to gp160 LAI the infected lab work canning [Abacioglu 1] RPEGIEEEGGERD	2001 s killing, and is not affect vaccine recipients – C8 ers – Abs binding this re  2994] RDRS) alters the antige	no Vaccine  cted by sCD4 [Pincus1993a]  8 was used as a control – the dominar egion do not neutralize, bind to infect nic exposure of this region on the vir in the virion, while the epitope IEEE	ted cells, nor serve as
683 B	331	gp160 (727–734)	gp41 (727–734 BH10 e: recombinant protein glu1994		omponent: gp160	Vaccine	murine (IgG1)

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizing	Immunogen	Species(Isotype)
		B31: Epitope bound	aries mapped by peptide sca	anning [Abacioglu1994]			
684	B33	References Abacios B33: There are two Baculovirus-express	glu1994, Bristow1994 MAbs in the literature name ed mis-folded rgp160 IIIB:1	pdrpegie ain: NL43 HIV component: gp160 ed B33, see also gp120, positions 123-142 NL43, MicroGenSys [Bristow1994]	no – MAb generat	Vaccine ed in a study of the humora	murine (IgG1)  Il immune response to
685	1576	• B33: Epitope bound gp160 (728–745)	gp41 (735–752 IIIB)	anning IgG1 [Abacioglu1994]  DRPEGIEEEGGERDRDRS	no	Vaccine	murine
002	1370		e: poliovirus <i>Strain:</i> IIIB 93	HIV component: gp41 peptide	no	, account	mame
686	1578	<ul><li>References Evans 19</li><li>1578: No neutralizin</li></ul>	989, Vella1993 ng activity – epitope may be	DRPEGIEEEGGERDRDRS  HIV component: gp41 peptide  formed by regions from both poliovirus a dized IIIB, but not RF or MN [Vella1993]		Vaccine	murine
687	1579	gp160 (728–745) Vaccine Vector/Type References Vella199	gp41 (735–752 IIIB) :: poliovirus <i>Strain:</i> IIIB	DRPEGIEEEGGERDRDRS  HIV component: gp41 peptide  at not RF or MN [Vella1993]	no	Vaccine	murine
688	1583	<ul><li>References Evans 19</li><li>1583: Neutralizing a</li><li>1583: Core epitope:</li></ul>	989, Vella1993, Sattentau19 activity, less broad than 157' ERDRD – Could neutralize		no uttentau1995c]	Vaccine	murine
689	1899	References Vella199	•	DRPEGIEEEGGERDRDRS  HIV component: gp41 peptide  Vella1993]	no	Vaccine	murine
690	1907	References Vella199	-	DRPEGIEEEGGERDRDRS  HIV component: gp41 peptide  [Vella1993]	no	Vaccine	murine
691	1908	References Evans 19	gp41 (735–752 IIIB) e: poliovirus <i>Strain:</i> IIIB 989, Vella1993, Sattentau19 IB, but not RF or MN [Vella		no	Vaccine	murine

gp160 Antibodies

**HIV Antibodies Tables** 

No.	MAb ID	HXB2 Location Author's Location Sequence	Neutralizing	Immunogen	Species(Isotype)
		• 1908: Cytoplasmic domain, epitope not exposed at the surface of HIV-1 inf	ected cells [Sattentau1995c]		
692	1909	gp160 (728–745) gp41 (735–752 IIIB) DRPEGIEEEGGERDRDR Vaccine Vector/Type: poliovirus Strain: IIIB HIV component: gp41 pep References Vella1993  • 1909: Neutralized HIV IIIB but not HIV RF [Vella1993]		Vaccine	murine
693	41-1	gp160 (728–745) gp41 (735–752 IIIB) DRPEGIEEEGGERDRDR Vaccine Vector/Type: peptide Strain: IIIB HIV component: gp41 peptide References Mani1994, Dalgleish1988  41-1: This antibody gp41(735-752 IIIB) [Dalgleish1988] seems to have been 41-1: Neutralizes HIV-1 but not HIV-2 strains [Dalgleish1988]	le	Vaccine nt MAb to gp41(584	murine (IgMκ) -609) [Mani1994]
594	41-2	gp160 (728–745) gp41 (735–752 IIIB) DRPEGIEEEGGERDRDR Vaccine Vector/Type: peptide Strain: IIIB HIV component: gp41 peptid References Dalgleish1988  41-2: Neutralizes HIV-1 but not HIV-2 strains [Dalgleish1988]		Vaccine	murine ( $\operatorname{IgM}\kappa$ )
595	41-3	gp160 (728–745) gp41 (735–752 IIIB) DRPEGIEEEGGERDRDR Vaccine Vector/Type: peptide Strain: IIIB HIV component: gp41 peptid References Dalgleish1988  • 41-3: Neutralizes HIV-1 but not HIV-2 strains [Dalgleish1988]		Vaccine	murine (IgM $\kappa$ )
596	ED6	gp160 (728–745)	S no		murine (IgM)
597	LA9 (121-134)	gp160 (728–745)	S no		murine (IgM)
698	1575	gp160 (728–745) gp41 (735–752 IIIB) DRPEGIEEEGGERDRDR Vaccine Vector/Type: poliovirus Strain: IIIB HIV component: gp41 pep Ab type C-term Donor C. Vella, NIBSC, Potters Bar UK References Evans1989, Vella1993, Buratti1997, Cleveland2000a  1575: Neutralizing activity, less broad than 1577 [Evans1989]  1575: Core epitope: IEEE – neutralized IIIB, but not RF or MN [Vella1993]  1575: Study shows that MAb 1575 can recognize the IEEE sequence in bot regions in different HIV-1 clades [Buratti1997]	otide ] h gp41, and in the HPG30 reg		murine n – motif is conserved in bot
699	88-158/02	gp160 (732–747) gp41 (732–752 IIIB) GIEEEGGERDRDRSIR  Vaccine Vector/Type: recombinant protein Strain: IIIB HIV component  References Niedrig1992a  • 88-158/02: Mild inhibition of in vitro activity at high MAb concentrations -  virion – domain non-immunogenic in humans [Niedrig1992a]		Vaccine at low concentration	murine (IgG2b) s – significant reactivity to

HIV Antibodies Tables gp160 Antibodies

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizing	Immunogen	Species(Isotype)
700	88-158/022	References Niedrig	;1992a	GIEEEGGERDRDRSIE  train: IIIB HIV compone.  y at high MAb concentratio		Vaccine  y at low concentrat	murine (IgG2b) ions – significant reactivity to
			n-immunogenic in humans	_	,	,	,
701	88-158/079	References Niedrig  • 88-158/079: Mild in	1992a nhibition of HIV in vitro at	_		Vaccine low concentration	murine (IgG1) s – weak binding to virion –
702	polyclonal	gp160 (733–736)  Vaccine Vector/Typ  Ab type C-term  References Clevelae  When PRGPDRPE  GERDRDR shifts t  The substitution 72	and2000b, McLain2001 GIEEEGGERDRDRS was he response to ERDRD [C 5 RG (P[R->G]GPDRPEC	IEEE HIV component: gp41 pept used as antigen an immuno leveland2000b] GIEEEGGERDRDRS) alter	L  odominant, non-neutralizing respective antigenic exposure of this report of the company of th	region on the virior	resulting in the loss of the
703	polyclonal	Ab type C-term References McLair • The substitution 72.	n2001 5 RG (P[R->G]GPDRPEC	HIV component: gp41 pept GIEEEGGERDRDRS) alter	L s the antigenic exposure of this appe GPDRPEG in the virion, wh		
704	В8	References Pincus:  • B8: Ab response in was to this mid-gp4 immunotoxins [Pincus]	1993b, Abacioglu1994 IIIB lab workers was com 1 region, but not among th	train: LAI HIV compone pared to gp160 LAI vaccine e infected lab workers – Ab	no nt: gp160 recipients – B8 was used as a cost binding this region do not neuron.		
705	1577	gp160 (739–743)  Vaccine Vector/Typ  Ab type C-term I  References Evans1  • 1577: Raised again	gp41 (735–752 IIIB) e: poliovirus Strain: IIIE Donor C. Vella or Morag F 989, D'Souza1991, Vella1	ERDRD  3 HIV component: gp41 p erguson (NIBSC, Potters B 993, Cleveland2000a eutralized African and Ame		Vaccine 989]	murine

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C	Ì
е	

No.	MAb ID	<b>HXB2</b> Location	<b>Author's Location</b>	Sequence	Neutralizin	g Immunogen	Species(Isotype)
		<ul><li>1577: Ab binding to</li><li>1577: UK Medical 1</li></ul>				000a]	
706	polyclonal	Ab type C-term References Clevela ERDRD-specific Ig MN and D clade vir immunodominant, r attachment of free v The substitution 725	nd2000b, McLain2001 G recognizes an externaliz us CBL-4, but HXB-2D (con-neutralizing response tirus, but does inhibit by an	ERDRD  HIV component: gp41 peptide  red loop of the gp41 C-terminal tail velade B) was not recognized — when to IEEE was observed, but immunizate event that precedes fusion-entry [CGIEEEGGERDRDRS) alters the antigreased exposure of the epitope GPD	PRGPDRPEGIEEEG tion GERDRDR shift leveland2000b] genic exposure of this	GERDRDRS was used s the response to ERD region on the virion r	d as antigen an PRD – NAb does not inhibit esulting in the loss of the
707	DZ	gp160 (822–855)	gp41 (827–860 BRU)	VAEGTDRVIEVVQGACRAIRHI IRQGLERIL	PRR- L	Vaccine	human (IgG1λ)

## **IV-C-14** Env Antibodies

No. MAb ID	HXB2 Location	<b>Author's Location</b>	Sequence	Neutralizi	ng Immunogen	Species(Isotype)
708	Env Vaccine Vector/Type: References Rodríguez		HIV component: gp12	) Adjuvant: GM-CSF	Vaccine	murine (IgG1)
	response to a gp120-v	accinia construct, but th	e breadth of the Ab resp	ony stimulating factor GM-CSF/ onse was greater, in particular to , as measured by Elispot assay [1	the C-term region of gp120 –	
709	Env	Env (384–467)			Vaccine	rabbit, Rhesus macaque
	References Michel 199 • Immunization with red	93	BsAg hybrid particles int	HsBAg HIV component: V3 or rabbits or macaques elicited an		hs anti-V3 or HIV-1
710	<ul><li>References Buonagur</li><li>BALB/c mice were gi absence of adjuvants.</li></ul>	o2002 ven intraperitoneal imm High dose-independent	nunization with virus-like	.94UG018, HIV-1 IIIB HIV co e particlea (VLPs) expressing rec ast both gp120 and p24 peptides ined [Buonaguro2002]	ombinant subtype A gp120 an	
711			-	Y  end to favor potent neutralizing A	HIV-1 infection, Vaccine Ab production, and discusses p	human possible vaccine
712	autologous NAbs to vi	gous NAb response in larl isolates were genera		P infections was delayed – for pati month 6, and there was no appare 196]		
713 102-135	<ul><li>References Scheffel19</li><li>102-135: Overlapping</li></ul>	999 peptides based on grou	ıp O HAM112 Env were	O) HIV component: gp160 tested for MAb reactivity – 102-to either individually [Scheffel19		murine (IgG1 $\kappa$ )
714 1025	Env References Berman 19 • 1025: Binds to 1/7 iso		n cases from a MN gp120	) vaccine trial [Berman1997]		

No.	MAb ID	HXB2 Location	<b>Author's Location</b>	Sequence	Neutralizing	Immunogen	Species(Isotype)
715	105-134	Env	gp41 (652–681 HAM112, O group)			Vaccine	murine (IgG1 $\kappa$ )
		References Scheffe	el1999	Strain: HAM112 (group O)			
		• 105-134: Overlapp	ing peptides based on gro	up O HAM112 Env were te	sted for MAb reactivity [Scheffel	1999]	
716	10E9	Env References Papsido		bit 10E9 binding [Papsidero	10001	HIV-1 infection	murine (IgG1)
717	126-50	Env <b>References</b> Robins	gp41 (HXB2) on1990b, Tyler1990, Rob	oinson1991, Xu1991	no	HIV-1 infection	human (IgG2κ)
		<ul><li>126-50: Serves as t</li><li>126-50: No enhance</li></ul>	ing activity for HIV-1 IIII arget for antibody-depending or neutralizing activity r a conformational epitop	lent cellular cytotoxicity AD y [Robinson1991]	OCC [Tyler1990]		
718	12H2	References Giraud • 12H2: Env in a Ser	nliki-Forest Virus (SFV)	HIV component: Env	no mice intramuscularly as naked F in is properly expressed [Giraud		murine ( $IgM\kappa$ ) use was induced to Env from
719	13.10 (No. 1	3) Env Donor Evan Hersh References Lake 19  • 13.10: First HIV-1  • 13.10: Heavy (V H  • 13.10: 13.10 is V F infected individuals	gp120 and Yoh-Ichi Matsumoto 89, Moran1993, Wisnew specific human-mouse hy I) and light (V lambdaII) II – V-region heavy chair	ski1996 bridoma that produces a MA chain sequenced – no enhan usage was examined and a	no  Ab that binds to gp120 and gp160 cing or neutralizing activity – ca bias of enhanced V H1 and V H2	HIV-1 infection  [Lake1989]  [led No. 13 [Moran199	
720	1B1	<ul><li>References Buchad</li><li>1B1: Generated by</li><li>1B1: The complete</li></ul>	cher1994, Purtscher1994, electrofusion of PBL from V, J and D(H) domain was	m HIV-1 positive volunteers as sequenced – unlike non-n	L ral Science, Vienna, Austria with CB-F7 cells [Buchacher199 eutralizing anti-gp41 MAb 3D6, antigenic pressure over long perio	five neutralizing MAbs	human s (2F5, 2G12, 1B1, 1F7, ar
721	1F7	Env <b>Donor</b> Herman Ka <b>References</b> Buchae • 1F7: Generated by	Env tinger, Inst. Appl. Microb cher1994, Purtscher1994, electrofusion of PBL from	oiol. University of Agricultu Kunert1998, Grant2000 n HIV-1 positive volunteers	L	HIV-1 infection	human s (2F5, 2G12, 1B1, 1F7, an

3D5) showed extensive somatic mutations giving evidence of persistent antigenic pressure over long periods [Kunert1998]

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizir	g Immunogen	Species(Isotype)
					pooled IgG from HIV-1+ subject vity—this is not the same as the		
722	2.2B	in an immune responding the native coalso by anti-V3 MA bind C11, 23A, and very strongly induce bind to SOSgp140,  2.2B: Ab binding cl IgG1b12, CD4 induced to SOSgp140,	ith the broadest neutralizing to the oligomer on the information of Env and exabs 19b and 83.1 – SOSgr M90, MAbs that bind to ed by CD4 in SOS gp140 in contrast to 2F5, which naracteristics of SOS gp14cible 17b, and 19b bound	e virion surface rather than of splore its potential as an important is not recognized by Capp120 C1 and C5, where it — anti-gp41 MAbs that binds to the only gp41 epito40 were tested using SPR and	no and 2F5, all have high affinity dissociated subunits – a disulfutunogen – SOS gp140 is recognous fregion MAbs that neutralize dinteracts with gp41 – MAbs that in the region that interacts with gp that is well exposed in national driph and the soon of the	de linked gp120-gp41 (nized by NAbs IgG1b) only TCLA strains, G3 at bind CD4 inducible th gp120, 7B2, 2.2B, Twe gp120-gp41 comple-gp41 bound by a disu	(SOS gp140) was created to 12, 2G12, and CD4-IgG2, and -42 and G3-519 – nor did it epitopes, 17b and A32 were 24, T15G1 and 4D4, did not xes [Binley1999] Ifide bond – NAbs 2G12, 2F5
723	30D	Env References Yang20  • 30D: Uncleaved sol T4 trimeric motif de and 2G12 relative to	gp120 002 uble gp140 (YU2 strain, lerived from T4 bacteriopho the gp120 monomer, in	R5 primary isolate) can be s	no tabilized in an oligomer by fus omer gp140∆683(-FT) showed ng MAbs F105, F91, 17b, 48d.	l strong preferential rec	cognition by NAbs IgG1b12
724	31710B	-		-	DCC against target cells infec	ted with IIIB, MN, SF-	human (IgG1) -2, and RF – bound and
725	38B5/C9	Env Vaccine Vector/Type	gp120 (SF162)  e: recombinant protein	Strain: SF162 HIV compo	no nent: gp120 Adjuvant: Ribi	Vaccine adjuvant (MPL+TDM)	human from transgenic mice $(\operatorname{IgG2}\kappa)$
		• 38B5/C9: Transgen panel of anti-HIV g not block sCD4 bin MAbs also enhance	2 ic mice (strain XenoMou p120 MAb-producing hyl ding—these MAbs were p d their binding—these M	bridomas by immunization v part of the same competition	J, pinter@phri.org s allowing production of fully with HIV SF162 gp120—11 of group, and enhanced binding reactive but could not neutrali	the MAbs were confo of the CD4BS MAb 38	rmation dependent, but did 8G3/A9 and anti-CD4BS
726	39H10/A11	Env	gp120 (SF162)		no nent: gp120 Adjuvant: Ribi	Vaccine	human from transgenic mice $(IgG2\kappa)$

Vaccine Vector/Type: recombinant protein Strain: SF162 HIV component: gp120 Adjuvant: Ribi adjuvant (MPL+TDM)

	MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizing	Immunogen	Species(Isotype)
		• 39H10/A11: Transg a panel of anti-HIV not block sCD4 bind MAbs also enhanced	genic mice (strain XenoMo gp120 MAb-producing hy ding—these MAbs were pa d their binding—these MA	bridomas by immunization art of the same competition	pinter@phri.org es allowing production of full with HIV SF162 gp120—11 o group, and enhanced binding c eactive but could not neutraliz	f the MAbs were confort the CD4BS MAb 38	ormation dependent, but did G3/A9 and anti-CD4BS
727	3D5	<ul><li>References Buchact</li><li>3D5: Generated by</li><li>3D5: The complete</li></ul>	her1994, Purtscher1994, K electrofusion of PBL from V, J and D(H) domain was	HIV-1 positive volunteers v sequenced – unlike non-ne	L Science, Vienna, Austria with CB-F7 cells [Buchacher19 stralizing anti-gp41 MAb 3D6 tigenic pressure over long per	, five neutralizing MAI	human bs (2F5, 2G12, 1B1, 1F7, an
728	3Н6		er MAb with this ID that r	ecognizes Rev [Orsini1995] protein-free medium [Pinter	1995]		murine
'29	40D3/C11	Donor Dr. Abraham References He2002 • 40D3/C11: Transge panel of anti-HIV g	n Pinter, Public Health Res nic mice (strain XenoMou p120 MAb-producing hybi	earch Institute, Newark, NJ se G2) carrying human gene	s allowing production of fully th HIV SF162 gp120—11 of t	human IgG2κ MAbs	mation dependent, but did
		MAbs also enhance		bs tended to be very cross-	eactive but could not neutraliz		

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizin	g Immunogen	Species(Isotype)
731	52G5/B9	Env	gp120 (SF162)		no	Vaccine	human from transgenic mice ( $IgG2\kappa$ )
			n Pinter, Public Health R	Strain: SF162 HIV comporesearch Institute, Newark, NJ		adjuvant (MPL+TDM)	
		<ul> <li>52G5/B9: Transgeni panel of anti-HIV gr not block sCD4 bind MAbs also enhanced</li> </ul>	ic mice (strain XenoMot o120 MAb-producing hy ling—these MAbs were d their binding—these M	use G2) carrying human general bridomas by immunization we part of the same competition IAbs tended to be very crossion E clade viruses [He2002].	th HIV SF162 gp120—11 of group, and enhanced binding of	the MAbs were confor of the CD4BS MAb 38	rmation dependent, but did 3G3/A9 and anti-CD4BS
732	55E4/H1	Env	gp120 (SF162)		no	Vaccine	human from transgenic mice (IgG2κ)
		panel of anti-HIV gp not block sCD4 bind MAbs also enhanced	o120 MAb-producing hy ling—these MAbs were d their binding—these M	use G2) carrying human general bridomas by immunization we part of the same competition IAbs tended to be very cross-to E clade viruses [He2002].	th HIV SF162 gp120—11 of group, and enhanced binding of	the MAbs were confor of the CD4BS MAb 38	rmation dependent, but did 3G3/A9 and anti-CD4BS
		not block sCD4 bind MAbs also enhanced	ling—these MAbs were d their binding—these M	part of the same competition IAbs tended to be very cross-	group, and enhanced binding	of the CD4BS MAb 38	3G3/A9 and anti-CD4BS
33	56C4/C8	Env	gp120 (SF162)	G. CELCO MIN	no	Vaccine	human from transgenic mice ( $IgG2\kappa$ )
			n Pinter, Public Health R	Strain: SF162 HIV comporesearch Institute, Newark, NJ		adjuvant (MPL+1DM)	
		panel of anti-HIV gp not block sCD4 bind MAbs also enhanced	o120 MAb-producing hy ling—these MAbs were d their binding—these M	use G2) carrying human genestly bridomas by immunization we part of the same competition IAbs tended to be very cross-to E clade viruses [He2002].	th HIV SF162 gp120—11 of group, and enhanced binding of	the MAbs were confor of the CD4BS MAb 38	rmation dependent, but did 8G3/A9 and anti-CD4BS
734	57B6/F1	Env	gp120 (SF162)		no	Vaccine	human from transgenic mice (IgG2κ)
		**	n Pinter, Public Health R	Strain: SF162 HIV comporesearch Institute, Newark, NJ	<b>01</b>	adjuvant (MPL+TDM)	

	MAb ID	HXB2 Location	Author's Location	Sequence	Neutrali	zing Immunogen	Species(Isotype)
		panel of anti-HIV g not block sCD4 bin MAbs also enhance	p120 MAb-producing hyb ding—these MAbs were p	•	th HIV SF162 gp120—11 group, and enhanced binding	of the MAbs were conforms of the CD4BS MAb 38	rmation dependent, but did
735	57H5/D7	Env	gp120 (SF162)		no	Vaccine	human from transgenic mice (IgG2κ)
			n Pinter, Public Health Res	Strain: SF162 HIV compon search Institute, Newark, NJ,		bi adjuvant (MPL+TDM)	· -
		panel of anti-HIV g not block sCD4 bin MAbs also enhance	p120 MAb-producing hybriding—these MAbs were pa	e G2) carrying human genes ridomas by immunization wi art of the same competition gabs tended to be very cross-re E clade viruses [He2002].	th HIV SF162 gp120—11 group, and enhanced binding	of the MAbs were conforms of the CD4BS MAb 38	rmation dependent, but did 8G3/A9 and anti-CD4BS
736	63G4/E2	Env	gp120 (SF162)		no	Vaccine	human from transgenic mice $(IgG2\kappa)$
		Donor Dr. Abrahan References He2002 • 63G4/E2: Transgen panel of anti-HIV g not block sCD4 bind	n Pinter, Public Health Res 2 ic mice (strain XenoMouse p120 MAb-producing hyb ding—these MAbs were p d their binding—these MA	Strain: SF162 HIV compones arch Institute, Newark, NJ, ee G2) carrying human genes ridomas by immunization with art of the same competition gas between the same competition gas and the same competition gas architectures [Hz2003].	pinter@phri.org  allowing production of ful th HIV SF162 gp120—11 troup, and enhanced bindin	ly human IgG2 $\kappa$ MAbs v of the MAbs were confo ng of the CD4BS MAb 38	vere used to rapidly create a rmation dependent, but did 8G3/A9 and anti-CD4BS
		and three X4 B clad	le viruses, as well as two E	ciade viruses [He2002].			ose wez bound to three Rs
737	65B12/C5	and three X4 B clad	le viruses, as well as two E gp120 (SF162)	ciade viruses [He2002].	no	Vaccine	human from transgenic mice (IgG2 $\kappa$ )
737	65B12/C5	Vaccine Vector/Typ Donor Dr. Abrahan References He2002  • 65B12/C5: Transge panel of anti-HIV g not block sCD4 bin MAbs also enhance	gp120 (SF162)  e: recombinant protein S n Pinter, Public Health Res nic mice (strain XenoMou p120 MAb-producing hyb ding—these MAbs were p	Strain: SF162 HIV componsearch Institute, Newark, NJ, see G2) carrying human generidomas by immunization with art of the same competition gabs tended to be very cross-reserved.	ent: gp120 Adjuvant: Ri pinter@phri.org s allowing production of fut th HIV SF162 gp120—11 troup, and enhanced binding	bi adjuvant (MPL+TDM) ally human IgG2κ MAbs of the MAbs were confo	human from transgenic mice (IgG2κ)  were used to rapidly create a rmation dependent, but did 8G3/A9 and anti-CD4BS

	MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizing Immunogen	Species(Isotype)
		<b>Donor</b> Phil Berman <b>References</b> Berman				
739	7-1054	Env References Scheffe • Binds HIV-2 gp36,		of group O MAbs [Scheffell	no 999]	murine
740	7B2	in an immune responding the native coalso by anti-V3 MA bind C11, 23A, and very strongly induc	th the broadest neutralizing onse to the oligomer on the information of Env and explos 19b and 83.1 – SOSgp1 M90, MAbs that bind to ged by CD4 in SOS gp140 –	virion surface rather than diss lore its potential as an immun 40 is not recognized by C4 re p120 C1 and C5, where it into anti-gp41 MAbs that bind in	no  2F5, all have high affinity for the native trimer, sociated subunits – a disulfide linked gp120-gp4 logen – SOS gp140 is recognized by NAbs IgG1 egion MAbs that neutralize only TCLA strains, Ceracts with gp41 – MAbs that bind CD4 inducible the region that interacts with gp120, 7B2, 2.2B, that is well exposed in native gp120-gp41 comp	1 (SOS gp140) was created to b12, 2G12, and CD4-IgG2, and G3-42 and G3-519 – nor did it le epitopes, 17b and A32 were T4, T15G1 and 4D4, did not
741	85G11/D8	Env  Vaccine Vector/Typ	gp120 (SF162)		no Vaccine	human from transgenic mice (IgG2 $\kappa$ )
		Donor Dr. Abrahan References He2002  • 85G11/D8: Transgreated of anti-HIV genot block sCD4 bin	n Pinter, Public Health Res 2 enic mice (strain XenoMou p120 MAb-producing hybroding and were part of the s	earch Institute, Newark, NJ, p se G2) carrying human genes ridomas by immunization with ame competition group—thes	allowing production of fully human $IgG2\kappa$ MA n HIV SF162 gp120—three of the MAbs were compared to the MAbs were all raised against a deglycosylated	bs were used to rapidly create a onformation dependent, but did
742	87E4/A8	Donor Dr. Abrahan References He2002 S5G11/D8: Transge panel of anti-HIV g not block sCD4 bin neutralize autologo  Env  Vaccine Vector/Typ Donor Dr. Abrahan References He2002 S7E4/A8: Transger panel of anti-HIV g not block sCD4 bin	e: recombinant protein Son Pinter, Public Health Resonant Protein Son Pinter, Public Health Pinter, Publi	earch Institute, Newark, NJ, page G2) carrying human geness ridomas by immunization with ame competition group—thes R5 and X4 B clade viruses, and train: SF162 HIV component earch Institute, Newark, NJ, page G2) carrying human genes a ridomas by immunization with ame competition group—thes	allowing production of fully human IgG2 $\kappa$ MA  a HIV SF162 gp120—three of the MAbs were of the MAbs were all raised against a deglycosylated and no E clade viruses [He2002].  no Vaccine  ant: deglycosylated gp120 Adjuvant: Ribi adjuv	bs were used to rapidly create a conformation dependent, but did form of gp120—they could not human from transgenic mice (IgG2\kappa) vant (MPL+TDM)

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No. MAb ID	HXB2 Location	Author's Location	Sequence	Neuti	ralizing Immunogen	Species(Isotype)
	panel of anti-HIV g not block sCD4 bine	ic mice (strain XenoMou p120 MAb-producing hy ding and were part of the	bridomas by immunize same competition gro	n genes allowing production of ation with HIV SF162 gp120— pup—these MAbs were all raise viruses, and no E clade viruses	three of the MAbs were coned against a deglycosylated f	nformation dependent, but did
744 A9	Env <b>Vaccine</b> <i>Vector/Typ</i> . <b>References</b> delReal		Strain: IIIB HIV com	ponent: gp120 Adjuvant: GN	Vaccine M-CSF	murine (IgG1)
	normal mice were g anti-gp120 response	gp120 specific, MAbs fro e used a high frequency of	m nude mice bound gr of VH81X, VHQ52, an	ocyte-macrophage colony stimu o120 but were polyreactive, and d VH7183 genes, a family used I gene 7183-2 [delReal1999]	from reconstituted mice we	ere half way between - the
745 B4	Env <b>Vaccine</b> <i>Vector/Typ.</i> <b>References</b> delReal	gp120 (IIIB)  e: chimeric GM-CSF S	Strain: IIIB HIV com	ponent: gp120	Vaccine	murine (IgM)
	<ul> <li>B4: Murine antibod normal mice were g anti-gp120 response</li> </ul>	ly response to the chimer pp120 specific, MAbs fro e used a high frequency of	m nude mice bound gr of VH81X, VHQ52, an	ocyte-macrophage colony stimu o120 but were polyreactive, and d VH7183 genes, a family used ad VH gene J606 [delReal1999]	I from reconstituted mice we d during fetal life and associ	ere half way between - the
746 B5	References delReal  B5: Murine antibod normal mice were g anti-gp120 response	11999 ly response to the chimer gp120 specific, MAbs fro	ic construction granulo m nude mice bound gp of VH81X, VHQ52, an	ponent: gp120 Adjuvant: GN ocyte-macrophage colony stimu o120 but were polyreactive, and d VH7183 genes, a family used	ulating factor GM-CSF/gp12 I from reconstituted mice we	ere half way between - the
747 B6	References delReal  B6: Murine antibod normal mice were g anti-gp120 response	ly response to the chimer pp120 specific, MAbs fro e used a high frequency of	ic construction granulo m nude mice bound gp of VH81X, VHQ52, an	ponent: gp120  ocyte-macrophage colony stimulo 120 but were polyreactive, and d VH7183 genes, a family used I gene J558 [delReal1999]	from reconstituted mice we	ere half way between - the
748 BAT267	Env <b>Vaccine</b> <i>Vector/Type</i> <b>References</b> Fung19	gp120 e: inactivated virus Str 987	ain: IIIB HIV compo	L ment: virus	Vaccine	murine (IgG1)
749 BAT401	Env <b>Vaccine</b> Vector/Type	gp120 e: inactivated virus Str	ain: IIIB HIV compo	L onent: virus	Vaccine	murine (IgG1)

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizing	Immunogen	Species(Isotype)
		References Fung19	87				
750	BAT509	Env Vaccine Vector/Type References Fung19		nin: IIIB HIV component: vi	L us	Vaccine	murine (IgG1)
751	C31	Env References Boyer1  C31: Broadly-reacti		high yield cultivation of huma	no n MAb [Boyer1991]	HIV-1 infection	human (IgG1κ)
752	D1	References Otteken  • D1: MAbs D1, D16	11996 5, had T37 bind to oligom	HIV component: oligomeric eric gp160 equally well – puls with a half life of 30 min [Otto	e label experiments of MAb b	Vaccine inding to noncleavable	murine (IgG) e gp160 revealed that these
753	D12	Donor Patricia Earl References Earl199 D12: Generated dur D12: One of 18 MA neutralizes IIIB and D12: This antibody [Richardson1996] D12: MAbs D10 an D12: MAbs D4, D1 that these MAbs boo D12: D12 was used required for corecep D12: A combination (gp140-GNC4) – gp	and Christopher Broder, 24, Broder1994, Richards ring a study of the influent Abs (e. g. D4 and D40) the SF2 [Broder1994] was blocked more strong and D12 are very easily bloco, D11, D12, and D41 alound with a delay, epitoper in WB of HIV-1 transment of the specificity – IIIBx, and of gp41 fusion with the b41 MAbs T4, D12, T3, and	HIV component: oligomeric NIH on 1996, Earl 1997, Otteken 1990 ice of the oligomeric structure at bind to a conformation-depend by human sera than other a cocked by human sera from HIV I bind only to complete oligom is forming with a half life of 30 cembrane proteins in a study who CD4-independent variant of II GNC4 trimeric sequences and and D50 bound less efficiently and T3 and D50 recognized to	6, LaBranche1999 of Env in determining the repondent epitope in gp41 that bir atti-gp41 MAbs (D20, D43, Determined the properties of the p	ad preferentially, but not not of HIV-1 CD4 independent of the period of	ot exclusively, to oligomers – meric ELISA assay  ncleavable gp160 revealed ndence map outside regions sulted in stable gp140 trimers 12 recognized the
754	D16	<ul> <li>Donor Patricia Earl</li> <li>References Earl199</li> <li>D16: Generated dur</li> <li>D16: Precipitates be D38, D40, D41, and</li> <li>D16: One of eleven of the MAb D50 that</li> </ul>	oth oligomeric gp140 and I D54 [Weissenhorn1996] MAbs (D16, D17, D31, at binds to the linear pepti	NIH rl1997 ice of the oligomeric structure I soluble monomeric gp41(21-	66)that lacks the fusion pepti 9, T37, and T45) that are conf	de and membrane and formation dependent a	hor, along with MAbs D16, and that can block the binding

	HXB2 Location	Author's Location	Sequence	Neutralizing	Immunogen	Species(Isotype)
55 D4	Env <b>Vaccine</b> <i>Vector/Type</i> <b>References</b> delReal		Strain: IIIB HIV component:	gp120	Vaccine	murine (IgG1)
	normal mice were gp anti-gp120 response	o120 specific, MAbs froused a high frequency	om nude mice bound gp120 but	acrophage colony stimulating f were polyreactive, and from re 83 genes, a family used during 558 [delReal1999]	econstituted mice were	half way between - the
56 D43	<b>Donor</b> Patricia Earl	gp41 (HXB2)  : protein HIV comporand Christopher Broder 4, Richardson1996, Ear	, NIH		Vaccine	murine (IgG)
	<ul><li>D43: This is a linear MAbs D20, D43, D6</li><li>D43: Partially confo</li></ul>	gp41 epitope, mapping 51, and T4 [Richardson rmation dependent – do	g in the region 635-678 – huma 1996] Desn't bind to short peptides, bu	of Env in determining the repe n sera blocked binding in oligo at does bind to the region spann 7-1 strains, not binding to JRFL	meric ELISA assay to	a similar extent for gp41
57 F223	Env <b>References</b> Cavacin	gp120		no	HIV-1 infection	human (IgG3λ)
	• F223: binds to HIV-cells – the antibody of	1 gp120 and to uninfect enhances HIV-1 infection e gene VH3-H.11 – N-1	on in a complement-dependent	59-kd auto-antigen expressed o manner – F223 light chains ha r recognition of both gp120 and	ve a strong homology	with VLgamma2, the hea
58 F285	• F223: binds to HIV-cells – the antibody of chain to the germline has autoreactivity [CE]  Env  References Wisnews	1 gp120 and to uninfect enhances HIV-1 infection e gene VH3-H.11 – N-1 avacini1999]  Env ski1995, Wisnewski199 – V-region heavy chain	on in a complement-dependent inked carbohydrates are key fo	manner - F223 light chains ha	ve a strong homology d the autoantigen – MA HIV-1 infection	with VLgamma2, the hea Ab 3D6 also uses VH3 an human (IgG1)
58 F285 59 F7	<ul> <li>F223: binds to HIV-cells – the antibody of chain to the germline has autoreactivity [C]</li> <li>Env</li> <li>References Wisnews</li> <li>F285: F285 is V H1 infected individuals</li> <li>Env</li> <li>Vaccine Vector/Type References delReal1</li> <li>F7: Murine antibody normal mice were granti-gp120 response</li> </ul>	1 gp120 and to uninfection than ces HIV-1 infection are the period of th	on in a complement-dependent inked carbohydrates are key for the strain: IIIB HIV component:  Strain: IIIB HIV component:  The construction granulocyte-mate on nude mice bound gp120 but of VH81X, VHQ52, and VH71	manner – F223 light chains ha r recognition of both gp120 and	we a strong homology of the autoantigen – Market HIV-1 infection and reduced V H3, we will be with the various various with the various of the various with the various variou	human (IgG1)  as noted among HIV  murine (IgG1)  was tested, MAbs from thalf way between – the ed with autoimmunity – I
	<ul> <li>F223: binds to HIV-cells – the antibody of chain to the germline has autoreactivity [C]</li> <li>Env</li> <li>References Wisnew:</li> <li>F285: F285 is V H1 infected individuals</li> <li>Env</li> <li>Vaccine Vector/Type References delReal!</li> <li>F7: Murine antibody normal mice were granti-gp120 response was a gp120 specific</li> <li>Env</li> <li>References Binley19</li> </ul>	I gp120 and to uninfective enhances HIV-1 infective enhances HIV-1 infective gene VH3-H.11 – N-1 (avacini1999)  Env ski1995, Wisnewski1996 – V-region heavy chain [Wisnewski1996] gp120 (IIIB) : chimeric GM-CSF (1999) (response to the chimer of 120 specific, MAbs frou a BALBe republic gp41 (LAI)	on in a complement-dependent inked carbohydrates are key for the strain: IIIB HIV component:  Strain: IIIB HIV component:  The construction granulocyte-mate on nude mice bound gp120 but of VH81X, VHQ52, and VH71	manner – F223 light chains har recognition of both gp120 and as of enhanced V H1 and V H4.  gp120 Adjuvant: GM-CSF acrophage colony stimulating factor were polyreactive, and from re 83 genes, a family used during 81X), previously found express no	we a strong homology of the autoantigen – Market HIV-1 infection and reduced V H3, we will be with the various various with the various of the various with the various variou	human (IgG1)  as noted among HIV  murine (IgG1)  was tested, MAbs from thalf way between – the ed with autoimmunity – I

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizing	Immunogen	Species(Isotype)
		• Fab A2: Uncharacte	rized epitope – variable r	regions sequenced [Binley199	06]		
762	Fab L9	Env References Binley1 • Fab L9: Uncharacte		egions sequenced [Binley199	no 6]	HIV-1 infection	human (IgG1 $\kappa$ )
763	G12	References delReal • G12: Murine antibo normal mice were g anti-gp120 response	1999 dy response to the chime p120 specific, MAbs fror used a high frequency of	n nude mice bound gp120 bu	macrophage colony stimulating t were polyreactive, and from re 183 genes, a family used during	econstituted mice were	half way between - the
764	G2	References delReal  G2: Murine antibod normal mice were g anti-gp120 response	1999 y response to the chimeri p120 specific, MAbs fror used a high frequency of	n nude mice bound gp120 bu	acrophage colony stimulating f t were polyreactive, and from re 183 genes, a family used during	econstituted mice were	half way between - the
765	H2	References Muller1			ed by immunization of BALBc	mice with H2 – they a	human ( $\operatorname{IgM}\kappa$ ) so react with seropositive
766	Н8	References delReal  H8: Murine antibod normal mice were g anti-gp120 response	1999 y response to the chimeri p120 specific, MAbs fror used a high frequency of	n nude mice bound gp120 bu	nacrophage colony stimulating f t were polyreactive, and from ro 183 genes, a family used during	econstituted mice were	half way between - the
767	HBW4	• HBW4: Heavy (V H	H2 – V-region heavy ch	I) chain sequenced [Moran19	93] a bias of enhanced V H1 and V	HIV-1 infection H4, and reduced V H	human (IgG1 $\lambda$ ) 3, was noted among HIV
768	HIVIG	Env <b>References</b> Nichols	gp120 2002		P	HIV-1 infection	human

No.	MAb ID	HXB2 Location	<b>Author's Location</b>	Sequence	Neutralizing	g Immunogen	Species(Isotype)
		neutralizing assay a	gainst a panel of six prima	ary isolates - both could ne	VIG derived from patients with butralize all isolates tested but the he effective concentration of NA	e NYBC-HIVIG dose req	uired for 50%
769	IVI-4G6	References Yin200 • IVI-4G6: A bi-spec	ific Ab (BFA) was made b		ts of gp41-specific MAb IVI-4Go ells [Yin2001]	Vaccine 6 and CD3-specific Mab	murine (IgG2b)  UCHT1 – the BFA
770	K14	Env References Teeuws K14: Did not bind to showed this was an K14: Reduced affin: K14: In a study of N	human (IgG1)  – competition experiments				
771	M25		Veronese1985, Watkins1		eavy and light chain in combinat	Vaccine ion, in contrast to M77 [V	murine ( $\operatorname{IgG}\kappa$ )  Watkins1996]
772	MAG 6B	<b>Donor</b> C. Y. Kang, <b>References</b> Kang 19	IDEC Inc 94 cid substitutions that reduc	Strain: HXB2 HIV comes binding 10 fold: 256 S/N	no <i>ponent:</i> gp120  7, 257 T/R or G or A, 262 N/T, 3	Vaccine 68 D/R or T, 370 E/R or	murine Q, 381 E/P, 384 Y/E, 421
773	MO28		ly was raised by in vitro s		no nant Env penv9 – the discontinuo on – this specificity is unusual ir		
774	MO30		ly was raised by in vitro s		no nant Env penv9 – the discontinuo on – this specificity is unusual ir		
775	MO43		ly was raised by in vitro s		no nant Env penv9 – the discontinuo brane region – this specificity is		
776	N2-4	Env <b>Donor</b> Evan Hersh	gp41 and Yoh-Ichi Matsumoto		no	HIV-1 infection	human (IgG1κ)

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizing	Immunogen	Species(Isotype)
			on1990b g activity for HIV-1 IIIB [F esearch and Reference Rea				
777	N70-2.3a	<ul><li>References Robinso</li><li>N70-2.3a: Broad rea</li></ul>	gp120 (dis) ason, Tulane University, La on1990a, Takeda1992 activity [Robinson1990a] for mediated enhancement		no a conformational site in the cart	HIV-1 infection  poxyl half of gp120, di	human (IgG1) stinct from 1.5e
778	P43110	References diMarzo	gp120 iosciences (Kensington, M o Veronese1992, VanCott1 ecognized denatured form		cott1995]		
779	P5-3	<ul><li>References Robinso</li><li>P5-3: No enhancing</li><li>P5-3: Poor immuno</li></ul>	gp120 and Yoh-Ichi Matsumoto on1990b, Pincus1991 g activity for HIV-1 IIIB [R toxin activity when couple esearch and Reference Rea	ed to RAC – isotype specific	ed as: IgG3lambda [Pincus1991	HIV-1 infection	human (IgG1λ)
780	T15G1	raised in an immune created to mimic the CD4-IgG2, and also G3-519 – nor did it 17b and A32 were v	with the broadest neutralize response to the oligomer enative conformation of E by anti-V3 MAbs 19b and bind C11, 23A, and M90, very strongly induced by C	on the virion surface rather inv and explore its potential d 83.1 – SOSgp140 is not r MAbs that bind to gp120 C CD4 in SOS gp140 – anti-gp	no  2 and 2F5, all have high affinity than dissociated subunits – a di as an immunogen – SOS gp140 ecognized by C4 region MAbs to 1 and C5, where it interacts with 41 MAbs that bind in the region e only gp41 epitope that is well	sulfide linked gp120-g is recognized by NAb hat neutralize only TC h gp41 – MAbs that bi n that interacts with gp	p41 (SOS gp140) was is IgG1b12, 2G12, and LA strains, G3-42 and ind CD4 inducible epitopes, 120, 7B2, 2.2B, T4, T15G1
781	T20	<ul> <li>Donor P. Earl, Nation</li> <li>References Earl 199</li> <li>T20: Generated duries</li> <li>T20: Pulse label expended ay, and that the energy of the</li></ul>	onal Institute of Allergy ar 14, Otteken1996, Sugiural ing a study of the influence periments of 4 MAbs (D20 pitope formed with a t 1/2 of 25 gp120 specific, conf	e of the oligomeric structur ), D27, T20, and T22) bindi of about 10 minutes [Ottek formation dependent MAbs	, Bethesda, MD e of Env in determining the repeng to noncleavable gp140 revea	led that these anti-CD4 up of MAbs labeled Al	BS MAbs bound with a II – all AII MAbs were

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizing	Immunogen	Species(Isotype)
782	T27	Donor P. Earl, National References Earl 1990 T27: Generated dur	onal Institute of Allergy a 94, Sugiura1999 ing a study of the influence				
					uses, and could only partially bloc		
783	T3	References Earl 199 T3: Generated durin T3: Partially confor D43, D38 and D45 T3: T3 partially cor potential [Zwick200 T3: A combination (gp140-GNC4) – gg	rmation dependent – does – MAbs in this competition mpetes with MAb Z13, bu [Olb] of gp41 fusion with the Co p41 MAbs T4, D12, T3, a	b, Yang2000 e of the oligomeric structurn't bind to short peptides, on group reacted with 9/10 at not MAb 4E10, both of GNC4 trimeric sequences and D50 bound less efficient	re of Env in determining the reper but does bind to the region spanning HIV-1 strains, not binding to JRF which bind to gp41 proximally to and disruption of the YU2 gp120-gntly to gp140-GNC4 than did pooled the trimer at greater levels than	ng 641-683 – bindi FL [Earl1997] the 2F5 epitope and gp41 cleavage site r ed sera, but T4 and	ng can be blocked by MAbs d have a broad neutralizing esulted in stable gp140 trimers D12 recognized the
784	T30	<ul><li>References Earl199</li><li>T30: Generated dur</li><li>T30: Binds in the re</li></ul>	ring a study of the influence egion 580 to 640, but does	ce of the oligomeric structs not bind to peptides span	no ure of Env in determining the repe ning this region – binding dependa a from HIV+ individuals [Earl199	s on N-linked glyco	
785	T4	References Earl 199  T4: Generated durin  T4: one of five MA neutralizes IIIB and  T4: Does not bind t [Weissenhorn 1996]  T4: MAbs T4 and T [Otteken 1996]  T4: This antibody, a both bind to the imm	94, Broder1994, Richardsing a study of the influence bs (T4, T6, T9, T10 and Tal SF2 [Broder1994] to soluble monomeric gp4 [T6 bind only to oligomer, along with 7 others (M10, munodominant region near	e of the oligomeric structure of the oligomeric structure (T35) in a competition ground (121-166) that lacks the formula and pulse chase experime (D41, D54, T6, T9, T10 and the two Cys in gp41 – m	L neric gp140 b, Otteken1996, Earl1997, Binley1 re of Env in determining the reper p that bind to a conformation-depo- usion peptide and membrane ancho nts indicate that the epitope is very and T35), can block the linear muri cost of these antibodies are oligom ocked by sera from HIV-1+ individe	toire of the Ab respendent epitope in good, only to the oligoverslow to form, require MAb D61, and the dependent — all of	onse [Earl1994] p41 and is oligomer specific – omer gp140, as does T6 niring one to two hours the human MAb 246-D, which

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizing Immunogen	Species(Isotype)
		an immune response mimic the native cor also by anti-V3 MA bind C11, 23A, and very strongly induce bind to SOSgp140, and to SOSgp140, and to SOSgp140, and to SOSgp140, and to SOSgp140 control of the total control of the	e to the oligomer on the v information of Env and ex ibs 19b and 83.1 – SOSgp M90, MAbs that bind to ed by CD4 in SOS gp140 in contrast to 2F5, which derived from SF162, a net cloop, were generated with ding of CD4i MAb 17b whom HIV-infected patients of gp41 fusion with the Co of gp41 fusion with the Co of gp41 MAbs T4, D12, T3, a equivalently to gp140(-), 40 (o-gp140) derived from	irion surface rather than dissond plore its potential as an immural 140 is not recognized by C4 regp120 C1 and C5, where it int — anti-gp41 MAbs that bind in binds to the only gp41 epitope attralization-resistant primary in hor without the gp120-gp41 center of the V3 loop is more exposed and D50 bound less efficiently and T3 and D50 recognized the R5 primary isolate US4 was	2F5, all have high affinity for the native trimer, indicated subunits – a disulfide linked gp120-gp41 (SC mogen – SOS gp140 is recognized by NAbs IgG1b1 egion MAbs that neutralize only TCLA strains, G3-eracts with gp41 – MAbs that bind CD4 inducible on the region that interacts with gp120, 7B2, 2.2B, To that is well exposed in native gp120-gp41 completed solute, and SF162AV2 a neutralization-susceptible cleavage site intact – all forms are recognized by old forms are less efficiently recognized than the clear on the fused form [Stamatatos2000] disruption of the YU2 gp120-gp41 cleavage site resto gp140-GNC4 than did pooled sera, but T4 and Date trimer at greater levels than gp140(-) [Yang2000 characterized for use as a vaccine reagent – antige cterized MAbs – T4 recognized o-gp140 [Srivastav	OS gp140) was created to 2, 2G12, and CD4-IgG2, and c-42 and G3-519 – nor did it epitopes, 17b and A32 were 4, T15G1 and 4D4, did not xes [Binley1999] isolate with 30 amino acids igomer-specific MAb T4 and yed forms by polyclonal ulted in stable gp140 trimers v12 recognized the line acute to the capture ELISA was used to
786	multiple Fabs	Env References Burton1	gp120 1991	· ·	HIV-1 infection om combinatorial library prepared from bone marro	human
707	multiple	individual [Burton19			Vaccine	
787	MAbs	Eliv	gp120	out: gp120	vaccine	murine
			va1996 sed as an immunogen, in c	contrast to gp120 bound to an a	anti-V3 MAb, few MAbs were generated and all bo 2F12, G1B8, G11F11, G9E8, G1B11, G1B6, G6F	
788	multiple MAbs	References Denisov • When gp120 was us	va1996 sed as an immunogen, in c	contrast to gp120 bound to an a		
788	multiple MAbs	• When gp120 was us to the denatured pro  Env  Vaccine Vector/Type References Denisov • When gp120-CD4 v	wa1996 sed as an immunogen, in obtein – MAbs generated w gp120 e: gp120-CD4 complex va1996 was used as an immunoge d protein – MAbs generated	contrast to gp120 bound to an agere: G1B12, G2F7, G9G8, G1  HIV component: gp120  n, in contrast to gp120 bound to an agere.	2F12, G1B8, G11F11, G9E8, G1B11, G1B6, G6F	2, G2E7 [Denisova1996]  murine  all bound better to the native

	MAb ID	HXB2 Location Author	r's Location Sequen	nce	Neutralizing	Immunogen	Species(Isotype)
		discontinuous epitope – 10 of GV4G10, GV1A8, GV10H5,	36 MAbs were mapped to 3 GV8E11, GV2H4, GV6E6	as an immunogen, it stimulated m linear epitopes and are mentioned , GV1F7, GV1G9, GV4G5, GV6 GV5C11, GV6B6, GV3C10 [Den	d elsewhere in th B12, GV1E8, C	his database, the others are:	GV5H1, GV4D5,
790	polyclonal	and IgG3 was also a more pote	ent inhibitor of viral fusion	s and IgG3 neutralization of HIV  – the IgG3 advantage was lost wheavy chain in comparison to IgG	hen only Fabs v	were considered, indicating	
791	polyclonal	References Earl2001 • Immunization of rabbits with a immunization of Rhesus maca	oligomeric gp140 induced ques with gp140 yielded st lizing activity could not be	HIV component: gp140, gp120 production of higher levels of crocking NAb against IIIB, modest against blocked by a V3 peptide – 3/4 va	oss-reactive neut gainst other lab	tralizing Abs than immuniza -adapted strains, and no NA	ation with gp120 – b activity against
792	polyclonal	References Cox1999  • 60 asymptomatic HIV-1 infect received placebo, and all were	red patients were vaccinated followed in a 5 year longit tervals in the study, and the	d with rec gp160 in alum, produce tudinal study – a mean of 78% of exaccine did not enhance ADCC 1	ed in a baculovi	82% of those receiving pla	cebo had demonstrable
							1 .8
793	polyclonal	Env gp160  Vaccine Vector/Type: modified  References Barouch2001b  Four rhesus macaques were va  The animals were infected wh  preservation of CD4+ T-cell co	(89.6) d vaccinia Ankara Strain. accinated with a modified ven challenged with pathogeounts, lower viral loads, and	: 89.6 HIV component: SIVmac raccinia Ankara (MVA) vaccine th enic SHIV-89.6P, but had potent C d no evidence of disease or morta dead by day 168 [Barouch2001b].	hat elicited stror CTL responses, ality by day 168	ng CTL responses as well as secondary NAb responses t	Rhesus macaque want: IL2/Ig s antibody responses. upon challenge, partial
793	polyclonal	Env gp160  Vaccine Vector/Type: modified References Barouch2001b  Four rhesus macaques were va The animals were infected wh preservation of CD4+ T-cell co had high viral load, progressed Env gp160 References Ahmad2001	(89.6) d vaccinia Ankara Strain. accinated with a modified ven challenged with pathoge ounts, lower viral loads, and to disease, and 2/4 were detected.	raccinia Ankara (MVA) vaccine the enic SHIV-89.6P, but had potent C d no evidence of disease or morta	c239 Gag/Pol ar hat elicited stror CTL responses, ality by day 168	nd HIV-1 89.6P Env Adjuring CTL responses as well as secondary NAb responses u after challenge—monkeys  HIV-1 infection	Rhesus macaque want: IL2/Ig s antibody responses. upon challenge, partial that got a sham vaccine human

No.	MAb ID	<b>HXB2</b> Location	<b>Author's Location</b>	Sequence	Neutralizing	Immunogen	Species(Isotype)
		M and O viruses inh			r binding or fusion – six broad tested in this study represented		
796	polyclonal	could neutralize 14 p non-neutralizing ser- key isolates, MN lab	dividuals from diverse geo primary isolates from HIV a—6/7 broadly neutralizin	-1 group M clades A-H and g sera were from African w tor), VI525 (envG/gagH, env	P attralize primary isolates to diff three O isolates, limited cross- omen, despite only 14/66 study A/gagA, R5X4) and CA9 (Gr	neutralizing sera neutry subjects being wome	ralized some isolates, and n—ability to neutralize three
797	polyclonal	References O'Haga • Microparticles were	n2000 used as an adjuvant for en	_	L t: gp120 Adjuvant: PLG+Minduced strong serum IgG response [O'Hagan2000]	•	murine, baboon
798	polyclonal	MF-59 References O'Haga • DNA vaccines of co	n2001 don-optimized Env and G	ag genes driven by CMV pro	V component: gp120 Adjuva  commotors and absorbed on to PL  e), comparable to gp120 in MF	.G microparticles were	
799	polyclonal	subsequently challer	IgG from chimpanzee seranged with the virulent SHI	V bearing the HIV-1 env DI	L  1 strains was used for passive a H12 – in vitro neutralization co h neutralization titer and limit	rrelated with protection	on in vivo [Shibata1999]
800	polyclonal			elected for study as they had	L P 1 anti-Env IgA – IgA neutralizi	HIV-1 infection	human (IgA) ed that was not directed at
801	polyclonal	References McElrat  • After 3 immunizatio persistent neutralizin	h2000 ns, 210/241 (87%) HIV-1 ng antibodies to homologo		nase II trial developed NAbs – ogous virus, measured at day		

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizin	g Immunogen	Species(Isotype)
802	polyclonal	• The murine Ab respresponse to a gp120	nez1999 onse to a chimeric of gra -vaccinia construct, but the	nulocyte-macrophage ne breadth of the Ab 1	p120 Adjuvant: GM-CSF/gp120 chi colony stimulating factor GM-CSF/g response was greater – a cellular respond Elispot [Rodríguez1999]	p120 in vaccinia was n	
803	polyclonal	Env Vaccine Vector/Type Donor Joseph Sodro References Yang200 Soluble Env trimers effectively than gp12 stabilized primers di	gp120 (YU2) e: stabilized Env trimer oski, Harvard Medical Sc 01 were created that were d 20, and Abs to the YU2 t id not neutralize primary	Strain: YU2, HXBc2 hool esigned to mimic fun rimer were cross-reac isolates outside the B		ze several primary and Bc2 stabilized trimer a	TCLA reactive strains - the
804	polyclonal	References Evans20 • Vaccination with QS	001 S21 adjuvant and rsgp120	elicited stronger and	mponent: gp120 Adjuvant: QS21, a more sustained neutralizing antibody a means to reduce the does of solubl	responses and lympho	human cyte proliferation with lowe
805	polyclonal	infection - HAART	ne development of anti-gr during primary infection	usually did not inhib	yes d during primary infection and sometithe development of weak NAb responsible to the concident with brief viremic properties.	onses against autologo	•
806	polyclonal		d an SIV mutated strain t		yes d 6th sites for N-linked glycosylation ected with the parental strain [Reitter]	_	macaque ith the mutant viruses had
807	polyclonal	titers, and neutralizing	ction of viral load to <400 ng Abs titers increased as	gainst primary isolate	yes a 12 month interval, 2/11 patients wer s US1, and CM237 – no NAB titer inc /-1 by HAART may augment immune	crease was seen to more	e readily neutralized isolate
808	polyclonal	Env  References Kaul200  Kaul et al. provide a protection [Kaul200	concise summary of the	findings concerning	yes he presence of Mucosal IgA in highly	HIV-1 exposed seronegative exposed, uninfected s	human (IgA) ubjects, arguing for a role in

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizing	g Immunogen	Species(Isotype)
809	polyclonal	References Nitayap  • A phase I/II trial wa	han2000 s conducted in 52 seron	egative Thais immunizing wi	yes  nt: gp120 Adjuvant: MF-59  th rgp120 SF2 – the vaccine wa		human loped NAb responses to the
810	polyclonal	Env Vaccine Vector/Type References Heeney The immune respon from challenge infect	gp120 (SF2)  e: recombinant protein 1998a ses induced in Rhesus metion, the other vaccinee	Strain: SF2 HIV componer nonkeys using two different is and controls became infect	yes nt: gp120, p24 Adjuvant: ISC mmunization strategies was stuced – protected animals had high roduced by circulating CD8+ T	Vaccine COM lied – one vaccine gro titers of heterologous	NAbs, and HIV-1-specific T
811	polyclonal	References Verscho  • Attempts were made homologous challen	or1999 to broaden immune res ge, with a second immu	ponses induced in Rhesus m nization with ISCOM-peptid	HIV component: gp120 Adjusted an Adjusted and Adjusted an	mals previously immu	nized that had resisted
812	polyclonal	• Immunization with a induced Abs could c rgp120CM235 and a within C2, and by rg	gp120 CM235 (CRF01) only neutralize subtype I gp120SF2 induced Abs gp120SF2 to multiple ep	induced Abs capable of neu 3 TCLA isolates – neither in to regions within C1, V1/V2 itopes within C3, V4, and C4	yes M235 (CRF01) HIV componer tralizing TCLA subtype E (CRI munogen induced Abs capable , V3, and C5, but unique respon – CM235 baboon sera bound 3 were within two to threefold for	F01) and subtype B is of neutralizing primarises were induced by the to 12-fold more stro	olates, while rgp120SF2 ry HIV-1 isolates – both rgp120CM235 to epitopes ngly than the SF2 baboon ser
813	polyclonal	Env  Vaccine Vector/Type References Barnett2  • SF162ΔV2 is a virus neutralization—whe neutralizing Ab titer SF162ΔV2, but not 91US056(R5), 92US immunized macaque	gp140 (SF162DeltaVer: DNA with CMV pron 2001 s that has a 30 amino acin incorporated into a co s against SF162 than did intact SF162, was used a 5714(R5), 92US660(R5)	notor Strain: SF162, SF162, SF162, dids deletion in the V2 loop the don-optimized DNA vaccined SF162 itself, and Abs that das the immunogen—Control (2), 92HT593(R5X4), and BZ15056(R5), 92US714(R5), 92	yes  2AV2 HIV component: gp140  at does not abrogate its infective with a CMV promoter and delicross-neutralized non-homologo MAbs 2F5 and 2G12 could neufor(R5X4), while after the first puse660(R5) and ADA(R5), but no	Vaccine  Adjuvant: MF-59C  ity but renders it high vered by gene gun, SI ous primary isolates we tralize all of the follow protein boost, the sera	rabbit, Rhesus macaque (IgG)  ly susceptible to F162ΔV2 gave higher ere obtained only when wing primary isolates: from two SF162ΔV2
		<u>U</u>					

No.	MAb ID	HXB2 Location	Author's Location	Sequence		Neutralizing	Immunogen	Species(Isotype)
				anti-Gag antibodies durin even in a backdrop of de				It of the loss of T-cell help and to the CD4 molecule
815	polyclonal	References Beddow • rgp120 derived from positive subjects – v neutralize homologo	s1999 a R5X4 subtype B virus accinee sera had more pous ous or heterologous virus	otent responses to linear V	I to vaccinate healthy V1/V2 and V3 epitopor F-cell lines – neutraliz	es than did the cation activity	sera from HIV-1+ ir was lost after re-ada	human vere compared with HIV-1 adividuals, but could only ptation to growth in PBMCs –
816	polyclonal	References Wagner  • A VLP is a non-infe linear domains – Ga response occurred or	1998b ctious virus-like particle g and Env specific CTL	were stimulated in each cot V3+CD4 – despite the	Pr55 gag – macaque ase, and Ab response	s were immun to gag and gp	ized with VLPs bound	Rhesus macaque and to either gp120 or V3+CD4, but the gp120 neutralizing sted by intervenous challenge
817	polyclonal	<ul><li>References Shiver 19</li><li>DNA vaccinations of</li></ul>	f BALBc mice with a gp				Vaccine ive response with Th	murine 11-like secretion of gamma
818	polyclonal	References Kim199 • A gag/pol, vif or CM dramatic increase in	7b IN160 DNA vaccine, wh	roliferative responses in	on with the plasmid e			murine ules B7 and IL-12, gave a CMN160 DNA vaccinated
819	polyclonal	Env References Bradney • Sera were taken from contemporary isolate	n long term non-progress	sors and evidence for vira	ıl escape was noted –	P serum could n	HIV-1 infection	human ologous isolates, but not
820	polyclonal	References Belshe1	998 by a HIV-1 gag/env in c	rgp120 boost Strain: Strain: Strain: Strain: Strain: Strain:	-	_	Vaccine n rgp120 against lab	human strains – 1/8 primary isolates

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizing	Immunogen	Species(Isotype)
821	polyclonal	References Belshe2 • A phase 2 trial was of protease (LAI), either	001 conducted in 435 voluntee	ers with vCP201, a canary poost – NAbs against MN v	L, MN, SF2 HIV component: Ga pox vector carrying gp120 (MN inverse obtained in 56% of those where	n vCP201, and SF2 in th	ne boost), p55 (LAI) and
822	polyclonal		rs to be a B cell superantig	gen that binds to members in the V_H region were co	of the V_H3 Ig gene family—the itical [Neshat2000].	gp120 binding site was	human (Ig V_H3) localized to the Fab
823	polyclonal	References Bai2000  • Murine rsgp41 antis	era recognized a common	HIV component: gp41 epitope on human IFN $\alpha$ (	aa 29-35 and aa 123-140) and on may be due to a cross-reactive g	, .	murine (IgG) and aa 125-142),
824	polyclonal	References Ross200 • gp120 was fused with	)1 th murine complement pro avidity maturation, after t	otein C3d in a DNA vaccir	: gp120 Adjuvant: C3d fusion e to enhance the titers of Ab to E LB/c mice with DNA on a gold b		
825	polyclonal	References Cherpel  Two animals were in gp140 envelope with lymphocytes were d 1 to 4 logs lower that HIV-1 SF162ΔV2 g of their CD8+ T lym	is 2001b, Cherpelis 2001a mmunized both intraderm an intact gp120-gp41 cleepleted in the animals and in those in the unvaccinate p140 envelope was used in those the p140 envelope and challenged	ally and intramuscularly at eavage site, and both devel I they were challenged wited animals [Cherpelis2001 in a DNA-prime plus protein with pathogenic SHIV(SI	weeks 0, 4, and 8 with a codon of oped lymphoproliferative response a SHIV162P4 – at peak viremia, b] n-boost vaccination methodology (162P4)—the vaccinated macaquintigens relative to non-vaccinated	optimized DNA vector exses and potent neutralizing plasma viral levels in the vin Rhesus macaques, the shad lower peak virem	expressing the SF162V2 ng Abs – CD8+ T e vaccinated animals were ne animals were depleted ia, rapidly cleared virus
826	polyclonal				P g ARV, and CD4 levels are correl	HIV-1 infection ated with HIV-1 specific	human  NAbs – no correlation
827	polyclonal	Env <b>Vaccine</b> <i>Vector/Type</i> <b>References</b> Bai2000	gp41 (539–684 BH10) c: recombinant protein I			Vaccine	murine (IgG)

No.	MAb ID	HXB2 Location	<b>Author's Location</b>	Sequence	Neutralizir	g Immunogen	Species(Isotype)
		There is a common	n epitope in HIV-1 gp41, a	nd IFNalpha and IFNbeta [B	ai2000]		
828	polyclonal	Abs – IgM Fab rea	ibody analysis by phage di activity is observed through cting a lack of maturation	nout the entire sequence of H	no monstrated that gp120 in HIV- IV-1 IIIB gp120 and is charac utralizing activity was observ	terized by low affinity l	binding and near germline
829	polyclonal	References Loche • High risk voluntee	er1999 ers were vaccinated with SI evere never high and took 6		L at: gp120 ases were studied – SF2 neutra a to develop – viral loads were	_	
830	polyclonal	References LaCas In this study, immufusion by formaldo CD4- and CCR5-t A retraction was p	sse1999, Nunberg2002 unogens were generated the chyde-fixation of co-cultur ransgenic mice that neutral	at were thought to capture trees of cells expressing HIV-1 lized 23/24 primary isolates (2002) noting that an unknow	yes gp120 ansient envelope-CD4-corecep Env and those expressing CD- from clades A-E [LaCasse199 n cytotoxic effect of these cor	4 and CCR5 receptors - 9]	- these cells elicited NAbs in
831	polyclonal	who were classifie and four subtype E likely to achieve so	ore HAART therapy and aft d as HAART failures – V3 3 clinical isolates were test	peptide antibody binding tit ed – subjects with strong ant	P measured in 8 individuals that ers to the B-consensus and M i-V3 and NAb humoral immut [AART – HIV-specific Ab res	N and SF2 variants, and ne responses before star	l neutralization of HIV-1 MN rting HAART were more
832	polyclonal	contemporaneous	m nonprogressors(LTNP) autologous isolate than we	re sera from short-term nonp	P terologous primary isolates ar rogressors and normal progres ) weeks, and not detected in a	ssors – in 4 individuals	followed from acute
833	polyclonal	Env <b>References</b> Moog	1997		P	HIV-1 infection	human

No.	MAb ID	<b>HXB2</b> Location	<b>Author's Location</b>	Sequence	Neutralizing	Immunogen	Species(Isotype)
		NAbs were not detected one year	cted in sera collected at the	e same time as the viruses d were highly specific to	were sampled early after sero-constant were isolated – NAbs detected as the virus present at the early phase	gainst the seroconversi	ion autologous strains were
834	polyclonal	Env			yes	HIV-1 infection	human
		interuption after 1-3 to HIV-1, presumabl rapidly appeared and absence of detectabl notion that virus-spe	years, and Env and Gag A years, and Env and Gag A y by limiting the concentral d correlated with spontane e NAbs, suggesting that concific B-cell priming, comb	Abs were low or undetector ration of viral antigens ne ous down-regulation of v ellular immune responses bined with CD8+ CTL in	ion, NAbs to autologous strains we'd by ELISA indicating, that early eded to drive B-cell maturation—iremia—prolonged control of virealone can control viremia under caluction, may be beneficial for HIV f virus transmission [Montefiori20]	HAART suppresses the suppresses that a patients with a virtual after stopping treatment after stopping treatment of the suppression of the suppres	he normal antibody response al rebound autologous NAbs atment persisted in the - these results support the
835	polyclonal	Env				HIV-1 infection	human (IgG)
		specifically recogniz	raries were screened using ted by Abs from HIV-1 in	fected individuals – the se	ubjects to identify mimotopes, per ora of simian SHIV-infected monk atralized HIV-1 isolates IIIB and I	eys also recognized th	1 1
836	polyclonal	Env Vaccine Vector/Type References Scala19	e: peptide HIV compone.	nt: mimotopes	L	Vaccine	murine (IgG)
		specifically recognize	zed by Abs from HIV-1 in	fected individuals – the se	ubjects to identify mimotopes, pe era of simian SHIV-infected monk atralized HIV-1 isolates IIIB and I	eys also recognized th	
837	polyclonal	Env Vaccine Vector/Type References Lebedev	-	component: Env, Gag	Adjuvant: Freund's adjuvant	Vaccine	murine (IgG)
		• Virus-like particles (	(VLPs) in the form of sphe		dsRNA enveloped in a polysacchand induced specific Abs against I		
838	polyclonal	Env	2002		P	HIV-1 infection	human
					lasma is observed, especially in A	African women, who te	nded to have
839	polyclonal	Env	10000		L	HIV-1 infection	human (IgG)
					%) in association with HIV-specifi	c IgG NAbs indicating	g that the HIV in the plasma

	MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizing	Immunogen	Species(Isotype)
840	polyclonal	Env <b>References</b> Kimura	Env 2002		P	HIV-1 infection	human (IgG)
		therapy, increasing i	in one patient, and declining	ng in one patient – 3/6 patien	in 13/19 HIV+ patients at init ts with no detectable NAb at tl bounds (blips) [Kimura2002]		
341	polyclonal	Env			P	HIV-1 exposed seronegative	human (IgA)
			a HIV-specific IgA that ca	n neutralize primary isolates negative (HEPS) individuals	is present saliva (11/15 tested) [Devito2000b]	and plasma (11/15) an	d cervicovaginal fluid
342	polyclonal	Env			P	HIV-1 exposed seronegative	human (IgA)
		transwall system tha	l tract, saliva and plasma f at provides a tight epithelia	al cell layer—50% of the IgA	ntly seronegative (HEPS) indiv samples studied were able to aal acquisition of HIV-1 [Devi	inhibit transcytosis of a	
343	polyclonal	Env			P	HIV-1 exposed seronegative	human (IgA)
		neutralize a B, A an	ne saliva, genital tract, and		sed persistently seronegative (lass of HIV across a transwall m		
		[Broliden2001]			ъ	HIV-1 exposed	
344	polyclonal	[Broliden2001] Env			P	seronegative	human (IgA)
44	polyclonal	Env  References Devito2  • IgA isolated from the cross-clade neutralize	ne saliva, genital tract, and zation of primary isolates	(A, B, C, D, and CRF01) - 6	sed persistently seronegative (10 HEPS individuals that wer atralize clade A and B primary	seronegative HEPS) Kenyan sex wor e persistently exposed t	kers mediated broad o a stable HIV+ B clade
	polyclonal	Env  References Devito2  IgA isolated from the cross-clade neutralize infected partner sho	ne saliva, genital tract, and zation of primary isolates	(A, B, C, D, and CRF01) - 6	sed persistently seronegative (170 HEPS individuals that wer	HEPS) Kenyan sex wor e persistently exposed to visolates, but not clades HIV-1 exposed	kers mediated broad o a stable HIV+ B clade
344		Env  References Devito2  IgA isolated from the cross-clade neutralize infected partner shoto [Devito2002]  Env  References Mazzol  Serum HIV-specifice productively infected	ne saliva, genital tract, and zation of primary isolates wed less breadth of neutra i1999  IgA is present in highly end individuals and exposed	(A, B, C, D, and CRF01) – 6. lization, and were able to new exposed persistently seronegal seronegatives at similar titer	sed persistently seronegative (I /10 HEPS individuals that wer atralize clade A and B primary	HEPS) Kenyan sex wor re persistently exposed to visolates, but not clades HIV-1 exposed seronegative absence of serum IgG- neutralizing activity, 2 of	kers mediated broad to a stable HIV+ B clade to C, D, or CRF01 human (IgA) - serum IgA can be found i
		Env  References Devito2  IgA isolated from the cross-clade neutralize infected partner shoto [Devito2002]  Env  References Mazzol  Serum HIV-specifice productively infected	ne saliva, genital tract, and zation of primary isolates wed less breadth of neutra i1999  IgA is present in highly end individuals and exposed	(A, B, C, D, and CRF01) – 6. lization, and were able to new exposed persistently seronegal seronegatives at similar titer	red persistently seronegative (I/10 HEPS individuals that wer attralize clade A and B primary  P  Tive individuals (HEPS) in the s – 5/15 sera from HEPS had in	HEPS) Kenyan sex wor re persistently exposed to visolates, but not clades HIV-1 exposed seronegative absence of serum IgG- neutralizing activity, 2 of	kers mediated broad to a stable HIV+ B clade to C, D, or CRF01 human (IgA) - serum IgA can be found i

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizing	Immunogen	Species(Isotype)
		HIV-specific anti-gr	o160 IgA is present in cerv	rical lavage from 6/13 HI	V-exposed seronegative Thai fema	le sex workers [Beyr	er1999]
847	polyclonal	References Chakral • A modified gp140 (	gp140ΔCFI), with C-term	mutations intended to mi	mic a fusion intermediate and stab		
			erminants as defined by bin n mice injected with a DNA		os $2F5$ , $2G12$ , $F105$ , and $b12$ , and $c02$ ].	enhanced humoral in	nmunity without diminishing
848	polyclonal	with GMCSF References Liao200 • HIV-envelope peption	2 des coupled to α2-macrog	lobin were much more in	4-V3 Adjuvant: Freund's adjuvant: Freund's adjuvant: Freund's adjuvant: Adjuvant: Freund's adjuvant: Freund'	nonophosphoryl lipid	
849	polyclonal	References Fouts20 • gp120-CD4 and gp1 using a chimeric HI	002 140-CD4 complexes were V-BAL gp120 with a mim	used for i.m. vaccination etic peptide that induces a	P  ain: IIIB HIV component: gp120  of rhesus macaques and neutralizi a CD4-triggered mimetic structure subtypes but did not react as well a	ng Ig was recovered = the sera and affinit	using affinity chromatography y purified Ab were broadly
850	polyclonal		iring primary infection wa		P s and had different effects on NAb nst autologous virus were induced		human e cases, α-Env Abs were
851	polyclonal	particles in the presonaive animals, with neutralizing Abs we	earance in the circulation in ence and absence of virus- half-lives ranging from 13 are present to help to remove	specific antibodies was me to 26 minutes, but clearate ve virions from the blood	L ing a continuous infusion of cell-fa neasured – the clearance of physica nce cold be acheived with a half la [Igarashi1999] high neutralization titer and limite	al and infectious viralife of 3.9-7.2 minutes	l particles is very rapid in s when chimpanzee
852	polyclonal	<ul><li>References Gupta2</li><li>Vaccine trial protocosafe and immunoger</li></ul>	002 ol 022A in 150 HIV-1 unir	nfected adults (130 compl nteers – NAb responses w	L 120 MN and gp41 LAI, rgp120 SF leted the study) showed high titer avere detected in 95% of vaccinees, rs [Gupta2002]	ALVAC vaccine in co	ombination with gp120 was

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizing	Immunogen	Species(Isotype)
853	101-342	Ab type C-term References Scheffe	el1999		D) HIV component: gp160 tested for MAb reactivity [Scheffe	Vaccine	murine (IgG2a $\kappa$ )
854	101-451	Env  Vaccine Vector/Typ  Ab type C-term  References Scheffe	gp120 (498–527 HAM112, O group) ee: recombinant protein	Strain: HAM112 (group 0	D) HIV component: gp160 tested for MAb reactivity [Scheffe	Vaccine	murine (IgG2b κ)
855	120-1	Env Vaccine Vector/Typ Ab type C-term References Chanhl	gp120 (503–532) ee: peptide 1986, Dalgleish1988		no	Vaccine	murine (IgMκ)
856	212A	References Robins  212A: Mutations th  212A: Binding enh  212A: Study shows bound monomer, di  212A: Binds efficie the 19 C-term amin  212A: Does not net  212A: Does not cor  212A: A panel of M	nat inhibit binding: C1 (4 anced by anti-V3 MAb 5 is neutralization is not pred not bind oligomer or neutry to sgp120 but not so a acids are deleted [Wyantralize TCLA strains or mpete with binding of MAbs were shown to bind	loore1996, Binley1997a, F 5 W/S) and V5 (463 N/D) G11 – reciprocal inhibition dicted by MAb binding to eutralize JRFL [Fouts1997] sluble gp120+gp41, sugges tt1997] primary isolates [Parren19 Ab generated in response the with similar or greater affe	ting its gp120 epitope is blocked b	80 LD/DL) and C5 (49) cociated with oligomeric y gp41 binding – does (llivan1998b) les to a deglycosylated	or variable loop deleted
857	522-149	Ab type C1 Done References Moore  522-149: Binding is (position 61, LAI) §  522-149: Does not  522-149: A panel of	gp120 amino acid substit neutralize JR-FL nor blo of MAbs were shown to b	ey1998, Yang2000 dies M91 and 1C1 – mutua ution – other C1 antibodies ck gp120 interaction with ind with similar or greater	no  Il binding-inhibition with anti-C1 as enhance binding to gp120 [Moor CCR-5 in a MIP-1beta-CCR-5 con affinity and similar competition produces a structure closely approx	e1996] npetition study [Trkola rofiles to a deglycosyla	1996a] ted or variable loop deleted

No.	MAb ID	HXB2 Location	<b>Author's Location</b>	Sequence	Neutra Neutra	lizing Immunogen	Species(Isotype)
		trimers (gp140-GNC F91) and CD4i (17b gp140-GNC4 glycop	(A) that preserve and expos and 48d) recognized gp14	se some neutralizing ep 0-GNC4 as well as gp1 ompared to gp120 – Ma	ences and disruption of the Y itopes while occluding some 20 or gp140 – non-neutralizi Abs directed at the extreme te	non-neutralizing epitopes – ( ng MAbs C11, A32, 522-149	CD4BS MAbs (F105 and P), M90, and #45 bound to the
858	L19				MAb L72 was used for the s	HIV-1 infection election of Fabs – six N-tern	human Fab (IgG1) n Fabs, L19 L34, L35, L52,
859	M90	Env Vaccine Vector/Type Ab type C1 Donor References diMarzo M90: Reactive only M90: Reacted with l M90: Reciprocal inf [Moore1996] M90: Binds efficient the 19 C-term amino M90: A panel of MA gp120 protein ( Delt M90: The MAbs wit in an immune respon mimic the native cor also by anti-V3 MAl bind C11, 23A, and very strongly induce bind to SOSgp140, i M90: A combination trimers (gp140-GNC F91) and CD4i (17b gp140-GNC4 glycop	gp120  r: protein HIV component r Fulvia di Marzo Veronese veronese1992, DeVico19 with native gp120, so bind both non-reduced (but not nibition of binding of other tly to sgp120 but not solub veronese1992, DeVico19 with native gp120, so bind both non-reduced (but not nibition of binding of other tly to sgp120 but not solub verone shown to bind we verone shown to show the verone shown to bind we verone shown to bind vero	et: Env e 195, Moore1996, Ditzel ls to a discontinuous ep denatured) covalently of anti-C1 MAbs – inhib ole gp120+gp41, sugges a C1 positions 31-82, an ith similar or greater aff itch a core protein produ g activity, IgG1b12, 2G virion surface rather the lore its potential as an i 40 is not recognized by p120 C1 and C5, where anti-gp41 MAbs that b inds to the only gp41 e GNC4 trimeric sequence se some neutralizing ep 0-GNC4 as well as gp1 ompared to gp120 – MA	no 1997, Wyatt1997, Binley1999; itope – reacts with multiple stross-linked gp120-CD4 compits CD4 binding site MAbs – sting its gp120 epitope is bloc	trains [diMarzo Veronese199] enhances binding of V2 MA ked by gp41 binding – does a profiles to a deglycosylated ximating full length folded mity for the native trimer, indistribution of the sulfide linked gp120-gp41 (Secognized by NAbs IgG1b12 lize only TCLA strains, G3-4 bis that bind CD4 inducible els with gp120-gp41 complexed gp120-gp41 cleavage site resonn-neutralizing epitopes – Ong MAbs C11, A32, 522-149	bs G3-4 and SC258  not bind to HXBc2 gp120 if or variable loop deleted core nonomer [Binley1998] licating that they were raised (OS gp140) was created to 2, 2G12, and CD4-IgG2, and 42 and G3-519 – nor did it pitopes, 17b and A32 were 4, T15G1 and 4D4, did not es [Binley1999] sulted in stable gp140 CD4BS MAbs (F105 and 2, M90, and #45 bound to the
860	MAG 104	Ab type C1 Donor References Kang 19 • MAG 104: Only obs		tion that reduces bindin	no omponent: gp120 g: 88 N/P and 106 E/A – doe	Vaccine s not bind to C1 region 20 m	murine ner peptides, tentative

No.	MAb ID	HXB2 Location	Author's Location	Sequence		Neutralizing	Immunogen	Species(Isotype)
861	MAG 45 (#45)	Vaccine Vector/Type Ab type C1 Dono	gp120 e: sCD4-gp120 complex r C. Y. Kang, IDEC Inc 94, Moore1996, Wyatt19		HIV component: gp120	no	Vaccine	murine
	•		erved amino acid substitu nsitive anti-C1 MAb [Ka		binding: 88 N/P – does no	t bind to C1 regi	on 20 mer peptides	s, tentative classification
		anti-CD4 binding si	te MAbs [Moore1996]			_	•	/3 5G11 – inhibits binding of gp41 binding – does not bind to
		HXBc2 gp120 if the MAG 45: Called #4 stable gp140 trimers (F105 and F91) and bound to the gp140-	2 19 C-term amino acids, 5 – a combination of gp4 5 (gp140-GNC4) that pres CD4i (17b and 48d) reco	in conjunction w 1 fusion with the serve and expose ognized gp140-G duced levels com	ith C1 positions 31-50, are GNC4 trimeric sequences some neutralizing epitopes NC4 as well as gp120 or gpapared to gp120 – MAbs di	deleted [Wyatt1] and disruption of while occluding p140 – non-neutr	997] f the YU2 gp120-g g some non-neutral calizing MAbs C11	gp41 cleavage site resulted in izing epitopes – CD4BS MAbs , A32, 522-149, M90, and #45 120 C1 (135/9 and 133/290) and
862	MAG 95	Ab type C1 Dono References Kang 19 MAG 95: Only obse	<b>r</b> C. Y. Kang, IDEC Inc 94	tion that reduces	HIV component: gp120 binding: 88 N/P – does no	no t bind to C1 region	Vaccine on 20 mer peptides	murine s, tentative classification
863	MAG 97	Ab type C1 Dono References Kang 19 MAG 97: Only obse	r C. Y. Kang, IDEC Inc 94	tion that reduces	HIV component: gp120 binding: 88 N/P – does no	no ot bind to C1 regio	Vaccine On 20 mer peptides	murine s, tentative classification
864		References Broder 1  There are two HIV-		002b ne binds to gp41,	one to gp120	onformation-dep	Vaccine endent epitope in g	murine (IgG)  gp41 and is oligomer specific –
	•	T9: This antibody, a both bind to the imm	long with 7 others (M10, nunodominant region nea	r the two Cys in		odies are oligom	er dependent – all o	the human MAb 246-D, which of the MAbs are reactive with

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizi	ng Immunogen	Species(Isotype)
		HIV entry – preincu bundles form prior t	bation of E/T cells at 31.5 to fusion – the preincubation	C enabled polyclonal anti- on 31.5 C step did not alter	B1.5 C) to re-evaluate the poter -N-HR Ab and anti-six-helix b the inhibitory activity of neut ability to inhibit fusion [Goldin	oundle Abs to inhibit fusion ralizing Abs anti-gp41 2F	on, indicating six-helix
865	p7	Env <b>Ab type</b> C1	gp120 (HXBc2)			HIV-1 infection	human Fab (IgG1)
		epitopes, p7, p20, and M/S and 493 P/K er	zed on solid phase by cap nd p35 – a C1 W/S substit nhanced binding – compet	ution at position 45 abolish	or selection of Fabs – three not need binding, a Y/D at position and G1- ad 212A, but not M91 and G3-	45 reduced binding, and 0	
866	L100	<ul> <li>L100: Does not neu</li> <li>L100: gp120 immol for C1 and C2 – gp1</li> </ul>	bilized on solid phase by c 120 C1 substitutions 69 W	rimary isolates [Parren1997 capture with sCD4 and then Land 76 P/Y abolish L10	[c] masked with Fab p7 allowed 0 binding, and C2 substitution 99, but not M85, 212A, and M	s 252 R/W, 256 S/Y, 262	N/T and 267 E/L abolish o
867	2/11c (211c, 2.11c, 211/c, 2-11c)	References Moore I  2/11c: Inhibits bind similar reactivity pa  2/11c: Called 211c  2/11c: Study shows monomer, did not b  2/11c: Called 2.11c could not be achieve  2/11c: Binds efficie the 19 C-term amine  2/11c: Called 211/c loop deleted core gr [Binley1998]	ing of anti-C1, -C5, -C4, -ttern to A32, but less crost-does not neutralize JR-F neutralization is not predicted ind oligomer or neutralize - One of 14 human MAb and at a maximal concentration of acids, in conjunction with a panel of MAbs were soligonarios.	1997a, Fouts 1997, Li 1997, V3 and anti-CD4 binding sereactive and lower affinite. L nor block gp120 interact cted by MAb binding to JR JRFL [Fouts 1997] setsted for ability to neutration of 67 mug/ml [Li 1997] able gp120+gp41, suggesting C1 positions 31-74, are deshown to bind with similar	ng its gp120 epitope is blocked deleted [Wyatt1997] or greater affinity and similar of the protein produces a structure	f some anti-V2 and CD4i among known human and ta-CCR-5 competition stu associated with oligomeric thich expressed HIV-1 IIII by gp41 binding – does competition profiles to a	rodent MAbs [Moore1996 dy [Trkola1996a] c env binding – 2/11c boun B env – 50% neutralization not bind to HXBc2 gp120 deglycosylated or variable
868	A32	Env Ab type C1-C4 D References Moore1	gp120 onor James Robinson, Tu 994b, Wyatt1995, Moore	lane University, New Orlea	no nns, LA, USA 16, Trkola1996a, Binley1997a,	HIV-1 infection Fouts1997, Burton1997,	human (IgG1) Wyatt1997, Boots1997,

Parren1997c, Sullivan1998b, Binley1998, Binley1999, Yang2000, Yang2002, Grundner2002

• A32: Reacted with virtually every gp120 monomer of every clade tested, most conserved gp120 monomer epitope known [Moore1994b]

**HIV Antibodies Tables** 

No. MAb ID HXB2 Location Author's Location Sequence Neutralizing Immunogen Species(Isotype)

- A32: Epitope is better exposed upon CD4 binding to gp120 binding of A32 enhances binding of 48d and 17b studies using a V1/V2 deletion mutant demonstrated that enhanced binding of 48d in the presence sCD4 involves the V1/V2 loops, with more significant involvement of V2 [Wyatt1995]
- A32: Review: epitope is distinct from CD4BS MAbs, 48d and 17b, and 2G12 [Moore1995b]
- A32: Reciprocal inhibition of binding of anti-C1, -C5, -C4, -V3 and anti-CD4 binding site MAbs induces binding of some anti-V2 and sCD4 inducible MAbs (48d and 17b) very similar competition pattern to 2/11c, A32 and 211/c are unique among known human and rodent MAbs [Moore1996]
- A32: Not neutralizing binds domains that interact with gp41 MIP-1alpha binding to CCR-5 expressing cells can be inhibited by gp120-sCD4 and binding of A32 does not block this inhibition [Wu1996]
- A32: Does not neutralize JR-FL, or any strain strongly partial inhibition of gp120 interaction with CCR-5 in a MIP-1beta-CCR-5 competition study [Trkola1996a]
- A32: Study shows neutralization is not predicted by MAb binding to JRFL monomeric gp120, but is associated with oligomeric env binding A32 bound
  monomer, did not bind oligomer or neutralize JRFL [Fouts1997]
- A32: Review [Burton1997]
- A32: Binds efficiently to sgp120 but not soluble gp120+gp41, suggesting its gp120 epitope is blocked by gp41 binding [Wyatt1997]
- A32: Does not neutralize TCLA strains or primary isolates [Parren1997c]
- A32: Abs that recognize discontinuous epitopes can identify mimotopes from a phage peptide display library A32 has a unique epitope involving mostly C2 but C1 and C4 contribute six quite variable phage inserts were recognized, with a consensus of LPWYN a central Trp was the most conserved element, consistent with W427 being an important residue for binding gp120 [Boots1997]
- A32: Enhances binding of CD4i MAbs 17b and 48d, and a MAb generated in response to gp120-CD4 complex, CG10 [Sullivan1998b]
- A32: A panel of MAbs were shown to bind with similar or greater affinity and similar competition profiles to a deglycosylated or variable loop deleted core gp120 protein (Delta V1, V2, and V3), thus such a core protein produces a structure closely approximating full length folded monomer [Binley1998]
- A32: The MAbs with the broadest neutralizing activity, IgG1b12, 2G12 and 2F5, all have high affinity for the native trimer, indicating that they were raised in an immune response to the oligomer on the virion surface rather than dissociated subunits a disulfide linked gp120-gp41 (SOS gp140) was created to mimic the native conformation of Env and explore its potential as an immunogen SOS gp140 is recognized by NAbs IgG1b12, 2G12, and CD4-IgG2, and also by anti-V3 MAbs 19b and 83.1 SOSgp140 is not recognized by C4 region MAbs that neutralize only TCLA strains, G3-42 and G3-519 nor did it bind C11, 23A, and M90, MAbs that bind to gp120 C1 and C5, where it interacts with gp41 MAbs that bind CD4 inducible epitopes, 17b and A32 were very strongly induced by CD4 in SOS gp140 anti-gp41 MAbs that bind in the region that interacts with gp120, 7B2, 2.2B, T4, T15G1 and 4D4, did not bind to SOSgp140, in contrast to 2F5, which binds to the only gp41 epitope that is well exposed in native gp120-gp41 complexes [Binley1999]
- A32: A combination of gp41 fusion with the GNC4 trimeric sequences and disruption of the YU2 gp120-gp41 cleavage site resulted in stable gp140 trimers (gp140-GNC4) that preserve and expose some neutralizing epitopes while occluding some non-neutralizing epitopes CD4BS MAbs (F105 and F91) and CD4i (17b and 48d) recognized gp140-GNC4 as well as gp120 or gp140 non-neutralizing MAbs C11, A32, 522-149, M90, and #45 bound to the gp140-GNC4 glycoprotein at reduced levels compared to gp120 MAbs directed at the extreme termini of gp120 C1 (135/9 and 133/290) and C5 (CRA-1 and M91) bound efficiently to gp140-GNC4 [Yang2000]
- A32: Uncleaved soluble gp140 (YU2 strain, R5 primary isolate) can be stabilized in an oligomer by fusion with a C-term trimeric GCN4 motif or using a T4 trimeric motif derived from T4 bacteriophage fibritin stabilized oligomer gp140 delta683(-FT) showed strong preferential recognition by NAbs IgG1b12 and 2G12 relative to the gp120 monomer, in contrast to poorly neutralizing MAbs F105, F91, 17b, 48d, and 39F which showed reduced levels of binding, and C11, A32, and 30D which did not bind the stabilized oligomer [Yang2002]
- A32: HIV-1 gp160deltaCT (cytoplasmic tail-deleted) proteoliposomes (PLs) containing native, trimeric envelope glycoproteins from R5 strains YU2 and JRFL, and X4 strain HXBc2, were made in a physiologic membrane setting as candidate immunogens for HIV vaccines 2F5 bound to gp160deltaCT with a reconstituted membrane ten-fold better than the same protein on beads anti-CD4BS MAbs IgG1b12 and F105, A32 (C1-C4), C11 (C1-C5), and 39F (V3) MAbs bound gp160deltaCT PLs indistinguishably from gp160deltaCT expressed on the cell surface non-neutralizing MAbs C11 and A32 bound with lower affinity than NAb IgG1b12 the MAb 17b was sCD4 inducible on gp160deltaCT PL [Grundner2002]

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizi	ing Immunogen	Species(Isotype)
369	C11 (c11)	Env	gp120		no	HIV-1 infection	human
			Oonor James Robinson, Tu				
				oore1996, Trkola1996a, Wu199	6, Binley 1997a, Fouts 199	7, Wyatt1997, Parren1997	c, Sullivan1998b,
		•	002, Grundner2002, Basm				
				W/S, 88 N/P) – V5 (463 N/D) –	and C5 (491 I/F, 493 P/K	and 495 G/K) and enhance	ee binding: C1 (36 V/L) –
			E/SM) – and DeltaV1/V2/				
				11 – reciprocal inhibition with			
				omplexes to inhibit MIP-1alpha			ā
				120 interaction with CCR-5 in	-		
				cted by MAb binding to JRFL r	nonomeric gp120, but is a	ssociated with oligomeric	Env binding – C11 bound
			oind oligomer or neutralize	= = = = = = = = = = = = = = = = = = = =	100 % 11 1 1	1 411' 1' 4' 1	.c cp4
				ble gp120+gp41, suggesting its		by gp41 binding – partial	re-exposure ii sCD4 was
				e 19 C-term amino acids are de imary isolates [Parren1997c]	eted [wyatt1997]		
				generated in response to gp12	O CD4 complex CC10 [S	ullivon 1000h]	
				ng activity, IgG1b12, 2G12 and		=	enting that they were raise
				e virion surface rather than diss			
		gnized by NAbs IgG1b12,					
				ol40 is not recognized by C4 re			
				gp120 C1 and C5, where it into			
				– anti-gp41 MAbs that bind in			
				binds to the only gp41 epitope			
				R5 primary isolate) can be stab			
				age fibritin – stabilized oligom			
				nomer, in contrast to poorly neu			
				ot bind the stabilized oligomer		, , ,	
				deleted) proteoliposomes (PLs)		c envelope glycoproteins t	From R5 strains YU2 and
				physiologic membrane setting	_		
				the same protein on beads – a			
				nguishably from gp160deltaCT			
				MAb 17b was sCD4 inducible of			
			_	CXCR4 binding site using CXC			MPLs) to reduce
				n the V3 loop and the beta19 st			
		1 01		MAbs 17b (CD4i) and F105 (			
				CR5 on PMPLs [Basmaciogull			
70	L81	Env	gp120	<del>_</del>	no	HIV-1 infection	human (IgG1)
-	-		OI .		== **		(-6-1)

Ab type C1-C5

References Ditzel1997, Parren1997c

• L81: gp120 immobilized on solid phase by capture with anti-CD4 BS MAb L72 was used for selection of Fabs – L81 binding is abolished by C1 substitution 45 W/S, C5 substitution 491 I/F, and C3 substitution L/A [Ditzel1997]

No.	MAb ID	HXB2 Location	<b>Author's Location</b>	Sequence	Neutralizing	Immunogen	Species(Isotype)
		• L81: Does not neutr	alize TCLA strains or pri	mary isolates [Parren1997c]			
871	2F19C	Ab type C3 References Matsush		APGK 2 ROD  on the cell surface, APGK is	no the core binding region [Mats	Vaccine ushita1995]	murine
872	B2C	Ab type C3 References Matsush		HYQ (core) 2 ROD or HIV-2 ROD [Matsushita199	L [5]	Vaccine	murine
873	polyclonal	had evolved from or	ere studied in 3 patients of preexisted in baseline por iruses – mutations in the	on HAART that rebounded – p pulations – HIV-1 rebound vin C3 region was responsible for	ruses from all 3 patients were	resistant to neutralizati	on by autologous IgG,
874	1024	Env Ab type C4 References Berman • 1024: Binds to 1/7 is		n cases from a MN gp120 vaco	cine trial [Berman1997]		
875	23A (2.3A)	References Thali 196  23A: Called 2.3A –  23A: C5 binding MA  23A: Study shows no monomer, did not bi  23A: The MAbs wit in an immune responsimite the native corralso by anti-V3 MA bind C11, 23A, and very strongly induce	Did not block ability of g Ab – does not inhibit gp12 eutralization is not predic nd oligomer or neutralize h the broadest neutralizin use to the oligomer on the aformation of Env and exp bs 19b and 83.1 – SOSgp M90, MAbs that bind to go d by CD4 in SOS gp140	Trkola1996a, Fouts1997, Bin p120-sCD4 complexes to inhi 20 interaction with CCR-5 in a ted by MAb binding to JRFL	bit MIP-1alpha binding – bind a MIP-1beta-CCR-5 competiti monomeric gp120, but is asso d 2F5, all have high affinity for sociated subunits – a disulfide nogen – SOS gp140 is recogni egion MAbs that neutralize on eracts with gp41 – MAbs that in the region that interacts with	on study [Trkola1996a ciated with oligomeric r the native trimer, indi linked gp120-gp41 (S zed by NAbs IgG1b12 ly TCLA strains, G3-4 bind CD4 inducible epg120, 7B2, 2.2B, T4 gp120-gp41 complexed	env binding – 23A bound cating that they were raised OS gp140) was created to , 2G12, and CD4-IgG2, and 2 and G3-519 – nor did it bitopes, 17b and A32 were , T15G1 and 4D4, did not

No. MAb	b ID	HXB2 Location	Author's Location	Sequence	Neutralizin	g Immunogen	Species(Isotype)
876 D732	24	References Moore I Sanders 2002, Gram D7324: Binding und D7324: Binds to the D7324: Epitope in C D7324: Called NEA glycosylation sites – infected people inhi D7324: Used to cap	or Aalto BioReagents Ltd, 990a, Sattentau 1991, Moc 2002, Xiang 2002a, Basma altered by gp120 binding the last 15 amino acids in gp C5 – Does not neutralize Jay 205 – gp120 capture EL - CD4 binding could only bited deglycosylation mos	aciogullari2002, Poignard2 o sCD4, in contrast to 110 120 – used for antigen cap R-FL nor block gp120 inte ISAs with MAbs D7324 (a inhibit deglycosylation what effectively when gp120 value for epitope mapping [M	yatt1995, Trkola1996a, Ditzel19 003, Herrera2003 5, 9284, 50-69 and 98-6 [Satter	beta-CCR-5 competition were compared in a studie by D7324, not by 920	n study [Trkola1996a] ly of orientation of 15, while Abs from HIV-1
877 10/46	6с	Ab type CD4BS References Cordell  10/46c: Increased by 10/46c: The most varied did not affect the ab	ariable amino acids in the ility of sCD4 or MAbs to	/V2 and V3 were deleted f V3 loop were replaced wit V1/V2, C1 and C4 to bind	rom gp120 [Jeffs1996] h serines to make the immunod – 10/46c was not affected by V hanced immunogenicity of cons	3 serine substitutions –	mice injected with serine
878 1027-	7-30-D	References Hioe200 • 1027-30-D: Ab resp MAbs or serum Ig f	00 conses, because of their cap from HIV+ individuals inh		ke and processing, can influence of gp120 specific T cells – C		
879 1125I (1125		References Tilley1991a, Tilley1  1125H: Binding to g SF-2 and IIIB – neu  1125H: Amino acid  1125H: Binding to s  1125H: Precipitation  1125H: Neutralizati involving 11 labs [C	991b, Thali1992a, Wyatt I gp120 inhibited by CD4 – tralization synergy with an substitutions in HXB2 tha soluble gp120 enhanced by n of Delta 297-329 env gly on was MN specific – faile 'Souza1995]	epitope is destroyed by recenti-V3 MAb 4117C [Tilley at strongly inhibit binding: by the presence of an anti-Vycoprotein, with has a deled to neutralize JRCSF, and	a1995, Warrier1996, Pincus199 luction, but not by removal of N	N-linked sugars – potent 70, 421, 427, 457, 470, 4 8b] ient that precipitation o	r neutralization of MN, RF, 480 [Thali1992a] f wild type [Wyatt1992]

Env Antibodies Tables HIV Antibodies Tables

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizing Immunogen	Species(Isotype)
		proportional to bin 1125H: Called 112 mutations that redu 1125H: A study of lysis against all fou 1125H: A neutraliz	ading [Pincus1996] 25h – summary of the implicuce NAb binding – probable 6 anti-Env MAbs and their ur strains [Alsmadi1998] zation assay was developed	cations of the crystal structe e mechanism of neutralizati ability to bind or direct AL based on hemi-nested PCR	to ricin A – immunotoxins mediated cell killing, but ure of the core of gp120 bound to CD4 and 17b with ion by CD4BS Ab is direct interference with CD4 bi DCC against target cells infected with IIIB, MN, SF-2 amplification of the LTR (HNPCR) – LTR-HNPCR say based on tests with 6 MAbs and 5 isolates [Yang	what is known about nding [Wyatt1998a] 2, and RF – bound and directed consistently revealed HIV
880	120-1B1	References Watkin  120-1B1: A neutra		•	${ m L}$ by growth of HXB2 in the presence of broadly neutra	human lizing sera – 120-1B1 was not
881		References Nyaml 1202-D: Using a w CD4-BS Abs ten and weakly bound 1202-D: Called 12binding site MAbs 830-D, 1027-30-D 1202-D: 26 HIV-1	A, C, and G clade isolates - 02-30D – Ab responses, bec or serum Ig from HIV+ ind , and 1202-30D strongly dir group M isolates (clades A	2000  I, 18 human MAbs were test telade specificity to virions  559/64-D, 558-D and 120 cause of their capacity to aldividuals inhibited proliferaminished proliferation [Hiotor H) were tested for bindi	sted for their ability to bind to a panel of 9 viruses from the sted for their ability to bind to a panel of 9 viruses from the sted by the sted of 9.2-D had similar reactivities [Nyambi1998] after antigen uptake and processing, can influence help the tive responses of gp120 specific T cells – CD4BS M	bind to any B clade viruses, ber T cell responses – anti-CD4 (Abs 654-D, 559/64-D, 588-D, S MAbs bound consistently to
882	1331E	Env Ab type CD4BS References Gorny 1331E: Inhibits sC compared – no MA	gp120 (IIIB) <b>Donor</b> Susan Zolla-Pazner 2000a  2D4 binding to rec gp120 LA was oligomer specific, th	r (Zollas01@mcrcr6.med.ng AI – binding of panel of 21 nough anti-V3 and CD4BS	HIV-1 infection	human (IgG1 k) sp120 monomers was C5 tended to favor the
883	1570 (1570A, 1570C, 1570D)	well exposed CD4 isolated from one i	nutated to form the PR12 pr binding domain (CD4bd) –	this proteins was used to s but all were determined to	HIV-1 infection  rminal amino acids and the V1, V2 and V3 hypervar select three new human CD4BS MAbs 1570, 1595 ar have the same V(H)3 region – 1570 was able to bind	nd 1599 – three MAbs were
		proteins from the r	A, D, C, D, and E subtypes [	[301132001]		

No. I	MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizing Immunogen	Species(Isotype)
		well exposed CD4	nutated to form the PR12 pr binding domain (CD4bd) –	this proteins was used to	erminal amino acids and the V1, V2 and V3 hypervaria select three new human CD4BS MAbs 1570, 1595 and oteins from the A, B, C, D, and E subtypes [Jeffs2001]	d 1599 – 1595 was able to
885 1	1599	well exposed CD4	nutated to form the PR12 pr binding domain (CD4bd) –	this proteins was used to	HIV-1 infection erminal amino acids and the V1, V2 and V3 hypervaria select three new human CD4BS MAbs 1570, 1595 and from the A, B, C, D, and E subtypes [Jeffs2001]	
	15e (1.5e, 1.5E, 15E)	References Robins Wyatt1993, Bagley Trkola1996a, McD Sullivan1998b, Bin  15e: Broadly neutr gp120-sCD4 bindin  15e: Cross-compet  15e: Binds to gp12  15e: gp120 mutant binding domain [H  15e: Precipitation of 15e: Amino acid st 470, 480 [Thali199  15e: Called N70-1  15e: Conformation gp120 [Moore1993  15e: Binding to De  15e: Called 15E — neutralization was  15e: Heavy chain i  15e: A mutation in  15e: MAbs against MAbs moderately 15e binding [Cook  15e: Cross-reactive 15e: Binds with hig 15e: The V4 and V	son1990a, Thali1991, Cordo 1994, Thali1994, Cook199 lougal1996, Wisnewski1996 alley1998, Trkola1998, Fout ralizing, binds multiple strain ing than MAbs G3-536 and the with MAbs ICR 39.13g 10 of HIV-1 IIIB, but not RI 11 st that affect 15e epitope bir 12 st that affect 15e epitope bir 13 could be bir 14 could be bir 15 could be bir 16 could be bir 17 could be bir 18 could be bir 19 could be bir 10 could be bir	ell1991, Ho1991b, Koup1 4, Moore1994b, Moore19 5, Binley1997a, Fouts199 s1998, Sullivan1998a, Par ns, competes with CD4 fo G3-537 [Ho1991b] and ICR 39.3b [Cordell19 F - mediates ADCC - deleading: 113, 257, 368, 370, protein, with a deleted V3 trongly inhibit binding, si ction of HIV-1 IIIB and M gp120 - neutralizes IIIB mutant glycoproteins is grant (HXB2 A281V) was son [Watkins1993] n is V_kappaI, Hum01/01: sistance to neutralization ( Cer block HIV infection of alCer, possibly through stee clades B and D, less so w an to oligomer, moderate 1.5e binding, in contrast	etion of the V3 loop from gp120 does not alter ADCC 421, 427, 475 – four of these coincide with amino aci loop, is much more efficient that precipitation of wild milar to [Ho1992], some additional, 88, 102, 117, 113,	ore1996, Poignard1996a, att1998a, Parren1998a, intophlet2003 ing – more potent blocking of activity [Koup1991] ds important for the CD4 type [Wyatt1992] 257, 368, 370, 421, 427, 457, + human sera binding to IIIB neutralizing sera – 15E  Tb) [Thali1994] tin and colon – anti-CD4 out did not completely block re1994b]

## No. MAb ID HXB2 Location Author's Location Sequence Neutralizing Immunogen Species(Isotype)

- 15e: gp120 binding enhanced by anti-V3 MAb 5G11 and anti-V2 MAb G3-136 binding inhibited by other CD4 binding site MAbs, antibodies that bind to gp120 only when CD4 is bound, and CD4-IgG [Moore1996]
- 15e: Anti-CD4BS MAbs 15e, 21h, and IgG1b12 did not cause gp120 dissociation from virus, or exposure of the gp41 epitope of MAb 50-69, in contrast to CD4i MAb 48d and anti-V3 neutralizing MAbs [Poignard1996a]
- 15e: Inhibits gp120 interaction with CCR-5 in a MIP-1beta-CCR-5 competition study [Trkola1996a]
- 15e: Neutralizes HIV-1 LAI less potently than V3 specific MAbs [McDougal1996]
- 15e: 15e is V H4 V-region heavy chain usage was examined and a bias of enhanced V H1 and V H4, and reduced V H3, was noted among HIV infected individuals [Wisnewski1996]
- 15e: Study shows neutralization is not predicted by MAb binding to JRFL monomeric gp120, but is associated with oligomeric Env binding 15e bound monomer, did not bind oligomer or neutralize JRFL [Fouts1997]
- 15e: One of 14 human MAbs tested for ability to neutralize a chimeric SHIV-vpu+, which expressed HIV-1 IIIB env 15e could only achieve 50% neutralization, but could act synergistically with anti-V3 MAb 694/98-D to achieve 90% [Li1997]
- 15e: Does not bind to HXBc2 gp120 if the 19 C-term amino acids, in conjunction with C1 positions 31-93, are deleted [Wyatt1997]
- 15e: Called 1.5E Binds to 7/7 isolates from breakthrough cases from a MN gp120 vaccine trial [Berman1997]
- 15e: Neutralizes TCLA strains, but not primary isolates [Parren1997c]
- 15e: Summary of the implications of the crystal structure of the core of gp120 bound to CD4 and 17b with what is known about mutations that reduce NAb binding probable mechanism of neutralization by CD4BS Ab is direct interference with CD4 binding [Wyatt1998a]
- 15e: The MAb and Fab binding to the oligomeric form of gp120 and neutralization were highly correlated authors suggest that neutralization is determined by the fraction of Ab sites occupied on a virion irrespective of the epitope [Parren1998a]
- 15e: A panel of MAbs were shown to bind with similar or greater affinity and similar competition profiles to a deglycosylated or variable loop deleted core gp120 protein (Delta V1, V2, and V3), thus such a core protein produces a structure closely approximating full length folded monomer CD4BS MAbs 15e, F91 and IgG1b12 bound better to the deleted protein than to wild type [Binley1998]
- 15e: Competes with CG-10 binding, a MAb raised against a gp120 CD4 complex, this was probably due to the disruption of CD4-gp120 by 15e [Sullivan1998b]
- 15e: No detectable neutralizing activity among primary isolates with different co-receptor usage some neutralization of TCLA strains [Trkola1998]
- 15e: CD4BS MAbs 15e, 21h, and F91 bind with even lower affinity than 205-43-1 and 205-42-15 to JRFL oligomer [Fouts1998]
- 15e: Called 1.5e the HIV-1 virus YU2 entry can be enhanced by MAbs binding to the CD4BS, V3 loop, and CD4i epitopes the activation for this enhanced entry state could be conferred on HxB2 by introducing the YU2 V3 loop, or the YU2 V3 and V1/V2 loops a similar effect is observed by sub-neutralizing concentrations of sCD4 and the effect is dependent of CCR5 1.5e enhances and does not neutralize YU2 env even at 50 ug/ml [Sullivan1998a]
- 15e: Six mutations in MN change the virus from a high-infectivity neutralization resistant phenotype to low-infectivity neutralization sensitive V3, CD4BS, and CD4i MAbs are 20-100 fold more efficient at neutralizing the sensitive form the mutation L544P reduced binding of all MAbs against gp120 by causing conformational changes [Park2000]
- 15e: Mutations in two gloosylation sites in the V2 region of HIV-1 ADA at positions 190 and 197 (187 DNTSYRLINCNTS 199) cause the virus to become CD4-independent and able to enter cells through CCR5 alone these same mutations tended to increase the neutralization sensitivity of the virus, including to 15e [Kolchinsky2001]
- 15e: A series of mutational changes were introduced into the YU2 gp120 that favored different conformations 375 S/W seems to favor a conformation of gp120 closer to the CD4-bound state, and is readily bound by sCD4 and CD4i MAbs (17b, 48d, 49e, 21c and 23e) but binding of anti-CD4BS MAbs (F105, 15e, IgG1b12, 21h and F91 was markedly reduced IgG1b12 failed to neutralize this mutant, while neutralization by 2G12 was enhanced 2F5 did not neutralize either WT or mutant, probably due to polymorphism in the YU2 epitope another mutant, 423 I/P, disrupted the gp120 bridging sheet, favored a different conformation and did not bind CD4, CCR5, or CD4i antibodies, but did bind to CD4BS MAbs [Xiang2002b]

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizing	Immunogen	Species(Isotype)
		MAbs directed againanti-V3 MAbs tested 2F5 – thus multiple sensitive MN-TCLA • 15e: Alanine scannic combinations of Alaincreased, binding by	nst the CD4 binding site (d (19b and 694/98-D) neuropitopes on R2 are functional strain and the typically rung mutagenesis was used anine substitutions that enline substituti	CD4BS), CD4-induced (Caralized R2, as did 2/3 and conal targets for neutralizate esistant MN-primary strait to compare substitutions to the compare substitutions and the compare bilding, and the compare substitutions are substitutions.	ximal limb of the V3 region cause CD4i) epitopes, soluble CD4 (sCD i-CD4BS MAbs (15e and IgG1b1 ion and the neutralization sensitivn [Zhang2002] that affected anti-CD4BS NAb b12 while binding of b12 to these gp12 F105, 15e, and F91) was reduced of	4), and HNS2, a broad 2), 2/2 CD4i MAbs (ity profile of R2 is into 2 – rec gp120s were 600 monomers was ger	adly neutralizing sera – 2/12 17b and 4.8D), and 2G12 and termediate between the highly engineered to contain terally maintained or
887	205-43-1	<ul> <li>205-43-1: Rank ord notably distinguishi</li> <li>205-43-1: To deterr was examined, and</li> </ul>	ng about neutralizing IgG nine the antigenicity of vir	Ib12 is that it depends on us killed by thermal and on the was found to be enhar	no  12 = 2G6 = 205-46-9 > 205-43-1 = residues in V2 [Fouts1998] chemical inactivation, retention of need (MAbs IgG1b12, 205-46-9, a osed [Grovit-Ferbas2000]	conformation-depend	dent neutralization epitopes
888	205-46-9	<ul> <li>205-46-9: Binds JR Parren98 – authors thus counteracts the 21h = F91, and the</li> <li>205-46-9: To deterr was examined, and</li> </ul>	propose a model where 20: neutralizing effect – rank only thing notably distingu- nine the antigenicity of vir	5-46-9 and 2G6 may inhil order of CD4BS antibodi hishing about neutralizing us killed by thermal and ones was found to be enhar	no  t IgG1b12 is neutralizing, 205-46- bit CD4 binding, but cause a confo- es oligomer binding is IgG1b12 = IgG1b12 is that it depends on res- chemical inactivation, retention of nced (MAbs IgG1b12, 205-46-9, a osed [Grovit-Ferbas2000]	ormational shift which 2G6 = 205-46-9 > 2 idues in V2 [Fouts19 conformation-dependent	n enhances CCR5 binding and 05-43-1 = 205-42-15 > 15e = 98] dent neutralization epitopes
889	21h (2.1H)	References Ho199 Poignard1996a, Wir Fouts1998, Xiang20 21h: Amino acid su 21h: Binding to De 21h: Conformations gp120 [Moore1993: 21h: Has strong cro 21h: Competition so comparable or prior	snewski1996, McKeating1 002b bstitutions in HXB2 that in lta V1/2 and Delta V1/2/3 al, does not bind denatured al ss-reactivity with gp120 m tudies with human sera fro to anti-V3 antibodies [Mo	Nyatt1993, Moore1993a, 1996b, Binley1997a, Fouts whibit binding, some sharmutant glycoproteins is glap120 – neutralizes IIIB monomers from most subtum seroconverting individual pore1994a	L Moore1994b, Moore1994a, Bagle, s1997, Li1997, Ugolini1997, Wyar ed with CD4 binding inhibition, 8 reater than binding to wildtype gp — reactive with SF-2 gp120 — stro ypes, A-F, with the least reactivity hals showed that anti-CD4 BS antim318. Compared to 15e and F105	tt1997, Parren1997c, 8, 113, 257, 368, 370 120 [Wyatt1993] ng inhibition of HIV- to clade E [Moore19 ibodies can arise very	Wyatt1998a, Parren1998a, , 421, 470, 480 [Thali1992a] + human sera binding to IIIB

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutr	alizing Immunogen	Species(Isotype)
No.	MAb ID	<ul> <li>21h: A mutation in</li> <li>21h: Binds with hig</li> <li>21h: Anti-CD4 bind anti-V3 MAb 5G11</li> <li>21h: Anti-CD4BS I CD4i MAb 48d and</li> <li>21h: 21h is V H3 — individuals [Wisned 21h: Called 2.1H — 21h: Study shows monomer, did not be 21h: One of 14 hun achieved at a maxin</li> <li>21h: Viral binding [Ugolini1997]</li> <li>21h: Binds both gp and C5 and deletion</li> <li>21h: Neutralizes TG</li> <li>21h: Summary of the control of the cont</li></ul>	gp41, 582 A/T, confers resigner affinity to monomer the ding site MAb – reciprocal – enhances binding of sor MAbs 15e, 21h, and IgG1b di anti-V3 neutralizing MAb V-region heavy chain usagwski1996]  Neutralizes HXB2, but faineutralizes HXB2, but faineutralization is not predicted in the predict of the digomer or neutralized nan MAbs tested for ability mal concentration of 67 multinhibition by 21h strongly of the V1V2 and V3 loog CLA strains, but not primate implications of the crystine in the implication of the crystine in	istance to neutralization (an to oligomer, moderate inhibition by anti-C1, -C ne anti-V3 and -V2 MAb: 12 did not cause gp120 dos [Poignard1996a] e was examined and a bial to neutralize chimeric ved by MAb binding to JR JRFL [Fouts1997] to neutralize a chimeric g/ml [Li1997] correlated with neutraliza 41 complex efficiently, sups do not diminish binding visolates [Parren1997c] al structure of the core of	falso confers resistance to I association rate [Sattentau 4 and other anti-CD4 bindis [Moore1996] issociation from virus, or eas of enhanced V H1 and Virus with gp120 from prim FL monomeric gp120, but SHIV-vpu+, which express tion (all other neutralizing ggesting its gp120 epitope g [Wyatt1997]	MAbs F105, 48d, 15e and 1 11995b] ing site antibodies – enhance exposure of the gp41 epitope 7 H4, and reduced V H3, was nary isolates in an HXB2 basis associated with oligomer sed HIV-1 IIIB env – 50% n MAbs tested showed some is not blocked by gp41 bind 17b with what is known about 17b with what 18b with 18b	7b) [Thali1994] ed by some anti-V2 MAbs and e of MAb 50-69, in contrast to as noted among HIV infected ckground [McKeating1996b] ic Env binding – 21h bound eutralization could not be
		binding – probable  21h: The MAb and determined by the f  21h: CD4BS MAbs with [Parren1998a]  21h: A series of mu gp120 closer to the 15e, IgG1b12, 21h neutralize either W different conformat	mechanism of neutralization Fab binding to the oligometraction of Ab sites occupied 15e, 21h, and F91 bind was [Fouts1998] Intational changes were introced CD4-bound state, and is read F91) was markedly recommend.	on by CD4BS Ab is directed on a virion irrespective in even lower affinity that be duced into the YU2 gp12 adily bound by sCD4 and luced—IgG1b12 failed to to polymorphism in the YCCR5, or CD4i antibodie	interference with CD4 bin cutralization were highly co of the epitope [Parren1998 in 205-43-1 and 205-42-15 20 that favored different co d CD4i MAbs (17b, 48d, 4) in neutralize this mutant, who CU2 epitope—another muta	nding [Wyatt1998a] orrelated – authors suggest to JRFL oligomer – conclusion formations—375 S/W see 19e, 21c and 23e) but binding the neutralization by 2G12 vant, 423 I/P, disrupted the grants.	hat neutralization is
890	28A11/B1	Env	gp120 (SF162)	-	L  conent: gp120 Adjuvant:	Vaccine Ribi adjuvant (MPL+TDM	human from transgenic mice (IgG2κ)
		Ab type CD4BS References He2002 28A11/B1: Transge panel of anti-HIV g 5145A, blocked sC	Donor Dr. Abraham Pinter 2 enic mice (strain XenoMou p120 MAb-producing hyb	r, Public Health Research se G2) carrying human good ridomas by immunization rmationally sensitive—4/	Institute, Newark, NJ, pinteness allowing production of with HIV SF162 gp120—66 could neutralize the auto	ter@phri.org of fully human IgG2κ MAbs -6 anti-CD4BS MAbs comp	s were used to rapidly create a eted with anti-CD4BS MAb ere broadly cross-reactive with

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizing	Immunogen	Species(Isotype)
891	2G6	References Fouts1 • 2G6: Binds to JRF neutralization – cor	998 L oligomer with an affinity nclusions of this paper cont	comparable to IgG1b12, burast with [Parren1998a] – a	ersity of Agricultural Science, on at does not neutralize the virus, authors propose a model where 2 interacts the neutralizing effect [	so binding of oligome 205-46-9 and 2G6 may	r is not always predictive of
892	35F3/E2		_		L  nent: gp120 Adjuvant: Ribi a stitute, Newark, NJ, pinter@ph	•	human from transgenic mice (IgG2κ)
		References He200  35F3/E2: Transger panel of anti-HIV § 5145A, blocked sC	2 nic mice (strain XenoMouse gp120 MAb-producing hyb	G2) carrying human generidomas by immunization v rmationally sensitive—4/6	allowing production of fully havith HIV SF162 gp120—6 anti- could neutralize the autologous	uman IgG2κ MAbs w CD4BS MAbs compe	ted with anti-CD4BS MAb
893	38G3/A9	Env	gp120 (SF162)		L	Vaccine	human from transgenic mice (IgG2 $\kappa$ )
		Ab type CD4BS References He200 38G3/A9: Transge panel of anti-HIV s	<b>Donor</b> Dr. Abraham Pinter 2 nic mice (strain XenoMous gp120 MAb-producing hyb	; Public Health Research In e G2) carrying human gene ridomas by immunization v	nent: gp120 Adjuvant: Ribi as a stitute, Newark, NJ, pinter@ph as allowing production of fully by the HIV SF162 gp120—6 anticould neutralize the autologous	uri.org numan IgG2κ MAbs w CD4BS MAbs compe	ted with anti-CD4BS MAb
			strains (not E clade)—380				ere broadly cross reactive with
894	428		gp120 wska1992a, Jeffs1996 mificant increased binding	when V1/V2 or V1/V2 and	V3 were deleted from gp120 [J	HIV-1 infection effs1996]	human
895		Ab type CD4BS References Karwo 448-D: Conformati 448-D: Called 448 MAbs 39.13g and 448-D: Did not me 448-D: Dissociatio	owska1992a, McKeating199 ional – reactive with IIIB gr D – blocks gp120-CD4 bind 39.3b [McKeating1992c] diate deposition of comple	2c, Spear1993, Laal1994, I ol 20 in RIP, but not WB as ding – substitutions at gp12 ment component C3 on HIV 9 – neutralizes IIIB, acts sy	0 residues 88, 113, 117, 257, 36 7 infected cells [Spear1993] nergistically with anti-V3 MAb	58 and 370 reduce bind	

No.	MAb ID	HXB2 Location	<b>Author's Location</b>	Sequence	Neutralizin	g Immunogen	Species(Isotype)
		<ul> <li>448-D: One of 14 h</li> <li>448-D: Summary o</li> <li>NAb binding – prol</li> <li>448-D: 26 HIV-1 gi</li> </ul>	numan MAbs tested for abil f the implications of the cry bable mechanism of neutral roup M isolates (clades A to	ity to neutralize a chimeric vstal structure of the core of ization by CD4BS Ab is dip b H) were tested for binding	epitopes to Th cells [Manca19] SHIV-vpu+, which expressed gp120 bound to CD4 and 17b eect interference with CD4 bin to 47 MAbs, including 6 CD eption of broadly reactive MA	HIV-1 IIIB env [Li1997) with what is known abo ding [Wyatt1998a] 4BS MAbs – CD4BS M	out mutations that reduce  Abs bound consistently to
896	44D2/D5				no nent: gp120 Adjuvant: Ribi a stitute, Newark, NJ, pinter@p		human from transgenic mice ( $IgG2\kappa$ )
		References He2002  • 44D2/D5: Transger panel of anti-HIV g 5145A, blocked sC	2 nic mice (strain XenoMouse p120 MAb-producing hybr D4 binding and were confo	e G2) carrying human generidomas by immunization wrationally sensitive—4/6	s allowing production of fully ith HIV SF162 gp120—6 anticould neutralize the autologou ttologous SF162, and while it	human IgG2 $\kappa$ MAbs we -CD4BS MAbs compete s strain SF162, and were	ed with anti-CD4BS MAb broadly cross-reactive with
 897	48-16	Env Ab type CD4BS References Fevrier • 48-16: Broadly crox ×10 <sup>-9</sup> M [Fevrier1	ss-reactive, reacts outside tl	ne CD4 binding site and V3	no region—competes with sera f	HIV-1 infection	human (IgG $\kappa$ ) ejects—binding affinity 2–5
898	50-61A	Env Ab type CD4BS References Fevrier • 50-61A: Neutralize		competes with sera from 4	L 5 seropositive subjects – bindi	HIV-1 infection  ng affinity 2.4 x 10-10 l	human (IgGκ)  M [Fevrier1995]
899	5145A	<ul><li>5145A: Potent and</li><li>5145A: Synergistic</li></ul>	broadly cross-reactive neut neutralization of HIV-1 wh			HIV-1 infection	human (IgG1)
		lysis against all fou • 5145A: Transgenic	ding [Pincus1996] 6 anti-Env MAbs and their r strains [Alsmadi1998] mice carrying human gene	s allowing production of fu	CC against target cells infected by human MAbs were used to viously described human MAI	rapidly create a panel o	f anti-HIV gp120 MAb

APCs [Hioe2001].

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizing	Immunogen	Species(Isotype)
		<ul><li>558-D: Blocks gp12 [McKeating1992c]</li><li>558-D: Using a who CD4BS Abs tended</li></ul>	ole virion-ELISA method, to bind weakly without c	18 human MAbs were te lade specificity to virions,	ot for 256 S/Y and 262 N/T, which sted for their ability to bind to a pa but bound well to soluble gp120 – )2-D had similar reactivities [Nyan	nel of 9 viruses from - 558-D did not bind t	clades A, B, D, F, G, and H –
901	559/64-D (559, 559-64D)	Env Ab type CD4BS I References Karwov Hioe2000, Nyambi2 559/64-D: Conform 559/64-D: Did not re 559/64-D: Called 55 from HIV-1 isolates virion surface relativ SF128a and to T-cel [Stamatatos1995] 559/64-D: Neutraliz 559/64-D: Called 55 559/64-D: Used in te 559/64-D: Four prini isolate inhibited by 838-D), anti-CD4bd loop (419-D, and 44 and not at all by MA and 98-6 [Hioe1997 559/64-D: Using a v H - CD4BS Abs ten and weakly bound ce 559/64-D: Binding of though anti-V3 and 9CL and 1331E bou 559/64-D: Ab respo MAbs or serum Ig f 1027-30-D, and 120 559/64-D: 26 HIV-1 to most isolates of ce 559/64-D: CD4BS M	gp120 (LAI)  Donor Susan Zolla-Pazne vska1992a, McKeating19 2000, Hioe2001, York200 ational – reactive with III nediate deposition of com 59-64D – The binding of with differences in cell to the gp120 monomer 1 tropic SF2 – binding of ing activity, no ADCC actions actions activity, no ADCC actions activity, no ADCC actions actions activity, no ADCC action	er (Zollas01@mcrcr6.med 92c, Spear1993, Stamatat 1 B gp120 in RIP, but not Vaplement component C3 of conformation-dependent a ropism was studied – CD4 as indicated by an increase anti-CD4BS MAbs to SF stivity, and no viral enhance increased binding when a cell neutralization assay not patterns of sensitivity asma tested, and was also 30-D and a cluster II of gp 1 (98-6) MAbs at higher cocktail of ten MAbs consisted, 18 human MAbs were out clade specificity to virit – 559/64-D, 558-D and 1 oluble oligomeric gp140 verter with the oligomer IG stacity to alter antigen uptation in the proliferation [Hioe2000 at A to H) were tested for bates of other clades with the oligomer liferation gp120, inhibit prolifer	L  Inyu), NYU Med Center, NY, NY  10s1995, Forthal1995, Jeffs1996, He  In HIV infected cells [Spear1993]  In HIV infected cells [Spear1993]  Inti-V2, anti-V3, and anti-CD4BS [Inti-V2]  In HIV infected cells [Spear1993]  Inti-V2, anti-V3, and anti-CD4BS [Inti-V2]  In HIV infected cells [Spear1993]  Inti-V2, anti-V3, and anti-CD4BS [Inti-V2]  In HIV infected cells [Spear1993]  In HIV infected ser somewhat oche in the half-maximal binding value in	MAbs to monomeric scluded in the oligomates to macrophage-troof dissociation of gp12 ted from gp120 [Jeffs at or plasma and MAb icular anti-V3 loop (4 192HT593 and 91US0 ted by some of the pol 338-D, 559/64-D, 654 at panel of 9 viruses from gp120 as compared – no MA onomer – CD4BS MA onomer – CD4BS MA onomer – CD4BS MAbs 654-D, 5 D4BS MAbs – CD4B Ab IgG1b12[Nyambids and IFNγ production	and virion-associated gp120 eric gp120 epitopes on the opic isolates SF162 and 20 from virion surface  s1996]  s – BZ167 was the only 19-D, 447-52D, 782-D, and 256 were neutralized by V3 dyclonal sera/plasma tested -D, 450-D, 670-D, 1281-D om clades A, B, D, F, G, and 25 bind to any B clade viruses, ab was oligomer specific, abs 559/64-D, 654-D, 729-D, — anti-CD4 binding site 59/64-D, 588-D, 830-D,  S MAbs bound consistently 2000] 2000] 2000] 2001

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizing	Immunogen	Species(Isotype)
		gp41 (2F5, F240) e TCLA: 168C and 3	each showed similar binding	g efficiency to Env derived f lines were much more susc	52D), CD4BS (IgG1b12, 559-64) from related pairs of primary and eptible to neutralization suggest	d TCLA lines (primar	y: 168P and 320SI, and
902	55D5/F9	Env	gp120 (SF162)		L	Vaccine	human from transgenic mice (IgG2κ)
		Ab type CD4BS References He200 • 55D5/F9: Transger panel of anti-HIV § 5145A, blocked sC	<b>Donor</b> Dr. Abraham Pinter 22 nic mice (strain XenoMouse gp120 MAb-producing hyb 2D4 binding and were confe	r, Public Health Research In e G2) carrying human genes ridomas by immunization w	nent: gp120 Adjuvant: Ribi adstitute, Newark, NJ, pinter@phi allowing production of fully huith HIV SF162 gp120—6 anti-Could neutralize the autologous MAbs [He2002].	ri.org ıman IgG2 <i>k</i> MAbs w CD4BS MAbs compe	ted with anti-CD4BS MAb
903	588-D (588)	References Karwo  588-D: Conformati  588-D: 4-fold incre  588-D: Weak neutr  588-D: Called 588  588-D: Using a wh CD4-BS Abs tende weakly bound a cla  588-D: Ab respons or serum Ig from H and 1202-30D stro  588-D: 26 HIV-1 g	wwska1992a, Buchbinder199 ional – reactive with IIIB glease in neutralization potentralization of IIIB – strong in – slight, not significant include virion-ELISA method, ed to bind weakly without cade A, C, and G clade isolates, because of their capacitative individuals inhibited progly diminished proliferation of the capacitation of the capaci	22, Moore 1993a, Jeffs 1996, p. 120 in RIP, but not WB asset of 588-D when combine whibition of HIV+ human se treased binding when V1/V2 18 human MAbs were tested lade specificity to virions, but the end of th	L u), NYU Med Center, NY, NY Nyambi1998, Hioe2000, Nyam ay [Karwowska1992a] d 1:1 with human MAb 447-D   ra binding to IIIB gp120 [Moore or V1/V2 and V3 were deleted d for their ability to bind to a pa ut bound well to soluble gp120 202-D reacted had similar reacti I processing, can influence helpe 120 specific T cells – CD4BS M g to 47 MAbs, including 6 CD4I ception of broadly reactive MAB	[Buchbinder1992] e1993a] from gp120 [Jeffs199] nel of 9 viruses from – 588-D did not bind vities [Nyambi1998] er T cell responses – a IAbs 654-D, 559/64-I	clades A, B, D, F, G, and H – to any B clade viruses, and anti-CD4 binding site MAbs D, 588-D, 830-D, 1027-30-D, MAbs bound consistently to
904	654-D (654-30D, 654/30D, 654-D100, 654.30D, 654	References Karwo Nyambi1998, Stam • 654-D: Dissociatio [Laal1994]	owska1993, Laal1994, Gorn natatos1998, Hioe1999, Gor on constant gp120 IIIB 0.00	y1994, Stamatatos1995, Li rny2000a, Hioe2000, Hioe2	L u), NYU Med Center, NY, NY 1997, Stamatatos 1997, Gorny 19 1001, Nyambi 2000, Verrier 2001, aergistically with anti-V3 MAb	Gorny2002	<u>-</u>

**Env Antibodies** 

No. MAb ID HXB2 Location Author's Location Sequence Neutralizing Immunogen Species(Isotype)

• 654-D: Called 654-30D – The binding of conformation-dependent anti-V2, anti-V3, and anti-CD4BS MAbs to monomeric and virion-associated gp120 from HIV-1 isolates with differences in cell tropism was studied – CD4BS loop epitopes are somewhat occluded in the oligomeric gp120 epitopes on the virion surface relative to the gp120 monomer as indicated by an increase in the half-maximal binding values to macrophage-tropic isolates SF162 and SF128a and to T-cell tropic SF2 – binding of anti-CD4BS MAbs to SF2 resulted in a significant amount of dissociation of gp120 from virion surface [Stamatatos1995]

- 654-D: Called 654-30D One of 14 human MAbs tested for ability to neutralize a chimeric SHIV-vpu+, which expressed HIV-1 IIIB env [Li1997]
- 654-D: Anti-CD4 BS MAb 654-30D and IgG1b12 have comparable binding affinities, neither mediates gp120-virion dissociation, but IgG1b12 can neutralize SF128A and SF162 and 654-D cannot 654-D actually enhances infection by both viruses in primary macrophages [Stamatatos1997]
- 654-D: Four primary isolates showed distinct patterns of sensitivity to neutralization by polyclonal sera or plasma and MAbs BZ167 was the only isolate inhibited by all polyclonal sera and plasma tested, and was also neutralized by 8/17 MAbs, in particular anti-V3 loop (419-D, 447-52D, 782-D, and 838-D), anti-CD4bd (559/64-D, 654-D and 830-D and a cluster II of gp41 directed MAb (98-6) isolates 92HT593 and 91US056 were neutralized by V3 loop (419-D, and 447-52D)and cluster II gp41 (98-6) MAbs at higher concentrations US4 was neutralized by some of the polyclonal sera/plasma tested and not at all by MAbs individually or by a cocktail of ten MAbs consisting of 419-D, 447-52D, 782-D, 838-D, 559/64-D, 654-D, 450-D, 670-D, 1281-D and 98-6 [Hioe1997b]
- 654-D: Called 654-D100 654-D100 and IgG1b12 neutralized viruses HIV-BRU and a mutated virus that lacks the V3 loop glycan equally effectively in contrast, sera from guinea pigs immunized with BRU gp120 neutralize viruses more effectively that lack the V3 glycan[Schonning1998]
- 654-D: Using a whole virion-ELISA method, 18 human MAbs were tested for their ability to bind to a panel of 9 viruses from clades A, B, D, F, G, and H CD4-BS Abs tended to bind very weakly without clade specificity to virions, but bound well to soluble gp120 654-D bound only to JRFL [Nyambi1998]
- 654-D: Called 654.30D deleting the V2 loop of neutralization-resistant HIV-1 isolate SF162 does not abrogate its replication in PBMC or macrophages, but it enhances its neutralization sensitivity to sera from patients with B clade infection up to 170-fold, and also enhances sensitivity to sera from clades A through F deletion of V2 but not V1 slightly allowed neutralization by CD4BS MAb 654.30D [Stamatatos1998]
- 654-D: The presence of leukocyte function-associated molecule 1 (LFA-1) promotes virus infectivity and hinders neutralization, and anti-LFA-1 MAbs can
  enhance the neutralizing effect of anti-HIV V3 MAb 447-52D and anti-HIV CD4BS MAb IgG1b12 non-neutralizing anti-HIV CD4BS MAb 654-D did
  not become neutralizing in the presence of anti-LFA-1 MAbs [Hioe1999]
- 654-D: Binding of panel of 21 MAbs to soluble oligomeric gp140 versus gp41 or gp120 monomers was compared no MAb was oligomer specific, though anti-V3 and CD4BS MAbs reacted better with the oligomer and V2 and C5 tended to favor the monomer CD4BS MAbs 559/64-D, 654-D, 729-D, 9CL and 1331E bound with a 5-13 fold preference for the oligomer [Gorny2000a]
- 654-D: Ab responses, because of their capacity to alter antigen uptake and processing, can influence helper T cell responses CD4BS MAbs or serum Ig from HIV+ individuals inhibited proliferative responses of gp120 specific T cells MAb 654-D strongly diminished proliferation there is a discrepancy in isotyping this antibody, previous reports indicated IgG1kappa, while Hioe suggests it is IgG1lambda [Hioe2000]
- 654-D: 26 HIV-1 group M isolates (clades A to H) were tested for binding to 47 MAbs, including 6 CD4BS MAbs CD4BS MAbs bound consistently to most isolates of clade D, but poorly to isolates of other clades with the exception of broadly reactive MAb IgG1b12 654-D had the weakest binding among CD4BS MAbs, binding to only 4/26 isolates [Nyambi2000]
- 654-D: CD4BS MAbs when complexed with gp120, inhibit proliferation of gp120-specific CD4 T-cells and IFN gamma production anti-CD4BS MAbs inhibit gp120 presentation by altering the uptake and/or processing of gp120 by the APCs, not by blocking of gp120 attachment to CD4 on the surface of APCs [Hioe2001]
- 654-D: A panel of 12 MAbs was used to identify those that could neutralize the dual-tropic primary isolate HIV-1 89.6—six gave significant neutralization at 2 to 10 ug/ml: 2F5, 50-69, IgG1b12, 447-52D, 2G12, and 670-D, while six did not have neutralizing activity: 654-D, 4.8D, 450-D, 246-D, 98-6, and 1281—no synergy, only additive effects were seen for pairwise combinations of MAbs, and antagonism was noted between gp41 MAbs 50-69 and 98-6, as well as 98-6 and 2F5 [Verrier2001].

No.	MAb ID	HXB2 Locatio	n Author's Location	Sequence	Neutralizing	Immunogen	Species(Isotype)
		bind to the tip of intact virions at MAbs were use conformation-s	of the V3 loop and cross-comp and the strength binding was his and as controls: anti-V3 447-52.	ete with the MAb 447-52I ghly correlated with perce D (anti-V3 MAb for comp	more cross-reactive, so six new VD and are conformationally sensiting the most continuous and neutralization using the ghost continuous and neutralization studies), binding site MAb control), and MAD	ve – MAbs showed co ell or PHA blast assay , 654 (anti-CD4BS us	ross-clade binding to native, y – five well-characterized ed as a
905	67G6/C4	Env	gp120 (SF162)		no	Vaccine	human from transgenic mice
			S <b>Donor</b> Dr. Abraham Pinte	-	oonent: gp120 Adjuvant: Ribi ad Institute, Newark, NJ, pinter@phi		$(IgG2\kappa)$
		panel of anti-H 5145A, blocked	IV gp120 MAb-producing hybds sCD4 binding and were confe	oridomas by immunization ormationally sensitive—4/	nes allowing production of fully he with HIV SF162 gp120—6 anti-06 could neutralize the autologous e autologous SF162, and its bindin	CD4BS MAbs compe strain SF162, and we	ted with anti-CD4BS MAb re broadly cross-reactive with
906	729-D (729-30D)	References Lac 729-D: Dissoci 729-D: In a mu but originally re 729-D: Called 729-D: Neutral 729-D: Binding	al1994, D'Souza1997, Li1997, ation constant gp120 IIIB 0.02 ltilaboratory blinded study, fai eported in [Laal1994] to be Igt 720-30D – one of 14 human Mizes TCLA strains, but not pring of panel of 21 MAbs to solub	Parren1997c, Gorny2000 5 – neutralizes IIIB, acts of the consistently neutral G1kappa [D'Souza1997] [Abs tested for ability to not the consistent of the consistent of the consistency	synergistically with anti-V3 MAb ize any of nine B clade primary iso eutralize chimeric SHIV-vpu+, wh	olates – reported here nich expressed HIV-1 compared – no MAb v	IIIB env [Li1997] was oligomer specific, though
907	830D (830-	and 1331E bou	nd with a 5-13 fold preference	-			human (IgG1κ)
201	(0.00-	Ab type CD4B References Hice 830D: Called 8 only isolate inh and 838-D), and V3 loop (419-D tested and not a 1281-D and 98- 830D: Summar	S pe 1997b, Wyatt 1998a, Hioe 20 pe 1997b, Wyatt 1998a, Hioe 20 pe 1997b, Wyatt 1998a, Hioe 20 pe 1997b, all polyclonal sera and ti-CD4bd (559/64-D, 654-D and 20 pe 1997b), and 447-52D) and cluster II pe 1997b] pe 1997b] pe 1997b pe 1997	nowed distinct patterns of second plasma tested, and was and 830-D and a cluster II of ap41 (98-6) MAbs at higher by a cocktail of ten MAbseystal structure of the core of	sensitivity to neutralization by polyalso neutralized by 8/17 MAbs, in of gp41 directed MAb (98-6) – iso er concentrations – US4 was neutronsisting of 419-D, 447-52D, 78 of gp120 bound to CD4 and 17b with direct interference with CD4 bind	particular anti-V3 lo lates 92HT593 and 9 alized by some of the 32-D, 838-D, 559/64- with what is known ab	a and MAbs – BZ167 was the op (419-D, 447-52D, 782-D, 1US056 were neutralized by polyclonal sera/plasma D, 654-D, 450-D, 670-D,

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutraliz	ing Immunogen	Species(Isotype)	
		or serum Ig from Hl		proliferative responses of	nd processing, can influence he gp120 specific T cells – CD4B			
908	9CL	<ul><li>References Gorny2</li><li>9CL: Binding of paranti-V3 and CD4BS</li></ul>	000a nel of 21 MAbs to soluble	oligomeric gp140 versus the oligomer and V2 and	nyu), NYU Med Center, NY, Ngp41 or gp120 monomers was 1 C5 tended to favor the monor 000a]	compared – no MAb was		
909	BM12	Env Ab type CD4BS References Kessler BM12: Broad cross		mary isolates – additive (	L effect in combination with MA	HIV-1 infection b 2F5 [Kessler1995]	human	
910	D20	Ab type CD4BS   References Earl199   D20: Generated dur   D20: Binding comp   D20: Human sera b D20: Pulse label expand that the epitope   D20: Used for compandependent anti-gp41   D20: A comparison broadly cross-reacti	4, Broder1994, Richardso ing a study of the influence letely blocked by pooled helocked binding in oligome periments of 4 MAbs (D20 formed with a t 1/2 of about a study of gp41 MAbs [Earl1997] of 25 gp120 specific, confi	stitute of Allergy and Info n1996, Otteken1996, Ear e of the oligomeric struct numan sera [Broder1994] ric ELISA assay to a sim D, D27, T20, and T22) bir out 10 minutes [Otteken19 antibodies – D20 binds to	ectious Diseases, NIH, Bethesd 11997, Sugiura1999 ure of Env in determining the r lar extent for gp41 MAbs D20 dding to noncleavable gp160 re	repertoire of the Ab responsible, D43, D61, and T4 [Rich evealed that these anti-CD expressed Env than any group of MAbs labeled A	ardson1996] 4 MAbs bound with a delay, of 38 conformation	
911	D21	Env gp120 (IIIB) Vaccine Vector/Type: vaccinia Strain: IIIB HIV component: oligomeric gp140  Ab type CD4BS Donor P. Earl, National Institute of Allergy and Infectious Diseases, NIH, Bethesda, MD  References Earl1994, Sugiura1999  D21: Generated during a study of the influence of the oligomeric structure of Env in determining the repertoire of the Ab response [Earl1994]  D21: A comparison of 25 gp120 specific, conformation dependent MAbs was done – D21 is part of a group of MAbs labeled A1 – all A1 MAbs were broadly cross-reactive with gp160 from B-clade R5, X4, and R5X4 viruses, blocked CD4 binding, were sensitive to mutations in gp120 positions 368 and 370 that directly contact CD4 [Sugiura1999]						
912	D24				no neric gp140 ectious Diseases, NIH, Bethesd	Vaccine la, MD	murine (IgG)	

No. MAb ID	HXB2 Location	Author's Location	Sequence	Neutra	alizing Immunogen	Species(Isotype)	
	<ul> <li>D24: A comparison</li> </ul>	of 25 gp120 specific, con seven clade B isolates BI	formation dependent MAb	s was done – D24 is part o	he repertoire of the Ab respo of a group of MAbs labeled I ted with B-I MAbs – B-I M.	B-I, that had limited	
913 D25	Env gp120 (IIIB) Vaccine Vector/Type: vaccinia Strain: IIIB HIV component: oligomeric gp140  Ab type CD4BS Donor P. Earl, National Institute of Allergy and Infectious Diseases, NIH, Bethesda, MD  References Earl1994, Sugiura1999  D25: Generated during a study of the influence of the oligomeric structure of Env in determining the repertoire of the Ab response [Earl1994]  D25: A comparison of 25 gp120 specific, conformation dependent MAbs was done – D25 is part of a group of MAbs labeled A1 – all A1 MAbs were broadly cross-reactive with gp160 from B-clade R5, X4, and R5X4 viruses, blocked CD4 binding, were sensitive to mutations in gp120 positions 368 a						
914 D28	Env Vaccine Vector/Type Ab type CD4BS   References Earl199 • D28: Generated dur • D28: A comparison	Donor P. Earl, National In 14, Sugiura 1999 ing a study of the influence of 25 gp 120 specific, con seven clade B isolates BI	formation dependent MAb	tious Diseases, NIH, Beth re of Env in determining t s was done – D28 is part c	Vaccine lesda, MD  the repertoire of the Ab responsion of a group of MAbs labeled I ted with B-I MAbs – B-I Materials.	B-I, that had limited	
D15 D35	Env gp120 (IIIB) Vaccine Vector/Type: vaccinia Strain: IIIB HIV component: oligomeric gp140  Ab type CD4BS Donor P. Earl, National Institute of Allergy and Infectious Diseases, NIH, Bethesda, MD  References Earl1994, Sugiura1999  D35: Generated during a study of the influence of the oligomeric structure of Env in determining the repertoire of the Ab response [Earl1994]  D35: A comparison of 25 gp120 specific, conformation dependent MAbs was done – D35 is part of a group of MAbs labeled B-I, that had limited cross-reactivity – of seven clade B isolates BH8 and B-al were they only two that consistently reacted with B-I MAbs – B-I MAbs fully blocked CD4 binding [Sugiura1999]						
916 D39	Env gp120 (IIIB) Vaccine Vector/Type: vaccinia Strain: IIIB HIV component: oligomeric gp140  Ab type CD4BS Donor P. Earl, National Institute of Allergy and Infectious Diseases, NIH, Bethesda, MD  References Earl1994, Sugiura1999  D39: Generated during a study of the influence of the oligomeric structure of Env in determining the repertoire of the Ab response [Earl1994]  D39: A comparison of 25 gp120 specific, conformation dependent MAbs was done – D39 is part of a group of MAbs labeled A1 – all A1 MAbs were broadly cross-reactive with gp160 from B-clade R5, X4, and R5X4 viruses, blocked CD4 binding, were sensitive to mutations in gp120 positions 368 370 that directly contact CD4 [Sugiura1999]						
917 D42			HIV component: oligome stitute of Allergy and Infec		Vaccine nesda, MD	murine (IgG)	

No.	MAb ID	HXB2 Location	<b>Author's Location</b>	Sequence	Neutralizing	Immunogen	Species(Isotype)
		• D42: A comparison	ing a study of the influence of 25 gp120 specific, con seven clade B isolates BI	formation dependent MAb	are of Env in determining the repeats was done – D42 is part of a grow two that consistently reacted with	up of MAbs labeled B	-I, that had limited
918	D52	Ab type CD4BS I References Earl199  D52: Generated dur  D52: A comparison	Oonor P. Earl, National Ir 4, Sugiura 1999 ing a study of the influence of 25 gp120 specific, con seven clade B isolates BI	ce of the oligomeric structu	eric gp140 ctious Diseases, NIH, Bethesda, Mare of Env in determining the repease was done – D52 is part of a grow two that consistently reacted with	ertoire of the Ab respon oup of MAbs labeled B	-I, that had limited
919	D53	Ab type CD4BS I References Earl199  D53: Generated dur  D53: A comparison	Oonor P. Earl, National Ir 4, Sugiura1999 ing a study of the influence of 25 gp120 specific, con seven clade B isolates BI	ce of the oligomeric structure of the oligomeric structure.	eric gp140 ctious Diseases, NIH, Bethesda, I are of Env in determining the repe bs was done – D53 is part of a gro two that consistently reacted with	ertoire of the Ab respon	-I, that had limited
920	D60	<ul><li>Ab type CD4BS I References Earl199</li><li>D60: Generated dur</li><li>D60: A comparison</li></ul>	<b>Donor</b> P. Earl, National Ir 4, Richardson1996, Sugiting a study of the influence of 25 gp120 specific, con seven clade B isolates BI	ura1999 ce of the oligomeric structu formation dependent MAb	no eric gp140 ctious Diseases, NIH, Bethesda, I are of Env in determining the repe s was done – D60 is part of a gro two that consistently reacted with	ertoire of the Ab respon oup of MAbs labeled B	-I, that had limited
921	DA48	markedly different the balance of the balance to balance the balance the balance to balance the balance	ler of Fab binding affinity han Fab binding affinity to to oligomeric form and no	o the mature oligomeric for	op 2 > 3B3 > b12 = DO8i > b11 > rm (3B3 > b12 > DO142-10 > Lo d for both Fabs and MAbs – auth ren1998a]	op $2 > b11 > L17 > b6$	6 > DO8i > b14 > DA48 >

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizing Immunogen	Species(Isotype)	
		state could be cont concentrations of s cross-linking as a	ferred on HxB2 by introduc sCD4 and the effect is dependent	ing the YU2 V3 loop, or the indent of CCR5 – Fab Ab fronhances YU2, it neutralizes	the CD4BS, V3 loop, and CD4i epitopes – the actival YU2 V3 and V1/V2 loops – a similar effect is obsergement DA48 also enhances YU2 entry, ruling out For HXBc2 – DA48 was obtained by panning libraries of 1998a	rved by sub-neutralizing interactions or Env	
922	DO8i	markedly different > b13) and binding fraction of Ab site.  • DO8i – the HIV-1 state could be conficencentrations of state.	HIV-1 infection  2 > 3B3 > b12 = DO8i > b11 > b3 > b14 > b13 > D0  In (3B3 > b12 > DO142-10 > Loop 2 > b11 > L17 > b  for both Fabs and MAbs – authors suggest that neutren 1998a]  the CD4BS, V3 loop, and CD4i epitopes – the activate YU2 V3 and V1/V2 loops – a similar effect is observent DO8i also enhances YU2 entry, ruling out Fc into hing libraries derived from bone marrow from a long	16 > DO8i > b14 > DA48 > b3 ralization is determined by the tion for this enhanced entry rved by sub-neutralizing eractions or Env cross-linking			
923	F105 (F-105)	Ab type CD4BS Donor Marshall Posner, Boston MA  References Posner1991, Thali1991, Thali1992a, Marasco1992, Wyatt1992, Posner1992b, Posner1992a, Moore1993a, Posner1993, Cavacini1993a, Cavacini1993b, Wyatt1993, Montefiori1993, Potts1993, Klasse1993a, Pincus1993b, Watkins1993, Marasco1993, Bagley1994, Thali1994, Cook1994 Cavacini1994b, Cavacini1994a, Earl1994, Chen1994a, Turbica1995, Posner1995, Cavacini1995, Sullivan1995, Khouri1995, Jagodzinski1996, Wolfe McDougal1996, Wisnewski1996, Pincus1996, Litwin1996, Chen1996, Parren1997c, D'Souza1997, Li1997, Cao1997b, Wyatt1997, Wyatt1998a, Cavacini1998b, Li1998, Cavacini1998a, Brand1998, Sullivan1998a, Kropelin1998, Sugiura1999, Giraud1999, Cavacini1999, Oscherwitz1999a, Robert-Guroff2000, Baba2000, Park2000, Yang2000, Si2001, Kolchinsky2001, York2001, Yang2002, Xu2002, Chakrabarti2002, Xiang2002b, Edwards2002, Grundner2002, Basmaciogullari2002, Zhang2002, Ferrantelli2002, Liu2002, Pantophlet2003  • F105: First description of F105, binds topographically near the CD4-binding site – inhibits binding of free, infectious virions to uninfected HT-H9 ced ose not react with virus adsorbed to uninfected HT-H9 cells – soluble rCD4 pre-bound to infected cells inhibits F105 binding – F105 inhibits infecti HT-H9 cells in standard neutralization assays with HIV-1 and MN strains [Posner1991]  • F105: F105 neutralization escape mutants result from changes in amino acids in discontinuous regions: C2, 256-262 and C3, 386-370 [Thali1991]  • F105: Amino acid substitutions that impair F105 neutralization inhibit gp120-CD4 interaction [Thali1992a]  • F105: MAb cDNA sequence – V H4 V71-4 rearranged with a D H D-D fusion product of dlr4 and da4, and with J H5 – V kappa is from the Humvk: germline gene joined with Jkappa 2 [Marasco1992]					

- F105: Precipitation of Delta 297-329 env glycoprotein, which has a deleted V3 loop, is much more efficient than precipitation of wild type [Wyatt1992]
- F105: F105 mediates ADCC against SF2 through the CD16+ population of PBMC does not mediate complement-dependent cytotoxicity [Posner1992b]
- F105: Significant enhancement of F105 binding to RF infected cells preincubated with V3-specific MAbs V3-2 and V3-1 [Posner1992a]
- The segment of the control of the co
- F105: Called F-105 neutralizes IIIB strong inhibition of HIV+ human sera binding to IIIB gp120 [Moore1993a]
- F105: F105 binds to and neutralizes selected lab strains and 3/9 HIV-1 primary isolates synergistic enhancement of neutralization by seropositive sera [Posner1993]
- F105: No neutralization of primary isolates observed (John Moore, pers comm)
- F105: Additive MN or SF2 neutralization when combined with anti-V3 MAbs 447-52D and 257-D [Cavacini1993a]

No. MAb ID HXB2 Location Author's Location Sequence Neutralizing Immunogen Species(Isotype)

- F105: Serum from all asymptomatic HIV-1 positive people tested block F105 binding, but only from 27% of symptomatic individuals [Cavacini1993b]
- F105: Binding to Delta V1/2 and Delta V1/2/3 mutant glycoproteins is 2.4- and 13-fold greater, respectively, than binding to wildtype gp120 [Wyatt1993]
- F105: Study of synergism between F105 and sera from vaccinated volunteers with V3-loop specific neutralization activity 2/3 sera demonstrated neutralization synergy, and 3/3 binding/fusion-inhibition synergy [Montefiori1993]
- F105: Study of synergism of neutralization and binding comparing F105 and sCD4 with the V3 MAbs: 50.1, 59.1, 83.1, and 58.2 synergy was observed, and the data suggest that binding of one ligand (F105) can increase the binding of the second (e. g. V3 loop MAbs) due to conformational changes [Potts1993]
- F105: The gp41 mutation 582(Ala to Thr) results in conformational changes in gp120 that confer neutralization resistance to a class of conformation sensitive neutralizing MAbs required >81 fold higher concentrations to neutralize the mutant than wild type [Klasse1993a]
- F105: Ab response in IIIB lab workers was compared to gp160 LAI vaccine recipients F105 was used as a control infected lab workers and some of the gp160 vaccinees had a MAb response that could inhibit gp120-CD4 binding, at lower titers than the infected lab workers [Pincus1993b]
- F105: A neutralization escape mutant (HXB2 A281V) was selected by growth of HXB2 in the presence of broadly neutralizing sera F105 neutralization was not affected by this mutation [Watkins1993]
- F105: Comparison of MAb F105 sequences with those of MAbs 21h and 15e [Bagley1994]
- F105: A mutation in gp41, 582 A/T, confers resistance to neutralization (also confers resistance to MAbs 48d, 21h, 15e and 17b) [Thali1994]
- F105: MAbs against the glycosphingolipid GalCer block HIV infection of normally susceptible CD4 negative cells from the brain and colon anti-CD4 MAbs moderately inhibit gp120 binding to GalCer, possibly through steric hindrance binding of GalCer to gp120 inhibited but did not completely block F105 binding[Cook1994]
- F105: Administered intravenously to four cynomologus monkeys, plasma pharmacokinetics and biological activity tested [Cavacini1994b]
- F105: Fab fragments show reduced capacity to neutralize IIIB, MN, and RF compared to intact IgG1, suggesting bivalent interaction may be important in binding and neutralization [Cavacini1994a]
- F105: Used as a positive control for CD4 BS antibodies in a study of the influence of oligomeric structure of Env in determining the repertoire of the Ab response [Earl1994]
- F105: A human CD4+ T lymphocyte line was transduced to express Fab fragments of F105 heavy and light chains are joined by an inter-chain linker in the transduced cells infected with HIV-1, the Fab binds intracellularly to the envelope protein and inhibits HIV-1 production secreted Fab fragments neutralize cell-free HIV-1 combined intra- and extracellular binding activities of the expressed Fab make transduced cells resistant to HIV-1 infection and also can protect surrounding lymphocytes by secreting neutralizing antibodies [Marasco1993, Chen1994a]
- F105: An immunoassay for titrating CD4BS serum antibody was developed using a gp120-coated solid phase and competition with MAb F105 109/110 French HIV-1+ sera and 51/56 HIV-1+ African sera had detectable CD4BS Abs using this assay, demonstrating CD4 binding site conservation among diverse subtypes CD4BS Abs were detected soon after seroconversion and persisted 0/21 HIV-2+ sera reacted, indicating that the HIV-1 and HIV-2 CD4BS Abs are not cross-reactive [Turbica1995]
- F105: Eight patient phase Ia trial for use as an immunotherapeutic no clinical or biochemical side effects observed, plasma levels of 10 ug/ml maintained for 21 days [Posner1995]
- F105: Efficient neutralization of T-cell adapted lines HXBc2 and MN, no neutralization of primary isolates 89.6, ADA and YU2 even some enhancement of infection of ADA and YU2 was observed [Sullivan1995]
- F105: Biotinylated F105 was used for competition studies with Ab derived from pregnant HIV-1+ women a correlation between maternal anti-CD4 BS Abs overlapping the F105 binding site and lack of HIV-1 transmission to infants was noted [Khouri1995]
- F105: Changing heavy chain from IgG1 to IgG3 increased neutralization efficiency [Cavacini1995]
- F105: The sulfated polysaccharide curdlan sulfate (CRDS) binds to the Envelope of T-tropic viruses and neutralizes virus deletion of the V3 loop results in less potent inhibition of F105 binding by CRDS binding site of F105 described as 256-257 ST, 368-370 DPE, 421 K, and 470-484 PGGGDMRDNWRSELY [Jagodzinski1996]
- F105: Phase I study MAb clearance in plasma has a 13 day half-life [Wolfe1996]

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- F105: Neutralizes HIV-1 LAI less potently than V3 specific MAbs [McDougal1996]
- F105: F105 is V H4 V-region heavy chain usage was examined and a bias of enhanced V H1 and V H4, and reduced V H3, was noted among HIV infected individuals [Wisnewski1996]
- F105: A panel of immunotoxins were generated by linking Env MAbs to ricin A immunotoxins mediated cell killing, but killing was not directly proportional to binding [Pincus1996]
- F105: Binding of F105 to oligomeric gp120 occurs despite the fact it cannot neutralize primary isolates [Litwin1996]
- F105: Intracellular co-expression of heavy and light chains of the Fab105 fragment MAb F105 was enhanced by inclusion of an internal ribosome entry site (IRES) sequence the Fab105 IRES expression cassette was cloned into an adeno-associated virus (AAV) shuttle vector, and transduced into human lymphocytes which were able to produce and secrete the Fab105 fragments while maintaining normal growth several primary HIV-1 patient isolates were effectively blocked [Chen1996]
- F105: Neutralizes TCLA strains, but not primary isolates [Parren1997c]
- F105: In a multilaboratory blinded study, failed to neutralize any of nine B clade primary isolates [D'Souza1997]
- F105: One of 14 human MAbs tested for ability to neutralize a chimeric SHIV-vpu+, which expressed HIV-1 IIIB env F105 could only achieve 50% neutralization alone all Ab combinations tested showed synergistic neutralization F105 has synergistic response with MAbs 694/98-D (anti-V3), 48d, 2F5, and 2G12, and also with HIVIG [Li1997]
- F105: Virus with the V1-V2 loop deleted was viable and more susceptible to neutralization by CD4i MAb 17b, and anti-V3 MAbs 1121, 9284, and 110.4, but not to a CD4BS MAb, F105 or sCD4 [Cao1997b]
- F105: Binds both gp120 and soluble gp120+gp41 complex efficiently, suggesting its gp120 epitope is not blocked by gp41 binding does not bind to HXBc2 gp120 if the 19 C-term amino acids, in conjunction with C1 positions 31-93, are deleted [Wyatt1997]
- F105: Summary of the implications of the crystal structure of the core of gp120 bound to CD4 and 17b with what is known about mutations that reduce NAb binding probable mechanism of neutralization by CD4BS Ab is direct interference with CD4 binding [Wyatt1998a]
- F105: Phase I dose escalation study, single dose of 100 or 500 mg/m2 was given to 4 HIV+ patients sustained levels, no immune response against F105, no toxicity, infused Ab retained function there was no evidence of anti-HIV-1 activity and virus was not diminished at day 1 or 7, by culture or plasma RNA [Cavacini1998b]
- F105: Neutralization synergy was observed when the MAbs 694/98-D (V3), 2F5 (gp41), and 2G12 (gp120 discontinuous) were used in combination, and even greater neutralizing potential was seen with the addition of a fourth MAb, F105 (CD4 BS) [Li1998]
- F105: The MAb F240 binds to the immunodominant region of gp41 and enhances infection in the presence of complement reactivity of F240 is enhanced by preincubation of cells with sCD4 or anti-CD4BS MAb F105 [Cavacini1998a]
- F105: Immunoprecipitation of gp120 and gp160 expressed from a rec Semliki Forest virus by F105 and IgG1b12 indicated that the SFV expressed HIV-1 Env was folded appropriately and SVF-HIV-1 Env vaccine gave the strongest anti-HIV-1 Env response in mice, when compared to an HIV-1 Env DNA vaccine and a rgp160 protein [Brand1998]
- F105: A comparison of 25 gp120 specific, conformation dependent MAbs was done and F105 was used for competition studies F105 did cross-compete with multiple CD4BS specific MAbs, however most could not neutralize even the autologous NL4-3 strains [Sugiura1999]
- F105: F105 enhances viral entry of viruses carrying the YU2 envelope glycoproteins, but neutralizes HXBc2 [Sullivan1998a]
- F105: Anti-C1 region MAb 87-135/9 blocks gp120 interaction with CD4+ cells blocking activity is additive when combined with antibodies which bind in the C4 region of gp120 (F105, 388/389, and b12) [Kropelin1998]
- F105: A mini-review of observations of passive administration of IgG NAbs conferring protection against intervenous or vaginal SHIV challenge, that considers why IgG MAbs might protect against mucosal challenge [Robert-Guroff2000]
- F105: A triple combination of 2F5, F105 and 2G12 effectively neutralized perinatal infection of macaque infants when challenged with SHIV-vpu+ the plasma half-life was 7.2 +/- 2.2 days [Baba2000]

No. MAb ID HXB2 Location Author's Location Sequence Neutralizing Immunogen Species(Isotype)

• F105: Host encoded intercellular adhesion molecule (ICAM-1) is incorporated by the HIV-1 virion and enhances viral infectivity – ICAM-1 does not modify virus sensitivity to antibodies 0.5beta or 4.8D or sCD4, but neutralizing ability of F105 was diminished in ICAM bearing virions in the presence of lymphocyte function-association antigen-1 (LFA-1) Ab [Fortin2000]

- F105: Six mutations in MN change the virus from a high-infectivity neutralization resistant phenotype to low-infectivity neutralization sensitive V3, CD4BS, and CD4i MAbs are 20-100 fold more efficient at neutralizing the sensitive form, although F105 was an exception and cannot neutralize either form of MN the mutation L544P reduced binding of all MAbs against gp120 by causing conformational changes [Park2000]
- F105: A combination of gp41 fusion with the GNC4 trimeric sequences and disruption of the YU2 gp120-gp41 cleavage site resulted in stable gp140 trimers (gp140-GNC4) that preserve and expose some neutralizing epitopes while occluding some non-neutralizing epitopes CD4BS MAbs (F105 and F91) and CD4i (17b and 48d) recognized gp140-GNC4 as well as gp120 or gp140 non-neutralizing MAbs C11, A32, 522-149, M90, and #45 bound to the gp140-GNC4 glycoprotein at reduced levels compared to gp120 MAbs directed at the extreme termini of gp120 C1 (135/9 and 133/290) and C5 (CRA-1 and M91) bound efficiently to gp140-GNC4 [Yang2000]
- F105: SHIV-HXBc2 is a neutralization sensitive non-pathogenic virus, and several *in vivo* passages through monkies yielded highly pathogenic SHIV KU-1—HXBc2 and the KU-1 clone HXBc2P3.2 differ in 12 amino acids in gp160—substitutions in both gp120 and gp41 reduced the ability of sCD4, IgG1b12, F105 and AG1121 to Env achieve saturation and full occupancy, and neutralize KU-1—17b and 2F5 also bound less efficiently to HXBc2P3.2, although 2G12 was able to bind both comparably [Si2001].
- F105: Mutations in two glcosylation sites in the V2 region of HIV-1 ADA at positions 190 and 197 (187 DNTSYRLINCNTS 199) cause the virus to become CD4-independent and able to enter cells through CCR5 alone these same mutations tended to increase the neutralization sensitivity of the virus, including to F105 [Kolchinsky2001]
- F105: Abs against the V3 loop (50.1, 58.2, 59.1, 257-D, 268-D, 447-52D), CD4BS (IgG1b12, 559-64D, F105), CD4i (17b), and to gp41 (2F5, F240) each showed similar binding efficiency to Env derived from related pairs of primary and TCLA lines (primary: 168P and 320SI, and TCLA: 168C and 320SI-C3.3), but the TCLA lines were much more susceptible to neutralization suggesting that the change in TCLA lines that make them more susceptible to NAbs alters some step after binding [York2001]
- F105: Uncleaved soluble gp140 (YU2 strain, R5 primary isolate) can be stabilized in an oligomer by fusion with a C-term trimeric GCN4 motif or using a T4 trimeric motif derived from T4 bacteriophage fibritin—stabilized oligomer gp140δ683(-FT) showed strong preferential recognition by NAbs IgG1b12 and 2G12 relative to the gp120 monomer, in contrast to poorly neutralizing MAbs F105, F91, 17b, 48d, and 39F which showed reduced levels of binding, and C11, A32, and 30D which did not bind the stabilized oligomer [Yang2002].
- F105: Passive immunization of neonate macaques with a combination of F105+2G12+2F5 conferred complete protection against oral challenge with SHIV-vpu+ or the combination b12+2G12+2F5 conferred partial protection against SHIV89.6 such combinations may be useful for prophylaxis at birth and against milk born transmission the synergistic combination of IgG1b12, 2G12, 2F5, and 4E10 neutralized a collection of HIV clade C primary isolates [Xu2002]
- F105: A modified gp140 (gp140deltaCFI), with C-term mutations intended to mimic a fusion intermediate and stabilize trimer formation, retained antigenic conformational determinants as defined by binding to CD4 and to MAbs 2F5, 2G12, F105, and b12, and enhanced humoral immunity without diminishing the CTL response in mice injected with a DNA vaccine [Chakrabarti2002]
- F105: A series of mutational changes were introduced into the YU2 gp120 that favored different conformations 375 S/W seems to favor a conformation of gp120 closer to the CD4-bound state, and is readily bound by sCD4 and CD4i MAbs (17b, 48d, 49e, 21c and 23e) but binding of anti-CD4BS MAbs (F105, 15e, IgG1b12, 21h and F91 was markedly reduced IgG1b12 failed to neutralize this mutant, while neutralization by 2G12 was enhanced 2F5 did not neutralize either WT or mutant, probably due to polymorphism in the YU2 epitope another mutant, 423 I/P, disrupted the gp120 bridging sheet, favored a different conformation and did not bind CD4, CCR5, or CD4i antibodies, but did bind to CD4BS MAbs [Xiang2002b]

No. MAb ID HXB2 Location Author's Location Sequence Neutralizing Immunogen Species(Isotype)

• F105: Truncation of the gp41 cytoplasmic domain of X4, R5, and X4R5 viruses forces a conformation that more closely resembles the CD4 bound state of the external Envelope, enhancing binding of CD4i MAbs 17b and 48d and of CD4BS MAbs F105, b12, and in most cases of glycosylation site dependent MAb 2G12 and the anti-gp41 MAb 246D – in contrast, binding of the anti-V2 MAb 697D and the anti-V3 MAb 694/98D were not affected – viruses bearing the truncation were more sensitive to neutralization by MAbs 48d, b12, and 2G12 – the anti-C5 MAb 1331A was used to track levels of cell surface expression of the mutated proteins [Edwards2002]

- F105: HIV-1 gp160δCT (cytoplasmic tail-deleted) proteoliposomes (PLs) containing native, trimeric envelope glycoproteins from R5 strains YU2 and JRFL, and X4 strain HXBc2, were made in a physiologic membrane setting as candidate immunogens for HIV vaccines—2F5 bound to gp160δCT with a reconstituted membrane ten-fold better than the same protein on beads, while such an affinity difference was not seen with F105 and 2G12—anti-CD4BS MAbs IgG1b12 and F105, A32 (C1-C4), C11 (C1-C5), and 39F (V3) MAbs bound gp160δCT PLs indistinguishably from gp160δCT expressed on the cell surface [Grundner2002].
- F105: gp120 mutants were used to define the CXCR4 binding site using CXCR4 displayed on paramagnetic proteoliposomes (PMPLs) to reduce non-specific gp120 binding—basic residues in the V3 loop and the β19 strand (RIKQ, positions 419-422) were involved, and deletion of the V1-V2 loops allowed CD4-independent CXCR4 binding—MAbs 17b (CD4i) and F105 (CD4BS) were used to study conformational changes in the mutants—the affinity of ΔV1 and ΔV1-V2 mutants for F105 was comparable to the wildtype—V3 mutants did not affect F105 binding—the K421A mutation in the β19 strand dramatically reduced F105 affinity, consistent with what is known about the F105 epitope [Basmaciogullari2002].
- F105: A rare mutation in the neutralization sensitive R2-strain in the proximal limb of the V3 region caused Env to become sensitive to neutralization by MAbs directed against the CD4 binding site (CD4BS), CD4-induced (CD4i) epitopes, soluble CD4 (sCD4), and HNS2, a broadly neutralizing sera 2/12 anti-V3 MAbs tested (19b and 694/98-D) neutralized R2, as did 2/3 anti-CD4BS MAbs (15e and IgG1b12), 2/2 CD4i MAbs (17b and 4.8D), and 2G12 and 2F5 thus multiple epitopes on R2 are functional targets for neutralization and the neutralization sensitivity profile of R2 is intermediate between the highly sensitive MN-TCLA strain and the typically resistant MN-primary strain [Zhang2002]
- F105: Review of NAbs that notes that F105 binds the CD4BS, in combination with other MAbs it can protect some macaques against SHIV infection, and that it has strong ADCC activity [Ferrantelli2002]
- F105: Review of NAbs that discusses mechanisms of neutralization, passive transfer of NAbs and protection in animal studies, and vaccine strategies [Liu2002]
- F105: Virion capture assays are not a good preditor of neutralization, and the presentation of epitopes using this assay seems to be different from that of functional Envelope spikes on primary isolates F105 and b6 could efficiently block the b12-mediated capture of infectious virions in a virus capture, but did not inhibit b12 neutralization while b12 was potent at neutralizing the three primary virions JR-CSF, ADA, and 89.6, the Abs F105, 19b, and Fab b6 were overall very poor neutralizers [Poignard2003]
- F105: Alanine scanning mutagenesis was used to compare substitutions that affected anti-CD4BS NAb b12 rec gp120s were engineered to contain combinations of Alanine substitutions that enhanced b12 binding, and while binding of b12 to these gp120 monomers was generally maintained or increased, binding by five non-neutralizing anti-CD4bs MAbs (b3, b6, F105, 15e, and F91) was reduced or completely abolished [Pantophlet2003]
- F105: NIH AIDS Research and Reference Reagent Program: 857

924 F91 (F-91)

Env gp120

No

**Ab type** CD4BS **Donor** James Robinson, University of Connecticut, Storrs

**References** Moore1993a, Moore1994b, Moore1996, Fouts1997, Mondor1998, Parren1998a, Binley1998, Fouts1998, Yang2000, Yang2002, Xiang2002b, Pantophlet2003

- F91: Called F-91 neutralizes IIIB reactive with SF-2 gp120 strong inhibition of HIV+ human sera binding to IIIB gp120 [Moore1993a]
- F91: Has strong cross-reactivity with gp120 monomers from most subtypes, A-F [Moore1994b]
- F91: Unusual pattern of reciprocal enhancement with several anti-V2 and V3 directed MAbs reciprocal inhibition of other CD4BS MAbs [Moore1996]
- F91: Study shows neutralization is not predicted by MAb binding to JRFL monomeric gp120, but is associated with oligomeric Env binding F91 bound monomer, did not bind oligomer or neutralize JRFL [Fouts1997]

No. MAb ID **HXB2** Location **Author's Location** Sequence **Neutralizing Immunogen** Species(Isotype) • F91: Weak inhibition of binding of Hx10 to CD4 positive or negative cells, weakly neutralizing [Mondor1998] • F91: The MAb and Fab binding to the oligomeric form of gp120 and neutralization were highly correlated – authors suggest that neutralization is determined by the fraction of Ab sites occupied on a virion irrespective of the epitope [Parren1998a] • F91: A panel of MAbs were shown to bind with similar or greater affinity and similar competition profiles to a deglycosylated or variable loop deleted core gp120 protein (Delta V1, V2, and V3), thus such a core protein produces a structure closely approximating full length folded monomer – CD4BS MAbs 15e, F91 and IgG1b12 bound better to the deleted protein than to wild type [Binley1998] • F91: CD4BS MAbs 15e, 21h, and F91 bind with even lower affinity than 205-43-1 and 205-42-15 to JRFL oligomer – conclusions of this paper contrast with [Parren1998a] [Fouts1998] • F91: A combination of gp41 fusion with the GNC4 trimeric sequences and disruption of the YU2 gp120-gp41 cleavage site resulted in stable gp140 trimers (gp140-GNC4) that preserve and expose some neutralizing epitopes while occluding some non-neutralizing epitopes – CD4BS MAbs (F105 and F91) and CD4i (17b and 48d) recognized gp140-GNC4 as well as gp120 or gp140 – non-neutralizing MAbs C11, A32, 522-149, M90, and #45 bound to the gp140-GNC4 glycoprotein at reduced levels compared to gp120 – MAbs directed at the extreme termini of gp120 C1 (135/9 and 133/290) and C5 (CRA-1 and M91) bound efficiently to gp140-GNC4 [Yang2000] • F91: Uncleaved soluble gp140 (YU2 strain, R5 primary isolate) can be stabilized in an oligomer by fusion with a C-term trimeric GCN4 motif or using a T4 trimeric motif derived from T4 bacteriophage fibritin – stabilized oligomer gp140 delta683(-FT) showed strong preferential recognition by NAbs IgG1b12 and 2G12 relative to the gp120 monomer, in contrast to poorly neutralizing MAbs F105, F91, 17b, 48d, and 39F which showed reduced levels of binding, and C11, A32, and 30D which did not bind the stabilized oligomer [Yang2002] • F91: A series of mutational changes were introduced into the YU2 gp120 that favored different conformations – 375 S/W seems to favor a conformation of gp120 closer to the CD4-bound state, and is readily bound by sCD4 and CD4i MAbs (17b, 48d, 49e, 21c and 23e) but binding of anti-CD4BS MAbs (F105, 15e, IgG1b12, 21h and F91 was markedly reduced – IgG1b12 failed to neutralize this mutant, while neutralization by 2G12 was enhanced – 2F5 did not neutralize either WT or mutant, probably due to polymorphism in the YU2 epitope – another mutant, 423 I/P, disrupted the gp120 bridging sheet, favored a different conformation and did not bind CD4, CCR5, or CD4i antibodies, but did bind to CD4BS MAbs [Xiang2002b] • F91: Alanine scanning mutagenesis was used to compare substitutions that affected anti-CD4BS NAb b12 - rec gp120s were engineered to contain

combinations of Alanine substitutions that enhanced b12 binding, and while binding of b12 to these gp120 monomers was generally maintained or increased, binding by five non-neutralizing anti-CD4bs MAbs (b3, b6, F105, 15e, and F91) was reduced or completely abolished [Pantophlet2003]

Env gp120 L HIV-1 infection human (IgG1)

925 GP13 (ARP3054)

Ab type CD4BS

## References

Schutten1993, Back1993, Bagley1994, Schutten1995a, Schutten1995b, Bolmstedt1996, Wisnewski1996, Schutten1996, Schutten1997, Vella2002

- GP13: Neutralized a broad range of HIV-1 strains from phylogenetically different subfamilies the following gp120 amino acid substitutions strongly inhibit binding: 256(S/Y), 257(T/G), 262(N/T), 368(D/R or K), 370(E/R or Q or D), 384(Y/E) [Schutten1993]
- GP13: Mutations in a neutralization resistant isolate obtained by passage of the IIIB isolate in chimpanzees reduced neutralization, but the escape was not
  as clear as seen with anti-V3 MAbs [Back1993]
- GP13: Neutralizes IIIB only slight inhibition of SI phenotype, and strong enhancement of NSI phenotype chimeric viruses, that incorporated different
  envs from the same donor [Schutten1995a]
- GP13: Neutralizes T-cell adapted viruses but not the SI strain 16.2, despite high binding affinity [Schutten1995b]
- GP13: Sera were obtained from guinea pigs vaccinated either with gp160, or with gp160 lacking N-linked glycans at N406, N448, and N463 these sera could block equally well both the CD4 BS MAb GP13 and the V3 MAb F58/H3 [Bolmstedt1996]
- GP13: GP13 is V H5 V-region heavy chain usage was examined and a bias of enhanced V H1 and V H4, and reduced V H3, was noted among HIV
  infected individuals [Wisnewski1996]
- GP13: IIIB neutralizing MAbs in vitro fail to neutralize in a mouse model it in vivo [Schutten1996]

Env Antibodies Tables

No. MA	Ab ID	HXB2 Location	Author's Location	Sequence	Neutralizing	g Immunogen	Species(Isotype)
		<ul> <li>GP13: Called ARP3 neutralization assays plasma/sera were sir</li> </ul>	054: Herpesvirus saimiris, and compared with a sta	-immortalized CD4+ T lym andard PBMC protocol – no N-2 cells) and PBMCs [Vell	d) an NSI-env chimeric virus [Sphocytes (HVS T cells) were usurralization sensitivities to a para [2002]	sed to isolate virus and p	
926 GP	244	<ul> <li>GP44: Exhibited a n binding: 256(S/Y), 2</li> </ul>	257(T/G), 262(N/T), 368( 1 – V-region heavy chain	neutralizing activity than G D/R or K), 370(E/R or Q or	L P13 and GP68 – the following g D) [Schutten1993] Dias of enhanced V H1 and V H		
927 GP	P68	<ul> <li>GP68: Neutralized a inhibit binding: 1170</li> <li>GP68: The gp41 mu sensitive neutralizing</li> <li>GP68: Neutralizes II envs from the same of GP68: GP68 is V H infected individuals</li> <li>GP68: The affect of enhanced, not X4 - 10 critical - tests with M enhanced or neutrali</li> </ul>	broad range of HIV-1 lat (K/W), 256(S/Y), 257(T/O) tation 582(Ala to Thr) resign MAbs – GP68 required IIB – only slight inhibition donor [Schutten1995a] 1 – V-region heavy chain [Wisnewski1996] Ab binding on infectivity the V3 region was the mand MAbs anti-V3 391/95-D and	G), 262(N/T), 368(D/R or Issults in conformational charmarkedly higher concentration of SI phenotype, and strousage was examined and a was studied by pseudotypi in determinant of Ab-mediand CD4BS-specific GP68 is was determined by Envelo	L  dillon2002 dlly different subfamilies – the factor of the conference of the confe	5(Y/H) [Schutten1993] dization resistance to a can wild type [Klasse1997/pe chimeric viruses, that [4, and reduced V H3, wherent phenotypes – R5 viron of the interaction bet	class of conformation [93a] at incorporated different was noted among HIV ruses were preferentially ween CCR5 and gp120 is
928 HF	F1.7	Env Ab type CD4BS References Chanh19 • HF1.7: An anti-Id an		i-CD4 MAb Leu-3a binds t	L precombinant gp160, suggesting	anti-idiotype g HF1.7 mimics CD4 [6	murine (IgM) Chanh1987]
929 HT	Γ5	<ul><li>References Moore 1</li><li>HT5: HT5, HT6, and</li><li>HT5: Despite highly</li><li>HT5: 205-46-9 was</li></ul>	994b, Moore1995a, Fouts d HT7 are also known as a cross-reactive binding to cross-reactive across clad 2, HT5, HT6, and HT7 ci	s1997, Fouts1998, Herrera2 205-43-1, 205-42-15, and 2 many primary and T-cell a les A-F, 205-43-1 very cross	L (weak) ox Biosystems, Houston, Texas 2003 05-46-9, respectively [Fouts199] dapted viral strains, only weakl -reactive but not quite as exten- monomeric gp120, bind equall	y neutralizes IIIB and M sive 205-46-9 [Moore19	994b]

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizin	g Immunogen	Species(Isotype)
		<ul> <li>HT5: Called 205-43 monomeric gp120, in neutralization activi suggests Env has tw by only b12 – Ab-gj</li> </ul>	3-1 – CD4BS MAbs b12 (indicating the topological ty of MAb b12 – the nonn to categories of binding sit	neutralizing) and 205-42 proximity of their epitop neutralizing MAbs partia te for CD4BS MAbs, on the use of monomeric	e not neutralizing – conclusions of 2-15, 204-43-1, 205-46-9 (nonneut pes, however, the nonneutralizing ally competed with b12 for Env bit is recognized by both b12 and non gp120 or Env-transfected cells do	ralizing) all cross-con CD4BS MAbs did not ading of the surface of neutralizing CD4BS N	npeted for binding to interfere with the Env-transfected cells – this MAbs, the other is recognized
930	HT6	References Moore 1  HT6: HT5, HT6, an HT6: Despite highly HT6: 205-46-9 was HT6: MAbs IgG1b1 IgG1b12 neutralizes HT6: HT5 and HT6 HT6: Called 205-42 monomeric gp120, i neutralization activi suggests Env has tw by only b12 – Ab-g	994b, Moore1995a, Fouts of HT7 are also known as a y cross-reactive binding to cross-reactive across clad 12, HT5, HT6, and HT7 cross JRFL [Fouts1997] is bind JRSF oligomer but well-15 – CD4BS MAbs b12 indicating the topological ty of MAb b12 – the nonner ocategories of binding site.	s1997, Fouts1998, Herre 205-43-1, 205-42-15, a many primary and T-ce es A-F, 205-43-1 was no ross-compete for binding with low affinity, and are (neutralizing) and 205-4 proximity of their epitopeutralizing MAbs partiate for CD4BS MAbs, on the use of monomeric	L (weak) mox Biosystems, Houston, Texas rra2003 nd 205-46-9, respectively [Fouts19 ell adapted viral strains, only weak of quite as extensively cross-reacti g to monomeric gp120, bind equal e not neutralizing – conclusions of 42-15, 204-43-1, 205-46-9 (nonner pes, however, the nonneutralizing elly competed with b12 for Env bin the recognized by both b12 and non gp120 or Env-transfected cells do	ly neutralizes IIIB and we [Moore1994b] ly well, inhibit gp120 this paper contrast wi attralizing) all cross-co CD4BS MAbs did not adding of the surface of neutralizing CD4BS M	-sCD4 interactions, but only ith [Parren1998a] [Fouts1998] impeted for binding to interfere with the Env-transfected cells – this MAbs, the other is recognized
931	HT7	References Moore I HT7: HT5, HT6, an HT7: Despite highly of other isolates [Moore I = 10.5] HT7: 205-46-9 was HT7: MAbs IgG1b1 IgG1b12 neutralizes HT7: Binds JRSF o [Parren1998a] – aut counteracts the neut HT7: Called 205-46 monomeric gp120, in neutralization activities suggests Env has two by only b12 – Ab-gi	994b, Moore 1995a, Fouts of HT7 are also known as by cross-reactive binding to core 1995a] cross-reactive across clad 12, HT5, HT6, and HT7 cross JRFL [Fouts 1997] ligomer with high affinity, hors propose a model whe cralizing effect [Fouts 1998 6-9 – CD4BS MAbs b12 (indicating the topological ty of MAb b12 – the nonner ocategories of binding site.	s1997, Fouts1998, Herre 205-43-1, 205-42-15, a p many primary and T-ce es A-F, 205-43-1 was cross-compete for binding at least as high as IgG1 are H7 may inhibit CD4 proximity of their epitopeutralizing MAbs partiate for CD4BS MAbs, on the use of monomeric	L (IIIB) Tanox Biosystems, Houston, Texastra2003 and 205-46-9, respectively [Fouts19] adapted viral strains, only neutross-reactive, but not quite as extern to monomeric gp120, bind equal b12, but IgG1b12 is neutralizing, binding, but cause a conformation 2-15, 204-43-1, 205-46-9 (nonneutroses, however, the nonneutralizing ally competed with b12 for Env binder recognized by both b12 and non gp120 or Env-transfected cells do	palizes IIIB well, with a lizes IIIB well, with a lizes IIIB well, with a lize IIIB well, with a lize IIIB well, inhibit gp120. H7 is not – conclusional shift which enhance ralizing) all cross-concD4BS MAbs did not a lize IIIB well a lize IIIB well, with a lize IIB well a li	-sCD4 interactions, but only as of this paper contrast with es CCR5 binding and thus appeted for binding to interfere with the Env-transfected cells – this MAbs, the other is recognized

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizing	g Immunogen	Species(Isotype)		
932	ICR 39.13g (ICR39.13g, 39.13g)	Ab type CD4BS A References Cordell McKeating1996b, A ICR 39.13g: Cross-	Armstrong1996a, Klasse competes with MAbs IC	d C. Dean McKeating1992c, M 1996, Peet1998, Vella R 39.3b and 15e [Co	acKeating 1993b, Moore 1993a, Thali 199 n 2002 rdell 1991]				
		<ul><li>[McKeating1992a]</li><li>ICR 39.13g: Neutra</li><li>ICR 39.13g: Confor [Moore1993a]</li></ul>	lization activity against	HXB10, RF, SF-2 and denatured gp120 – w	binding – exerts a synergistic effect in c d MN strains of HIV-1 [McKeating199; reak neutralization of IIIB – strong inhil	3b]			
		<ul> <li>ICR 39.13g: Kinetic neutralization with 2</li> <li>ICR 39.13g: The gr sensitive neutralizin</li> <li>ICR 39.13g: Called</li> </ul>	es of neutralization studi 2.3 molecules of IgG [M 41 mutation 582(Ala to g MAbs – ICR 39.13g re	ed – no lag for 39.3b cLain1994] Thr) results in confor equired moderately h	while ICR 39.13g and ICR 41.1i have rmational changes in gp120 that confer igher concentrations to neutralize the m lize chimeric virus with gp120 from pri	neutralization resistanutant than wild type	nce to a class of conformation [Klasse1993a]		
		<ul> <li>[McKeating1996b]</li> <li>ICR 39.13g: Post-attachment neutralization mechanism, in contrast to MAb 39.3b [Armstrong1996a]</li> <li>ICR 39.13g: Variants of LAI have differing neutralization susceptibility to 39.13g [Klasse1996]</li> <li>ICR 39.13g: The most variable amino acids in the V3 loop were replaced with serines to make the immunodominant V3 loop less immunogenic – these changes did not affect the ability of sCD4 or MAbs to V1/V2, C1 and C4 to bind – ICR 39.13g was not affected by V3 serine substitutions – mice injected with serine substituted gp120 had a reduced response relative to wildtype, and no enhanced immunogenicity of conserved regions [Peet1998]</li> <li>ICR 39.13g: Called ARP390/391, but no such entry was found at the UK Medical Research Council AIDS reagent web site: Herpesvirus saimiri-immortalized CD4+ T lymphocytes (HVS T cells) were used to isolate virus and perform HIV-1 neutralization assays, and compared with a standard PBMC protocol – neutralization sensitivities to a panel of MAbs and to homologous or heterologous plasma/sera were similar for HVS T cells (CN-2 cells) and PBMCs [Vella2002]</li> <li>ICR 39.13g: UK Medical Research Council AIDS reagent: ARP390</li> </ul>							
933	ICR 39.3b (39.3, 39.3b, ICR39.3b)	Ab type CD4BS References Cordell ICR 39.3b: also knot ICR 39.3b: Cross-cot ICR 39.3b: Conform ICR 39.3b: Kinetics ICR 39.3b: Neutrali ICR 39.3b: Called 3 ICR 39.3b: Called 3	own as 39.3, 39.3b and Io competes with MAbs ICF mational, does not bind to s of neutralization studie izes only if the antibody 19.3b – increased binding 19.3 – summary of the in	Dean Moore1993c, McLai CR39.3b 2 39.13g and 15e [Co o denatured IIIB [Mo d – no lag for 39.3b, is added prior to the a g when V1/V2 or V1/ uplications of the cryst	n1994, Armstrong1996a, Jeffs1996, W	ags of 5 and 15 min r ontrast to 39.13g [Arn (effs1996] d to CD4 and 17b wit	nstrong1996a] th what is known about		

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizing	Immunogen	Species(Isotype)
	•	ICR 39.3b: UK M	ledical Research Council AI	DS reagent: ARP39	91		
934	IgG1b12 (Fab	Env	gp120		LP	HIV-1 infection	human (IgG1κ)
	b12, Fab 3B3,	Ab type CD4BS	Donor D. Burton, Scripps	Research Institute,	La Jolla, CA, also J. Geltowsky and J. P	yati, R. W. Johnson	Pharmaceutical Research Inst.
	MAb	La Jolla, CA					
	IgG1b12,	References Burton	n1991, Barbas III1992, Rob	en1994, Burton199	4, Moore1994b, Sattentau1995a, Moore	1995a, Moore1995b	Parren1995, Trkola1995,
	IgG1-b12,	Ditzel1995, Sulliva	an1995, Yang1997c, Moore	1996, Gauduin1996	6, Poignard1996b, Poignard1996a, Trkol	a1996a, Sattentau19	96, McKeating1996a,
	IgG1 b12,	D'Souza1997, Sch	nutten1997, Mo1997, Fouts	1997, Li1997, Kessl	er II1997, Moore1997, Stamatatos1997,	Ditzel1997, Ugolini	1997, Wyatt1997,
	IgGB12,	Burton1997, Boots	s1997, Parren1997c, Parren	1997b, Parren1997a	, Valenzuela1998, Wyatt1998a, Mondor	1998, Parren1998a,	Connor1998, Binley1998,
	b4/12, b12,	Fouts1998, Takefn	nan1998, Parren1998b, Bra	nd1998, Schonning	1998, Sullivan1998a, Frankel1998, Krop	elin1998, Stamatato	s1998, Poignard1999,
	1b12, im-	Jackson1999, Hioe	e1999, Montefiori1999, Gir.	aud1999, Beddows1	999, Binley1999, Grovit-Ferbas2000, L	y2000, Nyambi2000	, Park2000, Si2001,
	munoglobulin	Kolchinsky2001, S	Saphire2001a, Saphire20011	b, Yang2001, York2	001, Zwick2001a, Zwick2001b, Zwick2	001c, Parren2001, P	oignard2001,
	G1b12,	Zeder-Lutz2001, S	Spenlehauer2001, Verrier20	01, Hofmann-Lehm	ann2001, Xu2001, Srivastava2002, Gold	ling2002b, Sanders2	002, Schulke2002, Yang2002,
	ARP3065,	Saphire2002, Scan	ılan2002, Xu2002, Chakrab	arti2002, Vella2002	, Xiang2002b, Edwards2002, Grundner	2002, Zhang2002, K	lasse2002, Ferrantelli2002,
	IgG1 b12)	Liu2002, Poignard	d2003, Pantophlet2003, Her	rera2003			
	•	IgG1b12: Fab b12	was derived from IgG1b12	. Fab 3B3 was deriv	ved from Fab b12 by random mutageness	is and selected for in	creased affinity to sgp120 –

- IgG1b12: Fab b12 was derived from IgG1b12, Fab 3B3 was derived from Fab b12 by random mutagenesis and selected for increased affinity to sgp120 database note
- IgG1b12: The original Fab fragment was derived from a combinatorial phage library from bone marrow of an HIV-1 positive individual who had been asymptomatic for six years [Burton1991]
- IgG1b12: Anti-CD4 binding site Fab, potent neutralizing activity, greater affinity for a subpopulation of gp120 molecules suggested to be in a mature confirmation mutations in gp120 that abrogate binding: 368 D/R or D/T, 370 E/R, and 477 D/V, of clone HXBc2 of LAI sensitive to V1 and V2 substitutions [Roben1994]
- IgG1b12: Very potent neutralization, of primary and lab strains, at concentrations that could be achieved by passive immunization reduced binding with A,C, and D clade viruses relative to B clade, poor reactivity with E clade isolates that were refractive to neutralization by sera from HIV-1+ donors could be neutralized by IgG1 b12 [Burton1994]
- IgG1b12: Cross-reactive with some gp120s, (but not all), from clades A-D not reactive with gp120 from clades E or F [Moore1994b]
- IgG1b12: Formalin inactivation of virus at 0.1% formalin for 10 hours at 4 degrees was optimal for inactivation of virus while maintaining epitope integrity [Sattentau1995c]
- IgG1b12: Anti-CD4 binding site MAb very potent neutralization of a number of primary isolates [Moore1995a]
- IgG1b12: Complete protection against HIV-1 infection was achieved in hu-PBL-SCID mice by passive immunization with physiologically relevant doses pharmacokinetics showed serum half-life of 30.2 +/- 1.3 hours for Fab b12 and 7.4 +/- 0.7 days for IgG1 b12 in mice, but IgG1 half-lives in human are generally between 21-23 days [Parren1995, Parren1997a]
- IgG1b12: Called BM12 broad cross-clade neutralization of primary isolates additive neutralization in combination with MAb 2F5 [Kessler1995]
- IgG1b12: Review: unusual properties for anti-CD4 BS MAb: sensitive to V2 substitutions, preferential recognition of the oligomer on the cell surface [Moore1995b]
- IgG1b12: Could potently neutralize primary isolates from within clade B, but showed a slight reduction in efficacy outside of clade B [Trkola1995]
- IgG1b12: Because Fab b12 shows reduction in binding when the V2 loop is deleted and when aa 183/184 PI/SG substitutions are made competition studies were done with Fab L78 and anti-V2 MAbs SC258 and 684-238 and they do not compete with IgG1b12 [Ditzel1995]
- IgG1b12: Fab b12 showed potent neutralization of T-cell-line-adapted strains, but much reduced neutralization of 3 primary isolates 2 of the 3 primary isolates also had reduced binding affinity, but the third was as efficiently immunoprecipitated as HXBc2 [Sullivan1995]
- IgG1b12: Saturation mutagenesis of the complementarity-determining region and optimization strategies were used to create very high affinity versions of this Fab increased affinity was dominated by a slowing of the off rate [Yang1997c]

Env Antibodies HIV Antibodies Tables

No. MAb ID HXB2 Location Author's Location Sequence Neutralizing Immunogen Species(Isotype)

• IgG1b12: Potent neutralizing ex vivo of virus taken directly from plasma of HIV-1 infected individuals – little correlation between neutralization sensitivity of passaged virus and plasma derived virus – more effective than MAb 19b [Gauduin1996]

- IgG1b12: Review: Unique among anti-CD4BS MAbs in terms of being potent against both lab adapted virus and primary isolates one of three MAbs (IgG1b12, 2G12, and 2F5) generally accepted as having significant potency against primary isolates [Poignard1996b]
- IgG1b12: Anti-CD4BS MAbs 15e, 21h, and IgG1b12 did not cause gp120 dissociation from virus, or exposure of the gp41 epitope of MAb 50-69, in contrast to CD4i MAb 48d and anti-V3 neutralizing MAbs [Poignard1996a]
- IgG1b12: Neutralizes JR-FL inhibits gp120 interaction with CCR-5 in a MIP-1beta-CCR-5 competition study [Trkola1996a]
- IgG1b12: Review: Only four epitopes have been described which can stimulate a useful neutralizing response to a broad spectrum of primary isolates, represented by the binding sites of MAbs: 447-52-D, 2G12, Fab b12, and 2F5 [Sattentau1996]
- IgG1b12: In a multilab evaluation of monoclonal antibodies, only IgG1b12, 2G12, and 2F5 could neutralize at least half of the 9 primary test isolates at a concentration of < 25 mug per ml for 90% viral inhibition IgG1b12 failed to neutralize only 1/9 primary isolates, although there was some variation between test sites [D'Souza1997]
- IgG1b12: Inhibited some SI- and NSI-env chimeric viruses but enhanced one NSI-env chimeric virus 3 fold [Schutten1997]
- IgG1b12: JRCSF was cultured in the presence of IgG1b12 until a 100-fold resistance to neutralization was selected resistance was due to three changes: V2 substitution D182N and C3 substitution P365L conferred resistance, and V2 D164N was also required for a viable virus IgG1b12 resistant virus remained sensitive to MAbs 2G12 and 2F5 [Mo1997]
- IgG1b12: Study shows neutralization is not predicted by MAb binding to JRFL monomeric gp120, but is associated with oligomeric Env binding –
   IgG1b12 bound monomer, oligomer, and neutralized JRFL [Fouts1997]
- IgG1b12: b12 was used in its IgG1 form of 14 human MAbs, the most potent neutralizer of SHIV-vpu+, which expressed HIV-1 IIIB env all Ab combinations tested showed synergistic neutralization b12 has a synergistic response with MAbs 694/98-D (anti-V3), 2F5, and 2G12 [Li1997]
- IgG1b12: 35 primary isolates were tested and all were neutralized by IgG1b12 (including 4, UG270, RW92/026, ZB20, and 301727 which been had reported as not neutralized by IgG1b12 [Trkola1995]) IgG1b12 could neutralize even when added after the virus to the culture selection for 400-fold increased affinity did not enhance neutralization by antibody IgG1b12 was more potent with greater breadth than MAb 2F5 [Kessler II1997]
- IgG1b12: Review: MAbs 2F5, 2G12 and IgG1b12 have potential for use in combination with CD4-IgG2 as an immunotherapeutic or immunoprophylactic homologous MAbs to these are rare in humans and vaccine strategies should consider including constructs that may enhance exposure of these MAbs' epitopes [Moore1997]
- IgG1b12: Viral binding inhibition by IgG1b12 strongly correlated with neutralization (all other neutralizing MAbs tested showed some correlation except 2F5) [Ugolini1997]
- IgG1b12: Major deletions in C1 and C5 and deletions of the V1V2 and V3 loops do not diminish binding [Wyatt1997]
- IgG1b12: This is a review that includes a description of IgG1b12, noting approximately equivalent affinities for sgp120 and unprocessed gp160, and somewhat enhanced affinity for the native oligomer on TCLA viruses primary viruses have reduced affinity, but still in the useful range for neutralization there can be complete protection in hu-PBL-SCID mice with Ab even when administered several hours after viral challenge competes with sCD4, but unlike other CD4BS antibodies, it is sensitive to mutations in V2 [Burton1997]
- IgG1b12: In this review, the technique and potential application of Fab expression and selection in phage display libraries, and subsequent production of IgG molecules is discussed b12 is exceptionally potent at neutralization and can successfully neutralize most B clade primary isolates, and many isolates from other subtypes as well 3B3 was derived from b12 by selection for higher affinity using the CDR walking strategy 3B3 has 8-fold enhancement of binding, a linear correlation was found between neutralization and affinity, and 3B3 can neutralize strains b12 cannot [Parren1997a]
- IgG1b12: Abs that recognize discontinuous epitopes can identify mimotopes from a phage peptide display library IgG1b12 blocks CD4 binding and is the most potent neutralizing Ab many 15 and 21-mer phage inserts were recognized, but it was not possible to derive a consensus common features were a W and at least one acidic residue, and one sequence was found multiple times: NWPRWWEEFVDKHSS, and this peptide could compete with gp120 two short stretches found in the phage peptides might mimic gp120 components of the epitope: positions 382-384, FFY(I), and 423-426 I(FV)I(V)NM [Boots1997]

No. MAb ID HXB2 Location Author's Location Sequence Neutralizing Immunogen Species(Isotype)

• IgG1b12: Fab b12 is unusual in that it binds to gp140 and monomeric gp120 with similar affinities, and with a higher affinity to the native oligomer—authors propose this antibody may be exceptional because it binds the virus rather than viral debris—IgG1b12 can protect against infection prior to or shortly after challenge of hu-PBL-SCID mice with TCLA strains and primary strains, but the serum concentrations required *in vivo* were higher than for *in vitro* neutralization [Parren1997c, Parren1997b].

- IgG1b12: MAb was slightly more efficient at neutralization than Fab inhibits viral binding to cells and viral entry doesn't affect CD4-independent binding to T-cells [Valenzuela1998]
- IgG1b12: Summary of the implications of the crystal structure of the core of gp120 bound to CD4 and 17b with what is known about mutations that reduce NAb binding probable mechanism of neutralization by CD4BS Ab is direct interference with CD4 binding IgG1b12 is an unusual CD4BS antibody because it is particularly potent as a neutralizing antibody and it is susceptible to changes in the V1-V2 stem loop structure, and so it may disrupt an interaction between CD4 and conserved amino acids on the V1-V2 stem [Wyatt1998a]
- IgG1b12: Enhances binding of Hx10 to CD4 positive or negative HeLa cells, inhibits binding to CD4+ T-cell line A3.01 neutralizes HeLa and A3.01 cell Hx10 infection [Mondor1998]
- IgG1b12: IgG1b12, Fab b12 and 3B3 derived from b12 were all included in this study the rank order of Fab binding affinity to monomeric gp120 (Loop 2 > 3B3 > b12 = DO8i > b11 > b3 > b14 > b13 > DO142-10 > DA48 > L17) was markedly different than Fab binding affinity to the mature oligomeric form (3B3 > b12 > DO142-10 > Loop 2 > b11 > L17 > b6 > DO8i > b14 > DA48 > b3 > b13) and binding to oligomeric form and neutralization were correlated for both Fabs and MAbs authors suggest that neutralization is determined by the fraction of Ab sites occupied on a virion irrespective of the epitope binding affinity of divalent IgG1b12 is 17-fold greater than monovalent Fab b12 [Parren1998a]
- IgG1b12: Ab from gp120 vaccinated individuals prior to infection, who subsequently became HIV infected, could not achieve 90% neutralization of the primary virus by which the individuals were ultimately infected these viruses were not particularly refractive to neutralization, as determined by their susceptibility to neutralization by MAbs 2G12, IgG1b12, 2F5 and 447-52D [Connor1998]
- IgG1b12: A panel of MAbs were shown to bind with similar or greater affinity and similar competition profiles to a deglycosylated or variable loop deleted core gp120 protein (Delta V1, V2, and V3), thus such a core protein produces a structure closely approximating full length folded monomer CD4BS MAbs 15e, F91 and IgG1b12 bound better to the deleted protein than to wild type [Binley1998]
- IgG1b12: Binds JRSF oligomer with high affinity, as do 205-46-9 and 2G6, but IgG1b12 is neutralizing, the other two are not conclusions of this paper contrast with Parren98 authors propose a model where 205-46-9 and 2G6 may inhibit CD4 binding, but cause a conformational shift which enhances CCR5 binding and thus counteracts the neutralizing effect rank order of CD4BS antibodies oligomer binding is IgG1b12 = 2G6 = 205-46-9 > 205-43-1 = 205-42-15 > 15e = 21h = F91, and the only thing notably distinguishing about neutralizing IgG1b12 is that it depends on residues in V2 [Fouts1998]
- IgG1b12: Induces Complement-mediated lysis in MN but not primary isolates primary isolates are refractive to CML [Takefman1998]
- IgG1b12: MAbs 2G12, 2F5 and b12 are broadly neutralizing, as are some human polyconal sera, but this paper describes a set of primary isolates that are resistant to all three MAbs and 2 broadly neutralizing sera results indicate that resistance levels of pediatric isolates might be higher than adult isolates resistance in general did not seem to be conferred by a loss of binding affinity for gp120 or gp41, rather by a more global perturbation of oligomeric Envelope [Parren1998b]
- IgG1b12: Immunoprecipitation of gp120 and gp160 expressed from a rec Semliki Forest virus by F105 and IgG1b12 indicated that the SFV expressed HIV-1 Env was folded appropriately and SVF-HIV-1 Env vaccine gave the strongest anti-HIV-1 Env response in mice, when compared to an HIV-1 Env DNA vaccine and a rgp160 protein [Brand1998]
- IgG1b12: MAbs 654-D100 and IgG1b12 neutralized viruses HIV-BRU and a mutated virus that lacks the V3 loop glycan equally effectively in contrast, sera from guinea pigs immunized with BRU gp120 neutralize viruses more effectively that lack the V3 glycan[Schonning1998]
- IgG1b12: Fab b12 the HIV-1 virus YU2 entry can be enhanced by MAbs binding to the CD4BS, V3 loop, and CD4i epitopes the activation for this enhanced entry state could be conferred on HxB2 by introducing the YU2 V3 loop, or the YU2 V3 and V1/V2 loops a similar effect is observed by sub-neutralizing concentrations of sCD4 and the effect is dependent of CCR5 Fab fragment b12 also enhances YU2 entry, ruling out Fc interactions or Env cross-linking as a mechanism, while neutralizing HXBc2 [Sullivan1998a]

**HIV Antibodies Tables** 

No. MAb ID HXB2 Location Author's Location Sequence Neutralizing Immunogen Species(Isotype)

- IgG1b12: anti-C1 region MAb 87-135/9 blocks gp120 interaction with CD4+ cells blocking activity is additive when combined with antibodies which bind in the C4 region of gp120 (F105, 388/389, and b12) [Kropelin1998]
- IgG1b12: Deleting the V2 loop of neutralization-resistant HIV-1 isolate SF162 does not abrogate its replication in PBMC or macrophages, but it enhances its neutralization sensitivity to sera from patients with B clade infection up to 170-fold, and also enhances sensitivity to sera from clades A through F deletion of V2, but not V1, diminished neutralization by CD4BS MAb IgG1b12, in contrast to 654.30D and IgGCD4 [Stamatatos1998]
- IgG1b12: Infection of dendritic cells cultured from CD14+ blood cells or from cadaveric human skin was blocked by neutralizing MAbs IgG1b12, or 2F5 and 2G12 delivered together, but not by control non-neutralizing anti-gp120 MAb 4.8D, indicating that NAbs could interrupt early mucosal transmission events [Frankel1998]
- IgG1b12: The presence of leukocyte function-associated molecule 1 (LFA-1) promotes virus infectivity and hinders neutralization, and anti-LFA-1 MAbs can enhance the neutralizing effect of anti-HIV V3 MAb 447-52D and anti-HIV CD4BS MAb IgG1b12 non-neutralizing anti-HIV CD4BS MAb 654-D did not become neutralizing in the presence of anti-LFA-1 MAbs [Hioe1999]
- IgG1b12: rgp120 derived from a R5X4 subtype B virus was used to vaccinate healthy volunteers and the resulting sera were compared with sera from HIV-1 positive subjects and neutralizing MAbs TCLA strains showed enhanced IgG1b12 neutralization sensitivity relative to PBMC-adapted lines IgG1b12 was able to bind, with low affinity, to the rgp120 monomer HIV-1 W61D [Beddows1999]
- IgG1b12: A meeting summary presented results regarding neutralization D. Burton and J. Mascola presented results concerning passive immunization and protection of hu-PBL-SCID mice and macaques, respectively, and both found combinations of MAbs that were able to achieve 99% neutralization in vitro corresponded to efficacy in vivo [Montefiori1999]
- IgG1b12: does not inhibit attachment of virus to cells and was used as a control of a study of neutralization by a MAb F58 based micro antibody [Jackson1999]
- IgG1b12: Hu-PBL-SCID mice were infected with HIV-1s JRCSF and SF162 to study the effect of NAbs on an established infection at day 6 post infection, mice were given 50 mg/kg of b12, an amount that would have been protective if given up to 8 hours post-infection, and 100-fold higher than the amount required for 90% neutralization in vitro no significant differences in the initial rate of decrease in viral load or the plateau levels of viral RNA between the b12 treated and control mice were seen in most of the Ab treated mice escape mutants were observed with varying patterns of mutations a combination of b12, 2G12 and 2F5 protected 1/3 mice, and an isolate from one of the other two was resistant to neutralization by all three MAbs [Poignard1999]
- IgG1b12: The MAbs with the broadest neutralizing activity, IgG1b12, 2G12 and 2F5, all have high affinity for the native trimer, indicating that they were raised in an immune response to the oligomer on the virion surface rather than dissociated subunits a disulfide linked gp120-gp41 (SOS gp140) was created to mimic the native conformation of Env and explore its potential as an immunogen SOS gp140 is recognized by NAbs IgG1b12, 2G12, and CD4-IgG2, and also by anti-V3 MAbs 19b and 83.1 SOSgp140 is not recognized by C4 region MAbs that neutralize only TCLA strains, G3-42 and G3-519 nor did it bind C11, 23A, and M90, MAbs that bind to gp120 C1 and C5, where it interacts with gp41 MAbs that bind CD4 inducible epitopes, 17b and A32 were very strongly induced by CD4 in SOS gp140 anti-gp41 MAbs that bind in the region that interacts with gp120, 7B2, 2.2B, T4, T15G1 and 4D4, did not bind to SOSgp140, in contrast to 2F5, which binds to the only gp41 epitope that is well exposed in native gp120-gp41 complexes [Binley1999]
- IgG1b12: To determine the antigenicity of virus killed by thermal and chemical inactivation, retention of conformation-dependent neutralization epitopes was examined, and exposure of CD4BS epitopes was found to be enhanced (MAbs IgG1b12, 205-46-9, and 205-43-1) binding to 2G12 and 447-52D epitopes was essentially unaltered the 17b CD4i epitope was also exposed [Grovit-Ferbas2000]
- IgG1b12: SF162 is a neutralization-resistant HIV-1 isolate N-linked glycosylation modifications in the V2 loop of the SF162 gp120 revealed that these sites prevent neutralization by CD4BS MAbs (IgG1b12 and IgGCD4), and protect against neutralization by V3 MAbs (447-D and 391-95D) V2-region glycosylation site mutations did not enhance neutralization resistance to V2 MAbs (G3.4 and G3.136) or CD4i MAbs (17b and 48d) V2 glycosylation site modification allows increased infection of macrophages, probably due to glycosylated forms requiring fewer CCR5 molecules for viral entry [Ly2000]

No. MAb ID HXB2 Location Author's Location Sequence Neutralizing Immunogen Species(Isotype)

• IgG1b12: 26 HIV-1 group M isolates (clades A to H) were tested for binding to 47 MAbs, including 6 CD4BS MAbs – CD4BS MAbs bound consistently to most isolates of clade D, but poorly to isolates of other clades with the exception of broadly reactive MAb IgG1b12, binding to 22 of 26 isolates tested – 8 MAbs were tested for neutralization and MAb IgG1b12 was most potent, with 90% neutralization of 3/5 isolates tested [Nyambi2000]

- IgG1b12: Fab b12 was used six mutations in MN change the virus from a high-infectivity neutralization resistant phenotype to low-infectivity neutralization sensitive V3, CD4BS, and CD4i MAbs are 20-100 fold more efficient at neutralizing the sensitive form the mutation L544P reduced binding of all MAbs against gp120 by causing conformational changes [Park2000]
- IgG1b12: SHIV-HXBc2 is a neutralization sensitive non-pathogenic virus, and several in vivo passages through monkey's yielded highly pathogenic SHIV KU-1 HXBc2 and the KU-1 clone HXBc2P3.2 differ in 12 amino acids in gp160 substitutions in both gp120 and gp41 reduced the ability of sCD4, IgG1b12, F105 and AG1121 to Env achieve saturation and full occupancy, and neutralize KU-1 17b and 2F5 also bound less efficiently to HXBc2P3.2, although 2G12 was able to bind both comparably [Si2001]
- IgG1b12: Mutations in two glcosylation sites in the V2 region of HIV-1 ADA at positions 190 and 197 (187 DNTSYRLINCNTS) cause the virus to become CD4-independent and able to enter cells through CCR5 alone these same mutations tended to increase the neutralization sensitivity of the virus, except the mutation 197 S/R which resulted in a carbohydrate addition to 195 N that disrupts the IgG1b12 binding site [Kolchinsky2001]
- IgG1b12: This paper describes the technical aspects of the crystallization of b12 at a resolution of 2.7 angstroms with all 12 Ig domains resolved [Saphire2001a]
- IgG1b12: This paper describes the biological implications of the crystal structure of b12 a remarkable feature of this antibody is a long protruding finger-like CDR H3 that can dock in the recessed CD4-binding site a contact residues in gp120 are modeled, with numbering based on the variable loop-deleted crystal structure of gp120 [Saphire2001b]
- IgG1b12: Primary isolates YU2 and ADA are more resistant to IgG1b12 neutralization than HXBc2: 90% Neutralization of HXBc2 is observed with 1.25 ug of IgG1b12, while ADA and YU2 require 2.5 and 5 ug respectively to achieve 50% neutralization, and 90% neutralization could not be achieved with 10 or 20 ug of IgG1b12, respectively [Yang2001]
- IgG1b12: Abs against the V3 loop (50.1, 58.2, 59.1, 257-D, 268-D, 447-52D), CD4BS (IgG1b12, 559-64D, F105), CD4i (17b), and to gp41 (2F5, F240) each showed similar binding efficiency to Env derived from related pairs of primary and TCLA lines (primary: 168P and 320SI, and TCLA: 168C and 320SI-C3.3), but the TCLA lines were much more susceptible to neutralization suggesting that the change in TCLA lines that make them more susceptible to NAbs alters some step after binding [York2001]
- IgG1b12: b12 recognizes a conformational epitope that overlaps with the CD4 binding site a phage displayed peptide library was used to identify a peptide which bound b12, called B2.1, which competes with b12 in competition assays B2.1 has significant homology to the D loop of gp120: upper case letters indicate residues B2.1 shares with gp120, heRsymFSDlenrcI one of the goals of defining peptide mimics to the b12 epitope is to develop an immunogen that can stimulate b12-like antibodies, but B2.1 cross-linked to phage and ovalbumin bound IgG1b12 did not elicit cross-reactive gp120 Abs in mice or rabbits [Zwick2001a]
- IgG1b12: This paper primarily concerns 4E10 and Z13, MAbs that both bind proximally to the 2F5 binding site to a conserved epitope, and that neutralize some primary isolates from clades B, C, and E broadly neutralizing MAbs 2F5, IgG1b12, and 4E10 and Z13 fail to neutralize different subsets of viruses [Zwick2001b]
- IgG1b12: Neutralization synergy between anti-HIV NAbs b12, 2G12, 2F5, and 4E10 was studied a classic fixed-ratio method was used, as well as a method where one Ab was fixed at a low neutralization titer and the other was varied using primary isolates, a two-four fold enhancement of neutralization was observed with MAb pairs, and a ten-fold enhancement with a quadruple Ab combination no synergy was observed with any MAb pair in the neutralization of TCLA strain HXB2 whole IgG1b12 and b12 Fab fragments behaved similarly in the neutralization assays there was no evidence for cooperativity of binding between b12 and 2G12 to envelope spikes expressed on the cell surface of TCLA or primary isolates [Zwick2001c]

Env Antibodies HIV Antibodies Tables

No. MAb ID HXB2 Location Author's Location Sequence Neutralizing Immunogen Species(Isotype)

• IgG1b12: Intravenous passive transfer of MAb b12 provides dose-dependent protection from infection to macaques vaginally challenged with the R5 virus SHIV(162P4) – the primary isolate HIV-1SF162 is neutralized 90% (IC90) by b12 at 2 μg/ml, and SHIV162P4, derived from HIV-1SF162, was neutralized by 90% at 2 μg/ml in PHA-activated PBMC from rhesus macaques – the 90% neutralization titers achieved in three groups of animals that were given 25-, 5-, and 1-mg/kg doses were approximately 1:400, 1:80, and 1:16, respectively – the half-life of IgG1 b12 in plasma was about 1 week, but while the peak b12 plasma concentration was immediately after the infusion, the peak vaginal fluid concentration was 7-14 days later [Parren2001]

- IgG1b12: Structural aspects of the interaction of neutralizing Abs with HIV-1 Env are reviewed Env essentially has three faces, one is largely inaccessible on the native trimer, and two that exposed but have low immunogenicity on primary viruses neutralization is suggested to occur by inhibition of the interaction between gp120 and the target cell membrane receptors as a result of steric hindrance and it is noted that the attachment of approximately 70 IgG molecules per virion is required for neutralization, which is equivalent to about one IgG molecule per spike the 2G12, 17b and b12 epitopes are discussed in detail the structure of CD4-bound gp120 reveals features that HIV has evolved to escape anti-CD4BS Abs like IgG1b12 despite profound functional constraints CD4BS Abs must first access the CD4 binding site, deeply recessed within the gp120 core, and the Fab of an Ab molecule is "wider" than CD4, and in addition the binding site is flanked by variable and glycosylated regions [Poignard2001]
- IgG1b12: Neutralizing synergy between MAbs 1b12, 2G12 and 2F5 was studied using surface plasmon resonance to determine the binding kinetics for these three MAbs with respect to monomeric and oligomeric env protein gp160 IIIB the 2G12 epitope is highly accessible on both monomeric and oligomeric Envs, 1b12 is highly accessible on monomers but not oligomers, and 2F5 on neither form binding of 2G12 exposes the 2F5 epitope on gp160 oligomers [Zeder-Lutz2001]
- IgG1b12: A luciferase-reporter gene-expressing T-cell line was developed to facilitate neutralization and drug-sensitivity assays luciferase and p24 antigen neutralization titer end points were found comparable using NAb from sera from HIV+ donors, and MAbs 2F5, 2G12 and IgG1b12 [Spenlehauer2001]
- IgG1b12: A panel of 12 MAbs was used to identify those that could neutralize the dual-tropic primary isolate HIV-1 89.6 six gave significant neutralization at 2 to 10 ug/ml: 2F5, 50-69, IgG1b12, 447-52D, 2G12, and 670-D six did not have neutralizing activity: 654-D, 4.8D, 450-D, 246-D, 98-6, and 1281 no synergy, only additive effects were seen for pairwise combinations of MAbs, and antagonism was noted between gp41 M Abs 50-69 and 98-6, as well as 98-6 and 2F5 [Verrier2001]
- IgG1b12: A combination of MAbs IgG1b12, 2F5, and 2G12 was given postnatally to four neonates macaques that were then challenged with highly pathogenic SHIV89.6P one of the four infants remained uninfected after oral challenge, two infants had no or a delayed CD4(+) T-cell decline the most potent combination included IgG1b12, which alone does not alone neutralize SHIV89.6P [Hofmann-Lehmann2001]
- IgG1b12: Twenty HIV clade C isolates from five different countries were susceptible to neutralization by anti-clade B MAbs in a synergistic quadruple combination of mAbs IgG1b12, 2G12, 2F5, and 4E10 [Xu2001]
- IgG1b12: Oligomeric gp140 (o-gp140) derived from R5 primary isolate US4 was characterized for use as a vaccine reagent antigen capture ELISA was used to compare the antigenicity of gp120 and o-gp140 using a panel of well characterized MAbs Abs directed against the CD4 binding site (IgGCD4 and IgG1b12) reacted slightly more strongly with the gp120 monomer than with the oligomer, as did sCD4 [Srivastava2002]
- IgG1b12: The fusion process was slowed by using a suboptimal temperature (31.5 C) to re-evaluate the potential of Abs targeting fusion intermediates to block HIV entry preincubation of E/T cells at 31.5 C enabled polyclonal anti-N-HR Ab and anti-six-helix bundle Abs to inhibit fusion, indicating six-helix bundles form prior to fusion the preincubation 31.5 C step did not alter the inhibitory activity of neutralizing Abs anti-gp41 2F5, or anti-gp120 2G12, IG1b12, 48d, and 17b [Golding2002b]
- IgG1b12: Deglycosylation of gp120 does not significantly affect IG1b12 binding, in contrast to MAB 2G12 [Sanders2002]
- IgG1b12: Ab binding characteristics of SOS gp140 were tested using SPR and RIPA SOS gp140 is gp120-gp41 bound by a disulfide bond NAbs 2G12, 2F5, IgG1b12, CD4 inducible 17b, and 19b bound to SOS gp140 better than uncleaved gp140 (gp140unc) and gp120 non-neutralizing MAbs 2.2B (binds to gp41 in gp140unc) and 23A (binds gp120) did not bind SOS gp140 SOS gp140-2F5-IgG1b12 formed multiple ring structures composed of two SOS gp140 proteins bridged by two Ab molecules, while 2F5 and 2G12 formed extended chains rather than closed rings [Schulke2002]

No. MAb ID HXB2 Location Author's Location Sequence Neutralizing Immunogen Species(Isotype)

• IgG1b12: Uncleaved soluble gp140 (YU2 strain, R5 primary isolate) can be stabilized in an oligomer by fusion with a C-term trimeric GCN4 motif or using a T4 trimeric motif derived from T4 bacteriophage fibritin—stabilized oligomer gp140Δ683(-FT) showed strong preferential recognition by NAbs IgG1b12 and 2G12 relative to the gp120 monomer, in contrast to poorly neutralizing MAbs F105, F91, 17b, 48d, and 39F which showed reduced levels of binding, and C11, A32, and 30D which did not bind the stabilized oligomer [Yang2002].

- IgG1b12: The crystal structure of IgG1b12 is resolved and is the first structure of an intact human Ab with an ordered, full length hinge the structure is extremely asymmetric and flexible with an antigen-binding site that has an unusually long CDR H3 region with a ten residue insertion that projects above the rest of the antigen-binding site this loop may be required for recognition of the recessed CD4 binding site of gp120 [Saphire2002]
- IgG1b12: Alanine scanning mutagenesis used in conjunction with competition and replacement studies of N-linked carbohydrates and sugars suggest that the 2G12 epitope is formed from mannose residues contributed by the glycans attached to N295 and N332, with the other N-linked carbohydrates in positions N339, N386, and N392 playing a role in maintaining conformation relevant to 2G12 binding N295A and N332A mutants showed essentially unchanged anti-CD4BS NAb b12 binding affinities, while N339A, N386A and N392A mutants displayed significantly lowered b12 affinity, presumably due to conformational changes [Scanlan2002]
- IgG1b12: Passive immunization of neonate macaques with a combination of F105+2G12+2F5 conferred complete protection against oral challenge with SHIV-vpu+ or the combination b12+2G12+2F5 conferred partial protection against SHIV89.6 such combinations may be useful for prophylaxis at birth and against milk born transmission the synergistic combination of IgG1b12, 2G12, 2F5, and 4E10 neutralized a collection of HIV clade C primary isolates [Xu2002]
- IgG1b12: A modified gp140 (gp140ΔCFI), with C-term mutations intended to mimic a fusion intermediate and stabilize trimer formation, retained antigenic conformational determinants as defined by binding to CD4 and to MAbs 2F5, 2G12, F105, and b12, and enhanced humoral immunity without diminishing the CTL response in mice injected with a DNA vaccine [Chakrabarti2002].
- IgG1b12: Called ARP3065: Herpesvirus saimiri-immortalized CD4+ T lymphocytes (HVS T cells) were used to isolate virus and perform HIV-1 neutralization assays, and compared with a standard PBMC protocol neutralization sensitivities to a panel of MAbs and to homologous or heterologous plasma/sera were similar for HVS T cells (CN-2 cells) and PBMCs [Vella2002]
- IgG1b12: A series of mutational changes were introduced into the YU2 gp120 that favored different conformations 375 S/W seems to favor a conformation of gp120 closer to the CD4-bound state, and is readily bound by sCD4 and CD4i MAbs (17b, 48d, 49e, 21c and 23e) but binding of anti-CD4BS MAbs (F105, 15e, IgG1b12, 21h and F91 was markedly reduced IgG1b12 failed to neutralize this mutant, while neutralization by 2G12 was enhanced 2F5 did not neutralize either WT or mutant, probably due to polymorphism in the YU2 epitope another mutant, 423 I/P, disrupted the gp120 bridging sheet, favored a different conformation and did not bind CD4, CCR5, or CD4i antibodies, but did bind to CD4BS MAbs [Xiang2002b]
- IgG1b12: Truncation of the gp41 cytoplasmic domain of X4, R5, and X4R5 viruses forces a conformation that more closely resembles the CD4 bound state of the external Envelope, enhancing binding of CD4i MAbs 17b and 48d and of CD4BS MAbs F105, b12, and in most cases of glycosylation site dependent MAb 2G12 and the anti-gp41 MAb 246D in contrast, binding of the anti-V2 MAb 697D and the anti-V3 MAb 694/98D were not affected viruses bearing the truncation were more sensitive to neutralization by MAbs 48d, b12, and 2G12 the anti-C5 MAb 1331A was used to track levels of cell surface expression of the mutated proteins [Edwards2002]
- IgG1b12: Truncation of the gp41 cytoplasmic domain of X4, R5, and X4R5 viruses forces a conformation that more closely resembles the CD4 bound state of the external Envelope, enhancing binding of CD4i MAbs 17b and 48d and of CD4BS MAbs F105, b12, and in most cases of glycosylation site dependent MAb 2G12 and the anti-gp41 MAb 246D in contrast, binding of the anti-V2 MAb 697D and the anti-V3 MAb 694/98D were not affected viruses bearing the truncation were more sensitive to neutralization by MAbs 48d, b12, and 2G12 the anti-C5 MAb 1331A was used to track levels of cell surface expression of the mutated proteins [Edwards2002]
- IgG1b12: HIV-1 gp160ΔCT (cytoplasmic tail-deleted) proteoliposomes (PLs) containing native, trimeric envelope glycoproteins from R5 strains YU2 and JRFL, and X4 strain HXBc2, were made in a physiologic membrane setting as candidate immunogens for HIV vaccines—2F5 bound to gp160ΔCT with a reconstituted membrane ten-fold better than the same protein on beads—anti-CD4BS MAbs IgG1b12 and F105, A32 (C1-C4), C11 (C1-C5), and 39F (V3) MAbs bound gp160ΔCT PLs indistinguishably from gp160ΔCT expressed on the cell surface—non-neutralizing MAbs C11 and A32 bound with lower affinity than NAb IgG1b12—the MAb 17b was sCD4 inducible on gp160ΔCT PL [Grundner2002].

No. MAb ID

**HXB2** Location

Sequence **Neutralizing Immunogen** Species(Isotype) • IgG1b12: A rare mutation in the neutralization sensitive R2-strain in the proximal limb of the V3 region caused Env to become sensitive to neutralization by MAbs directed against the CD4 binding site (CD4BS), CD4-induced (CD4i) epitopes, soluble CD4 (sCD4), and HNS2, a broadly neutralizing sera – 2/12 anti-V3 MAbs tested (19b and 694/98-D) neutralized R2, as did 2/3 anti-CD4BS MAbs (15e and IgG1b12), 2/2 CD4i MAbs (17b and 4.8D), and 2G12 and 2F5 – thus multiple epitopes on R2 are functional targets for neutralization and the neutralization sensitivity profile of R2 is intermediate between the highly sensitive MN-TCLA strain and the typically resistant MN-primary strain [Zhang2002]

- IgG1b12: A broad review of NAbs that mentions IgG1b12 as an example of a NAb that does not alter the conformation of gp120, but interferes with CD4 binding [Klasse2002]
- IgG1b12: Review of NAbs that notes IgG1b12 is a recombinant IgG1 from a phage displayed Fab generated against gp120 from a B clade infected individual, that it binds the CD4BS, that alone or in combination with other MAbs it can protect some macaques against SHIV infection, and that it has strong ADCC activity [Ferrantelli2002]
- IgG1b12: Review of NAbs that discusses mechanisms of neutralization, passive transfer of NAbs and protection in animal studies, and vaccine strategies [Liu2002]
- IgG1b12: Virion capture assays are not a good preditor of neutralization, and the presentation of epitopes using this assay seems to be different from that of functional Envelope spikes on primary isolates - F105 and b6 could efficiently block the b12-mediated capture of infectious virions in a virus capture, but did not inhibit b12 neutralization – b12 was potent at neutralizing the three primary virions JR-CSF, ADA, and 89.6, but anti-V3 Abs 447-52D and 19b, which did not neutralize JR-CSF and ADA captured amounts of p24 equal to or higher than the amounts captured by the neutralizing Ab b12 [Poignard2003]
- IgG1b12: Called b12 Alanine scanning mutagenesis was used to compare substitutions that affected anti-CD4BS NAb b12 binding to those that affect binding of sCD4 and two non-neutralizing anti-CD4BS Abs b3 and b6 – while the epitope maps overlapped, there were some differences observed – binding of CD4 was never in enhanced, indicating it had evolved to be optimal – rec gp120s were engineered to contain combinations of Alanine substitutions that enhanced b12 binding, and while binding of b12 to these gp120 monomers was generally maintained or increased, binding by five non-neutralizing anti-CD4bs MAbs (b3, b6, F105, 15e, and F91) was reduced or completely abolished – 2G12 binding was largely unperturbed, indicating these proteins were not grossly misfolded – for twelve mutants, b12 neutralization sensitivity and affinity correlated, but for five mutants neutralization efficiency was maintained or increased despite a decrease in affinity [Pantophlet2003]
- IgG1b12: Called b12 CD4BS MAbs b12 (neutralizing) and 205-42-15, 204-43-1, 205-46-9 (nonneutralizing) all cross-competed for binding to monomeric gp120, indicating the topological proximity of their epitopes, however, the nonneutralizing CD4BS MAbs did not interfere with the neutralization activity of MAb b12 – the nonneutralizing MAbs partially competed with b12 for Env binding of the surface of Env-transfected cells – this suggests Env has two categories of binding site for CD4BS MAbs, one recognized by both b12 and nonneutralizing CD4BS MAbs, the other is recognized by only b12 – Ab-gp120 interactions based on the use of monomeric gp120 or Env-transfected cells do not predict the outcome of HIV-1 neutralization assays, and they should be interpreted with caution [Herrera2003]
- IgG1b12: UK Medical Research Council AIDS reagent: ARP3065

Author's Location

• IgG1b12: NIH AIDS Research and Reference Reagent Program: 2640

935 IgGCD4 (IgG-CD4)

Env gp120 Ab type CD4BS

human (IgG)

References Capon1989, Stamatatos1998, Ly2000, Srivastava2002

- IgGCD4: An antibody-like immunoadhesins molecule was constructed incorporating the gp120-binding domain of CD4 [Capon1989]
- IgGCD4: Deleting the V2 loop of neutralization-resistant HIV-1 isolate SF162 does not abrogate its replication in PBMC or macrophages, but it enhances its neutralization sensitivity to sera from patients with B clade infection up to 170-fold, and also enhances sensitivity to sera from clades A through F – deletion of V2 but not V1 slightly enhanced neutralization by CD4BS MAb IgGCD4 [Stamatatos1998]

No.	MAb ID	HXB2 Location	<b>Author's Location</b>	Sequence	Neutralizing	Immunogen	Species(Isotype)
		sites prevent neutral glycosylation site m modification allows  • IgGCD4: Oligomeriused to compare the	ization by CD4BS MAbs autations did not alter neut infection of macrophages ic gp140 (o-gp140) derives antigenicity of gp120 and	(IgG1b12 and IgGCD4), a ralization resistance to V2 , probably due to glycosyl d from R5 primary isolate l o-gp140 using a panel of	lycosylation modifications in the and protect against neutralization MAbs (G3.4 and G3.136) or CD ated forms requiring fewer CCR5 US4 was characterized for use as well characterized MAbs – Abs with the oligomer, as did sCD4 [S	by V3 MAbs (447-D 4i MAbs (17b and 48d molecules for viral e a vaccine reagent – a directed against the Cl	and 391-95D) – V2-region d) – V2 glycosylation site ntry [Ly2000] ntigen capture ELISA was
936	L28	V3 loop and by subs	at 257 T/R, 368 D/R, 370 I	G, 381 E/P, 382 F/L, 420 I/	L S 102 E/L and 463 N/D reduce bir /R, 435 Y/H or Y/R – binding is s		
937	L33	Env Ab type CD4BS References Ditzel19 • L33: binding is sens		heavy and light chain vari	L able region sequence is available	HIV-1 infection [Ditzel1995]	human (IgG1κ)
938	L41		at 133 D/R, 256 S/Y, 257 The brary after masking with I		L  E/Q or E/R, 384 Y/E, and 421 K/I  – binding is sensitive to deglycos		
939	L42		at 257 T/R, 368 D/R, 370 I		L  reduce binding – binding was signegion sequence is available [Ditz]		human (IgG1κ)  by 381 E/P and 382 F/L –
940	L52	Env Ab type CD4BS References Ditzel19 L52: Binding is sen		- heavy and light chain var	L iable region sequence is available	HIV-1 infection [Ditzel1995]	human (IgG1 $\kappa$ )
941	L72	References Ditzel19	997	EC Pharmaceuticals Corp	La Jolla, CA lection library [Ditzel1997]		murine
942	M12	Env <b>Vaccine</b> Vector/Type	gp120 (IIIB) e: vaccinia Strain: IIIB	HIV component: oligom	L eric gp140	Vaccine	murine (IgG)

No.	MAb ID	HXB2 Location	<b>Author's Location</b>	Sequence	Neutral	izing Immunogen	Species(Isotype)
		<ul> <li>References Earl1994.</li> <li>M12: There is a p15 g</li> <li>M12: Generated durin</li> <li>M12: A comparison of broadly cross-reactive</li> </ul>	sugiura1999 gag specific MAb also na ng a study of the influence of 25 gp120 specific, con with gp160 from B-clac	med M12 e of the oligomeric structormation dependent MA le R5, X4, and R5X4 viru	cure of Env in determining the bs was done – M12 is part of uses, blocked CD4 binding, wed with 21 ug/ml of M12 [5]	e repertoire of the Ab res f a group of MAbs labele were sensitive to mutation	
943	M13	<ul> <li>Ab type CD4BS Do References Earl1994.</li> <li>M13: Generated durin</li> <li>M13: A comparison of broadly cross-reactive</li> </ul>	onor P. Earl, National Ins., Sugiura 1999  ng a study of the influence of 25 gp 120 specific, con with gp 160 from B-clace	e of the oligomeric structormation dependent MA le R5, X4, and R5X4 viru	ectious Diseases, NIH, Bethe ture of Env in determining the bs was done – M13 is part of	e repertoire of the Ab res f a group of MAbs labele were sensitive to mutation	
944	M6	<ul> <li>Ab type CD4BS Do</li> <li>References Earl1994</li> <li>M6: Generated during</li> <li>M6: A comparison of</li> </ul>	onor P. Earl, National Ins., Sugiura1999 g a study of the influence 25 gp120 specific, confound from B-clade R5, X	of the oligomeric structuormation dependent MAb	ectious Diseases, NIH, Bethe are of Env in determining the s was done – M6 is part of a	repertoire of the Ab resp group of MAbs labeled A	murine (IgG)  onse [Earl1994]  A1 – all A1 MAbs were broadly 20 positions 368 and 370 that
945	MAG 116	<b>Ab type</b> CD4BS <b>Do</b> <b>References</b> Kang199	<b>onor</b> C. Y. Kang, IDEC I 4		-	Vaccine 370 E/R or Q, 384 Y/E, 42	murine 21 K/L – neutralizes MN, IIIB
946	MAG 12B	Env Vaccine Vector/Type: Ab type CD4BS Do References Kang199	<b>onor</b> C. Y. Kang, IDEC I 4		L nponent: gp120  C/R, 368 D/R or T, 370 E/R	Vaccine or Q, 384 Y/E, 477 D/V –	murine weak neutralization of IIIB
947	MAG 29B		onor C. Y. Kang, IDEC I	Strain: HXB2 HIV con	L nponent: gp120	Vaccine	murine

**Env Antibodies** 

No.	MAb ID	<b>HXB2</b> Location	Author's Location	Sequence	N	eutralizing	Immunogen	Species(Isotype)
		• MAG 29B: Amino a of IIIB [Kang1994]	acid substitutions that red	uce binding 10 fold: 257	T/R, 368 D/R or T, 370	E/R or Q, 3	84 Y/E, 386 N/Q, 4	421 K/L – weak neutralization
948	MAG 3B	Ab type CD4BS I References Kang19 • MAG 3B: Amino ac	eid substitutions that redu	Inc			Vaccine 8 D/R or T, 370 E/I	murine R or Q, 381 E/P, 384 Y/E, 421
		K/L, 475 M/S, 477 I	D/V [Kang1994]					
949	MAG 55 (#5	Vaccine Vector/Type	gp120 e: sCD4-gp120 complex <b>Donor</b> C. Y. Kang, IDEC 94, Moore1996		Domponent: gp120		Vaccine	murine
		D/V – neutralizes M • MAG 55: Called #5	IN, IIIB and RF [Kang19	94] nhibited by other anti-CI	D4 binding site MAbs, a	and by some	C1-C5 MAbs – bin	1 K/L, 470 P/L, 475 M/S, 477 ading enhanced by anti-V3
950	MAG 72 (L72)	Ab type CD4BS I References Kang19 • MAG 72: Amino ac neutralizes MN, IIIE		Hariharam, IDEC Pharm ce binding 10 fold: 257 T	aceuticals Corp, La Joll V/R or A or G, 262 N/T,	la, CA 368 D/R or		murine 34 Y/E, 421 K/L, 477 D/V –
951	MAG 86	Ab type CD4BS I References Kang19 • MAG 86: Amino ac	id substitutions that redu	Inc			Vaccine 2 or Q, 384 Y/E, 42	murine 1 K/L, 470 P/L, 477 D/V –
		neutralizes MN, IIII	3 and RF [Kang1994]					
952	MAG 96	<b>Ab type</b> CD4BS I <b>References</b> Kang19	gp120 e: sCD4-gp120 complex <b>Donor</b> C. Y. Kang, IDEC 94 id substitutions that redu	Inc			Vaccine  - weak neutralizat	murine ion of IIIB [Kang1994]
953	MTW61D	Env <b>Ab type</b> CD4BS <b>References</b> Sullivan	gp120 (W61D) n1998a		L		HIV-1 infection	human

Env Antibodies Tables

No. MAb ID	HXB2 Location	<b>Author's Location</b>	Sequence		Neutralizing	g Immunogen	Species(Isotype)
	entry state could be concentrations of st cross-linking as a n		troducing the YU2 V3 loc endent of CCR5 – Fab frag zing HXBc2 – MTW61D	op, or the YU2 V3 and gment MTW61D also was obtained by pann	d V1/V2 loo enhances Y	ps – a similar effect i U2 entry, ruling out I	
954 S1-1	Env Ab type CD4BS References Lake19	gp120 992, Moran1993, Wisnews	.ki1996	]	L	HIV-1 infection	human (IgG1λ)
	<ul> <li>S1-1: Neutralizes I inhibits sCD4-gp12</li> </ul>	IIB and MN without comp 20 binding [Lake1992]	plement, and neutralizes R				tive but not denatured gp120 –
	• S1-1: Heavy (V HI [Moran1993]	I) and light (V lambdaIII) o	chain sequenced – no enha	ancing activity – simi	lar germline	sequence to MAb 86	, but very different activity
			sage was examined and a	bias of enhanced V H	I1 and V H4,	, and reduced V H3, v	was noted among HIV infected
955 T13	Ab type CD4BS References Earl19 T13: Generated du T13: A comparisor	ring a study of the influence	nstitute of Allergy and Info ce of the oligomeric struct formation dependent MA	neric gp140 fectious Diseases, NIF ture of Env in determi bs was done – T13 is	ning the repo	ertoire of the Ab resp MAbs labeled group	murine (IgG) onse [Earl1994] Cb, that was type-specific for
956 T49	Ab type CD4BS References Earl19 T49: Generated du T49: A comparisor	ring a study of the influence	nstitute of Allergy and Info ce of the oligomeric struct formation dependent MA	neric gp140 fectious Diseases, NIF ture of Env in determi bs was done – T49 is	ning the repo	ertoire of the Ab resp MAbs labeled group	murine (IgG) onse [Earl1994] Cb, that was type-specific for
957 T56	Ab type CD4BS References Earl19 T56: Generated du T56: A comparisor	ring a study of the influence	nstitute of Allergy and Info ce of the oligomeric struct formation dependent MA	neric gp140 fectious Diseases, NIF ture of Env in determi bs was done – T56 is	ning the repo	ertoire of the Ab resp MAbs labeled group	murine (IgG)  onse [Earl1994]  Cb, that was type-specific for
958 TH9	Env <b>Ab type</b> CD4BS <b>References</b> D'Sou:	gp120 <b>Donor</b> Michael Fung, Tar za1995, Yang1998	nox Biosystem, USA	1	L		human (IgG1κ)

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizing Immunogen	Species(Isotype)
		involving 11 labs[D • TH9: A neutralizat	o'Souza1995] ion assay was developed ba	ased on hemi-nested PCR a	olates, or a D subtype primary isolate, by most labs in amplification of the LTR (HNPCR) – LTR-HNPCR consed on tests with 6 MAbs and 5 isolates [Yang1998]	
959	anti-CD4BS summary	Ab type CD4BS References Thali19 • Shared components 457 [Thali1993] • Anti-CD4 binding s	gp120 993, Moore1996 s of MAb epitopes and the	discontinuous CD4 binding	g regions included Thr 257, Asp 368, Glu 370, Lys 421 inding to monomeric gp120, and they differ in precise	
960	b11	markedly different > b13) and binding	r of Fab binding affinity to than Fab binding affinity to to oligomeric form and ne	the mature oligomeric for	2 > 3B3 > b12 = DO8i > b11 > b3 > b14 > b13 > DO1 rm (3B3 > b12 > DO142-10 > Loop 2 > b11 > L17 > b0 d for both Fabs and MAbs – authors suggest that neutrater [1998a]	6 > DO8i > b14 > DA48 > b3
961	b13	<ul> <li>b13: Fab b13 was u but not by b13 [Par</li> <li>b13: The rank orde markedly different &gt; b13) and binding</li> </ul>	ren1995, Parren1997a] r of Fab binding affinity to than Fab binding affinity to to oligomeric form and ne	BL SCID mouse study – an monomeric gp120 (Loop 2) the mature oligomeric for	imals were protected from HIV-1 SF2 infection by IgC 2 > 3B3 > b12 = DO8i > b11 > b3 > b14 > b13 > DO1- rm (3B3 > b12 > DO142-10 > Loop 2 > b11 > L17 > book d for both Fabs and MAbs – authors suggest that neutration (2008)	42-10 > DA48 > L17) was 6 > DO8i > b14 > DA48 > b3
962	b14	markedly different > b13) and binding	r of Fab binding affinity to than Fab binding affinity to to oligomeric form and ne	the mature oligomeric for	2 > 3B3 > b12 = DO8i > b11 > b3 > b14 > b13 > DO1 rm (3B3 > b12 > DO142-10 > Loop 2 > b11 > L17 > b0 d for both Fabs and MAbs – authors suggest that neutraten 1998a]	6 > DO8i > b14 > DA48 > b3
963	b3		gp120 1997c, Parren1998a, Pantoj LA strains, but not primary			human

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No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutra	lizing Immunogen	Species(Isotype)
		markedly different > b13) and binding fraction of Ab sites  • b3: Alanine scannin two non-neutralizin enhanced, indicatin and while binding of	than Fab binding affinity to oligomeric form and no occupied on a virion irresting mutagenesis was used to g anti-CD4BS Abs b3 and g it had evolved to be option of b12 to these gp120 more	to the mature oligomeric be on the mature oligomeric be outralization were correlated by the epitope [Patto compare substitutions of the patto be of the epitope of the epi	ted for both Fabs and MAbs arren1998a] that affected anti-CD4BS NA naps overlapped, there were s	0 > Loop 2 > b11 > L17 > b - authors suggest that neutral ab b12 binding to those that some differences observed - ations of Alanine substitution by five non-neutralizing an	26 > DO8i > b14 > DA48 > b3 calization is determined by the affect binding of sCD4 and binding of CD4 was never in that enhanced b12 binding, ati-CD4bs MAbs (b3, b6,
964	b6	References Parrent  b6: Neutralizes TC  b6: The rank order markedly different > b13) and binding fraction of Ab sites  b6: Virion capture a functional Enveloped did not inhibit b12 were overall very p  b6: Alanine scanning two non-neutralizing enhanced, indicating and while binding of	than Fab binding affinity to oligomeric form and no occupied on a virion irrespondent and a good predict of the spikes on primary isolated the spikes on primary isolated the properties of the	mard2003, Pantophlet2003, y isolates [Parren1997c] monomeric gp120 (Loop to the mature oligomeric feettralization were correlated to the epitope [Palitor of neutralization, and the seen F105 and b6 could eight was potent at neutralizing 12003] to compare substitutions of the while the epitope remail – rec gp120s were enomers was generally mail	2 > 3B3 > b12 = DO8i > b1 form (3B3 > b12 > DO142-10 ted for both Fabs and MAbs arren1998a] I the presentation of epitopes ficiently block the b12-media g the three primary virions Ju- that affected anti-CD4BS NA- maps overlapped, there were se	0 > Loop 2 > b11 > L17 > b - authors suggest that neutral using this assay seems to be ated capture of infectious v R-CSF, ADA, and 89.6, the b b12 binding to those that some differences observed - tions of Alanine substitution by five non-neutralizing and	26 > DO8i > b14 > DA48 > b3 calization is determined by the de different from that of irions in a virus capture, but Abs F105, 19b, and Fab b6 affect binding of sCD4 and binding of CD4 was never in ins that enhanced b12 binding, nti-CD4bs MAbs (b3, b6,
965	polyclonal	Env Vaccine Vector/Typ Ab type CD4BS References Truong • Antibodies raised a	1996 gainst recombinant anti-p	55 virus-like particles wi	no : LAI HIV component: V3, th the p24 region 196-226 del and strong Gag responses we	leted, bearing inserts of eith	
966	D33		s was found to be required			Vaccine	murine (IgG)
	_ 55	Vaccine Vector/Typ Ab type CD4BS, C References Earl199	e: vaccinia Strain: IIIB Sterm, N-term <b>Donor</b> P. 94, Sugiura1999	Earl, National Institute of	meric gp140 of Allergy and Infectious Disc eture of Env in determining the	eases, NIH, Bethesda, MD	

No. MAb ID

**HXB2** Location

**Author's Location** 

HIV Antibodies Tables Env Antibodies

Neutralizing Immunogen

Species(Isotype)

Sequence

	• D33: A comparison of 25 gp120 specific, conformation dependent MAbs was done – D33 is part of a group of MAbs labeled A1 – all A1 MAbs were broadly cross-reactive with gp160 from B-clade R5, X4, and R5X4 viruses, blocked CD4 binding, were sensitive to mutations in gp120 positions 368 and 370 that directly contact CD4 – D33 was unusual for the group of A1 MAbs, because while it blocked CD4 binding completely, but competed with MAbs that did not in a BIAcore assay – both the N- and C-terminal ends of gp120 are involved in D33 binding [Sugiura1999]							
967	Env gp120 Ab type CD4BS, CD4i, V3, V2 References Moore2001  • Moore and colleagues review structural aspects of gp120 and how the relationship between genetic subtype and serotype – they suggest the to elicit neutralizing antibodies against a significant proportion of prindiscussed, such as Ab binding to defective spikes, which does not affective spikes.	primary goal in vaccine efforts should be to mary isolates – assay artifacts that can result	design an immunogen that can be shown t in confused interpretations are also					
968 17b	<ul> <li>Env gp120</li> <li>Ab type CD4i Donor James Robinson, Tulane University, New Ork References</li> <li>Thali1993, Moore1993d, Thali1994, Beretta1994, Wyatt1995, Satten Fouts1997, Li1997, Weinberg1997, Ditzel1997, Cao1997b, Wyatt1995, Sullivan1998a, Binley1998, Stamatatos1998, Oscherwitz1999a, Hoff Stamatatos2000, Yang2000, Rizzuto2000, Si2001, Kolchinsky2001, Yang2002, Dowd2002, Xiang2002b, Xiang2002a, Edwards2002, Gru</li> <li>17b: 48d and 17b have similar epitopes, and the pair are unique amor</li> <li>17b: Epitope is better exposed upon CD4 binding to gp120 – compet 370 E/D, 382 F/L, 420 I/R, 433A/L, 438 P/R and 475 M/S confer dec</li> <li>17b: Binding of 48d is much more influenced by sequence variation at 17b: A mutation in gp41, 582 A/T, confers resistance to neutralizatio</li> <li>17b: Studies using a V1/V2 deletion mutant demonstrated that enhant significant involvement of V2 – similar effect observed for 48d and A</li> <li>17b: Binds with higher affinity to monomer and oligomer, slow associtifferent kinetics [Sattentau1995b]</li> <li>17b: Many MAbs inhibit binding (anti-C1, -C5, -C4, -CD4BS) – anti – enhances binding of some anti-V2 MAbs [Moore1996]</li> <li>17b: Binding did not result in significant gp120 dissociation from vir [Poignard1996a]</li> <li>17b: MIP-1α binding to CCR-5 expressing cells can be inhibited by 17b: Neutralizes JR-FL – inhibits gp120 interaction with CCR-5 in a</li> <li>17b: Study shows neutralization is not predicted by MAb binding to monomer, oligomer, and neutralized JRFL in the presence of sCD4, be 17b: One of 14 human MAbs tested for ability to neutralize a chimer combination with anti-V3 MAb 694/98-D [Li1997]</li> <li>17b: 48d binds to the IIIB protein and not IIIB V3 peptide, while binded and in the presence of the line presence of the li</li></ul>	tau1995b, Moore1996, Poignard1996a, Wu 27, Parren1997c, Kwong1998, Wyatt1998a, iman1999, Binley1999, Grovit-Ferbas2000, York2001, Zhang2001a, Poignard2001, Sriv undner2002, Basmaciogullari2002, Zhang20 ng human and rodent MAbs es with 15e and 21h, anti-CD4 binding site 1 creased sensitivity to neutralization [Thali19 among molecular clones of LAI than is bind n (also confers resistance to MAbs F105, 48 ced binding of 17b in the presence sCD4 im 32 [Wyatt1995] ciation rate, poor neutralization of lab strain 1-V3 MAb 5G11 enhances binding, as do C1 cion, in contrast to 48d, although the gp41 ep gp120-sCD4 — binding of 17b blocks this i MIP-1beta-CCR-5 competition study [Trko JRFL monomeric gp120, but is associated w out if sCD4 was not present, 17b only bound ic SHIV-vpu+, which expressed HIV-1 IIIB ding to the Can0A V3 peptide, suggesting C	Moore1998, Rizzuto1998, Sullivan1998b, Ly2000, Park2000, Salzwedel2000, Park2002, Golding2002b, Schulke2002, 2002, Arthos2002  MAbs – 113 D/R, 252 R/W, 257 T/A or G, 293]  ling of 17b [Moore1993d]  Bd, 21h and 15e) [Thali1994]  volves the V1/V2 loops, with more  – this is in contrast to 48d, which has very  1-C4 discontinuous epitopes A32 and 2/11c  pitope of MAb 50-69 was exposed  inhibition [Wu1996].  cla1996a]  vith oligomeric Env binding – 17b bound  I monomer [Fouts1997]  env – 17b has synergistic response in					

Env Antibodies HIV Antibodies Tables

No. MAb ID HXB2 Location Author's Location Sequence Neutralizing Immunogen Species(Isotype)

• 17b: Virus with the V1-V2 loop deleted was viable and more susceptible to neutralization by CD4i MAb 17b, and anti-V3 MAbs 1121, 9284, and 110.4, but not to a CD4BS MAb, F105, or sCD4 [Cao1997b]

- 17b: Binds to sgp120 efficiently, but not soluble gp120+gp41, suggesting its gp120 epitope is blocked by gp41 binding partial re-exposure if sCD4 was bound could not bind to HXBc2 gp120 if the 19 C-term amino acids were deleted in conjunction with amino acids 31-93 in C1, but binding was restored in the presence of sCD4 [Wyatt1997]
- 17b: Neutralizes TCLA strains, but not primary isolates [Parren1997c]
- 17b: 17b Fab was co-crystallized with a gp120 core and CD4, and it's binding site can be directly visualized—17b binds to the "bridging sheet" of gp120, an antiparallel beta sheet region, contacting residues from the C4 region and the V1/V2 stem—the contact area is small for an Ab-antigen interactive surface, and dominated in the Ab by the heavy chain—the center of the binding region has hydrophobic interactions, and the periphery charge interactions, acidic on 17b and basic on gp120 [Kwong1998]
- 17b: Summary of the implications of the crystal structure of a gp120 core bound to CD4 and 17b, combined with what is known about mutations that reduce NAb binding to gp120 probable mechanism of neutralization is interference with chemokine receptor binding mutations in 88N, 117K, 121K, 256S, 257T, N262, Delta V3, E370, E381, F 382, R 419, I 420, K 421, Q 422, I 423, W 427, Y 435, P 438, M 475 of HXBc2 (IIIB) reduce binding the only variable residues in gp120 that contact 17b are 202T and 434M the contact points for 17b with the crystallized incomplete gp120 are mostly in the heavy chain of the Ab, and there is a gap between 17b's light chain and the partial gp120 which may be occupied by the V3 loop in a complete gp120 molecule the authors propose that the V2 and V3 loops may mask the CD4i Ab binding site, and that the V2 loop may be repositioned upon CD4 binding [Wyatt1998a]
- 17b: Moore and Binley provide a commentary on the papers by [Rizzuto1998], [Wyatt1998a] and [Kwong1998] they point out 17b shares binding elements in gp120 with chemokine receptor molecules, and that CD4 needs to bind to gp120 first to make the 17b epitope accessible and it may be sterically blocked in the CD4 bound virus, thus making it a poor NAb for primary isolates [Moore1998]
- 17b: Site directed mutagenesis of a WU2 protein with the V1-V2 loops deleted revealed key residues for 17b-gp120 interaction and interaction of gp120 and CCR5 mutations in residues that reduced 17b by 70% were R/D 419, I/R 420, Q/L 422, Y/S 435, I/S 423, K/D 121 and K/D 421–17b can neutralize HIV-1 strains that use different chemokine receptors, supporting a common region in gp120 in chemokine-receptor interaction [Rizzuto1998]
- 17b: sCD4 induces 17b binding in primary isolates and TCLA strains amino acids that reduce the efficiency of binding were determined and found also to compromise syncytia formation and viral entry V1V2 deletion or sCD4 binding can expose the 17b epitope for both HXBc2 and macrophage tropic YU2 neutralizing potency of 17b is probably weak due to poor exposure of the epitope 17b epitope exposure upon sCD4 binding can occur over a wide range of temperatures, consistent with the energy of CD4 binding being sufficient to drive the V1/V2 loop into a new conformation [Sullivan1998b]
- 17b: The HIV-1 virus YU2 entry can be enhanced by MAbs binding to the CD4BS, V3 loop, and CD4i epitopes the activation for this enhanced entry state could be conferred on HxB2 by introducing the YU2 V3 loop, or the YU2 V3 and V1/V2 loops, and the presence of V1/V2 increased the enhancement a similar effect is observed by sub-neutralizing concentrations of sCD4 and the effect is dependent of CCR5 17b enhances YU2 enhanced viral entry 10-fold, whereas HXBc2 was neutralized [Sullivan1998a]
- 17b: A panel of MAbs was shown to bind with similar or greater affinity and similar competition profiles to a deglycosylated or variable loop deleted core gp120 protein (Delta V1, V2, and V3), thus such a core protein produces a structure closely approximating full length folded monomer CD4i MAbs 17b and 48d bound better to the deleted protein than to wild type [Binley1998]
- 17b: Deleting the V2 loop of neutralization-resistant HIV-1 isolate SF162 does not abrogate its replication in PBMC or macrophages, but it enhances its neutralization sensitivity to sera from patients with B clade infection up to 170-fold, and also enhances sensitivity to sera from clades A through F deletion of V2 but not V1 enabled neutralization by CD4i MAbs 17b and 48d [Stamatatos1998]
- 17b: A CD4-independent viral variant of IIIB, IIIBx, was generated on CXCR4-expressing cells IIIBx exhibited greater exposure of the 17b and 48d epitopes and enhanced neutralization by CD4i MAbs and by polyclonal human sera the 17b epitope has significant overlap with the CCR5 coreceptor binding site [Hoffman1999]

No. MAb ID HXB2 Location Author's Location Sequence Neutralizing Immunogen Species(Isotype)

• 17b: The MAbs with the broadest neutralizing activity, IgG1b12, 2G12 and 2F5, all have high affinity for the native trimer, indicating that they were raised in an immune response to the oligomer on the virion surface rather than dissociated subunits – a disulfide linked gp120-gp41 (SOS gp140) was created to mimic the native conformation of Env and explore its potential as an immunogen – SOS gp140 is recognized by NAbs IgG1b12, 2G12, and CD4-IgG2, and also by anti-V3 MAbs 19b and 83.1 – SOSgp140 is not recognized by C4 region MAbs that neutralize only TCLA strains, G3-42 and G3-519 – nor did it bind C11, 23A, and M90, MAbs that bind to gp120 C1 and C5, where it interacts with gp41 – MAbs that bind CD4 inducible epitopes, 17b and A32 were very strongly induced by CD4 in SOS gp140 – anti-gp41 MAbs that bind in the region that interacts with gp120, 7B2, 2.2B, T4, T15G1 and 4D4, did not bind to SOSgp140, in contrast to 2F5, which binds to the only gp41 epitope that is well exposed in native gp120-gp41 complexes [Binley1999]

- 17b: To determine the antigenicity of virus killed by thermal and chemical inactivation, retention of conformation-dependent neutralization epitopes was examined, and exposure of CD4BS epitopes was found to be enhanced (MAbs IgG1b12, 205-46-9, and 205-43-1) binding to 2G12 and 447-52D epitopes was essentially unaltered the 17b CD4i epitope was also exposed [Grovit-Ferbas2000]
- 17b: SF162 is a neutralization-resistant HIV-1 isolate N-linked glycosylation modifications in the V2 loop of the SF162 gp120 revealed that these sites prevent neutralization by CD4BS MAbs (IgG1b12 and IgGCD4), and protect against neutralization by V3 MAbs (447-D and 391-95D) V2-region glycosylation site mutations did not alter neutralization resistance to V2 MAbs (G3.4 and G3.136) or CD4i MAbs (17b and 48d) V2 glycosylation site modification allows infection of macrophages, probably due to glycosylated forms requiring fewer CCR5 molecules for viral entry [Ly2000]
- 17b: Six mutations in MN change the virus from a high-infectivity neutralization resistant phenotype to low-infectivity neutralization sensitive V3, CD4BS, and CD4i MAbs are 20-100 fold more efficient at neutralizing the sensitive form the mutation L544P reduced binding of all MAbs against gp120 by causing conformational changes [Park2000]
- 17b: sCD4 can activate fusion between effector cells expressing Env and target cells expressing coreceptor (CCR5 or CXCR4) alone without CD4 CD4i MAbs 17b and 48d have little effect on a standard cell fusion assay but potently block sCD4 activated fusion 17b was broadly cross-reactive inhibiting sCD4 activated fusion with Env from clades A, B, C, D, E, F, and F/B [Salzwedel2000]
- 17b: Soluble gp140 derived from SF162, a neutralization-resistant primary isolate, and SF162AV2 a neutralization-susceptible isolate with 30 amino acids deleted from the V2 loop, were generated with or without the gp120-gp41 cleavage site intact all forms are recognized by oligomer-specific MAb T4 and show enhanced binding of CD4i MAb 17b when sCD4 is bound the fused forms are less efficiently recognized than the cleaved forms by polyclonal neutralizing sera from HIV-infected patients the V3 loop is more exposed on the fused form [Stamatatos2000]
- 17b: A combination of gp41 fusion with the GNC4 trimeric sequences and disruption of the YU2 gp120-gp41 cleavage site resulted in stable gp140 trimers (gp140-GNC4) that preserve and expose some neutralizing epitopes while occluding some non-neutralizing epitopes CD4BS MAbs (F105 and F91) and CD4i (17b and 48d) recognized gp140-GNC4 as well as gp120 or gp140 non-neutralizing MAbs C11, A32, 522-149, M90, and #45 bound to the gp140-GNC4 glycoprotein at reduced levels compared to gp120 MAbs directed at the extreme termini of gp120 C1 (135/9 and 133/290) and C5 (CRA-1 and M91) bound efficiently to gp140-GNC4 [Yang2000]
- 17b: Mutagenesis defines Ile-420, Lys-421, Gln-422, Pro-438, and Gly-441 to be important residues for CCR5 binding these positions are located on two strands that connect the gp120 bridging sheet and outer domain, suggesting a mechanism for conformational shifts induced by CD4 binding to facilitate CCR5 binding [Rizzuto2000]
- SHIV-HXBc2 is a neutralization sensitive non-pathogenic virus, and several in vivo passages through monkey's yielded highly pathogenic SHIV KU-1 HXBc2 and the KU-1 clone HXBc2P3.2 differ in 12 amino acids in gp160 substitutions in both gp120 and gp41 reduced the ability of sCD4, IgG1b12, F105 and AG1121 to Env achieve saturation and full occupancy, and neutralize KU-1 17b and 2F5 also bound less efficiently to HXBc2P3.2, although 2G12 was able to bind both comparably [Si2001]
- 17b: Mutations in two glycosylation sites in the V2 region of HIV-1 ADA at positions 190 and 197 (187 DNTSYRLINCNTS 199) cause the virus to become CD4-independent and able to enter cells through CCR5 alone—these same mutations tended to increase the neutralization sensitivity of the virus, including to 17b—only the CD4i antibodies 17b and 48d showed an increased affinity of the CD4 independent viruses relative to wild-type [Kolchinsky2001].

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No. MAb ID HXB2 Location Author's Location Sequence Neutralizing Immunogen Species(Isotype)

• 17b: Abs against the V3 loop (50.1, 58.2, 59.1, 257-D, 268-D, 447-52D), CD4BS (IgG1b12, 559-64D, F105), CD4i (17b), and to gp41 (2F5, F240) each showed similar binding efficiency to Env derived from related pairs of primary and TCLA lines (primary: 168P and 320SI, and TCLA: 168C and 320SI-C3.3), but the TCLA lines were much more susceptible to neutralization suggesting that the change in TCLA lines that make them more susceptible to NAbs alters some step after binding – 17b bound at somewhat greater levels to 168C than to 168P, but this is not a general feature of 17b binding to primary versus TCLA strains [York2001]

- 17b: 17b binds to a CD4 inducible epitope which partially overlaps the CCR5 binding site JRFL, YU2, 89.6, and HXB2 and their C1-, V1/V2-, C5 -deletion mutants were used to study how 17b binding affects gp120-CD4 interactions 17b reduced CD4-gp120 interactions by decreasing the on-rate and increasing the off-rate of sCD4, while enhanced binding of sCD4 binding was observed for the 17b-bound, V1/V2 deleted gp120s 17b was considered to be a surrogate for CCR5, and the authors suggest that 17b binding may shift V1/V2 into a position that interferes with CD4 binding, forcing a release [Zhang2001a]
- 17b: Structural aspects of the interaction of neutralizing Abs with HIV-1 Env are reviewed Env essentially has three faces, one is largely inaccessible on the native trimer, and two that exposed but have low immunogenicity on primary viruses neutralization is suggested to occur by inhibition of the interaction between gp120 and the target cell membrane receptors as a result of steric hindrance and it is noted that the attachment of approximately 70 IgG molecules per virion is required for neutralization, which is equivalent to about one IgG molecule per spike the 2G12, 17b and b12 epitopes are discussed in detail the 17b epitope is masked prior to CD4 binding by the V1-V2 loop and in contrast to sCD4, the binding of cell surface CD4 to virus does not appear to make the epitope accessible to binding by 17b to allow neutralization [Poignard2001]
- 17b: Oligomeric gp140 (o-gp140) derived from R5 primary isolate US4 was characterized for use as a vaccine reagent antigen capture ELISA was used to compare the antigenicity of gp120 and o-gp140 using a panel of well characterized MAbs 17b recognized both gp120 monomer and o-gp140 [Srivastava2002]
- 17b: The fusion process was slowed by using a suboptimal temperature (31.5 C) to re-evaluate the potential of Abs targeting fusion intermediates to block HIV entry preincubation of E/T cells at 31.5 C enabled polyclonal anti-N-HR Ab and anti-six-helix bundle Abs to inhibit fusion, indicating six-helix bundles form prior to fusion the preincubation 31.5 C step did not alter the inhibitory activity of neutralizing Abs anti-gp41 2F5, or anti-gp120 2G12, IG1b12, 48d, and 17b [Golding2002b]
- 17b: Ab binding characteristics of SOS gp140 were tested using SPR and RIPA SOS gp140 is gp120-gp41 bound by a disulfide bond NAbs 2G12, 2F5, IgG1b12, CD4 inducible 17b, and 19b bound to SOS gp140 better than uncleaved gp140 (gp140unc) and gp120 non-neutralizing MAbs 2.2B (binds to gp41 in gp140unc) and 23A (binds gp120) did not bind SOS gp140 [Schulke2002]
- 17b: Uncleaved soluble gp140 (YU2 strain, R5 primary isolate) can be stabilized in an oligomer by fusion with a C-term trimeric GCN4 motif or using a T4 trimeric motif derived from T4 bacteriophage fibritin—stabilized oligomer gp140Δ683(-FT) showed strong preferential recognition by NAbs IgG1b12 and 2G12 relative to the gp120 monomer, in contrast to poorly neutralizing MAbs F105, F91, 17b, 48d, and 39F which showed reduced levels of binding, and C11, A32, and 30D which did not bind the stabilized oligomer [Yang2002].
- 17b: CD4 residue Phe43 significantly contributes to the affinity of CD4-gp120 interactions despite decreased affinities for gp120, CD4 proteins and CD4-mimetic peptides lacking a Phe side-chain enhance binding of gp120 to 17b in a manner similar to Phe-bearing ligands indicating the Phe42 interaction is not critical for CD4-induced conformational changes in gp120 [Dowd2002]
- 17b: A series of mutational changes were introduced into the YU2 gp120 that favored different conformations 375 S/W seems to favor a conformation of gp120 closer to the CD4-bound state, and is readily bound by sCD4 and CD4i MAbs (17b, 48d, 49e, 21c and 23e) but binding of anti-CD4BS MAbs (F105, 15e, IgG1b12, 21h and F91 was markedly reduced IgG1b12 failed to neutralize this mutant, while neutralization by 2G12 was enhanced 2F5 did not neutralize either WT or mutant, probably due to polymorphism in the YU2 epitope another mutant, 423 I/P, disrupted the gp120 bridging sheet, favored a different conformation and did not bind CD4, CCR5, or CD4i antibodies, but did bind to CD4BS MAbs [Xiang2002b]

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutra	lizing Immunogen	Species(Isotype)
		non-progressor – 23. ELISA antigen captud 420, also important to CCR5 binding site [1]  17b: Truncation of the external Envelop MAb 2G12 and the abearing the truncation expression of the multiple of the external Envelop MAb 2G12 and the abearing the truncation expression of the multiple of the HIV-1 gp16OΔt and X4 strain HXBc reconstituted membrace MAbs bound gp16OΔ affinity than NAb Ig  17b: gp120 mutants non-specific gp120 the allowed CD4-indeperor day1 and day1-varecognized by 17b expression with known the interest of the sensitive MN-TCLA and the interest of the sensitive MN-TCLA for the two N-term to gp120—coding sensitive management of two	e and 21c were converted ure assay – critical bindin for CCR5 binding, and all Xiang2002a] he gp41 cytoplasmic dom be, enhancing binding of Canti-gp41 MAb 246D – ir on were more sensitive to atated proteins [Edwards2 CT (cytoplasmic tail-delev2, were made in a physio rane ten-fold better than the ACT PLs indistinguishabl G1b12—the MAb 17b was were used to define the Coinding—basic residues in endent CXCR4 binding—2 for 17b was dramatically except in the presence of sign in the neutralization sensit the CD4 binding site (d. (19b and 694/98-D) neutepitopes on R2 are functional strain and the typically rininal domains of CD4, telequences of D1D2 and Ige	to hybridomas to ince gresidues are mapped five can block CCR ain of X4, R5, and X CD4i MAbs 17b and a contrast, binding of neutralization by MA (002) ted) proteoliposomes logic membrane settine same protein on bey from gp160\(\Delta\)CT exas sCD4 inducible on EXCR4 binding site unto the V3 loop and the MAbs 17b (CD4i) are increased and no logic CD4—mutations in the this region [Basmack sitive R2-strain in the CD4BS), CD4-inductralized R2, as did 2/ onal targets for neutralized R2, as did 2/ onal targets for neutralized D1 and D2, who (atp were fused to creat MAb 17b can also en 2002].	e proximal limb of the V3 region ed (CD4i) epitopes, soluble CD4 3 anti-CD4BS MAbs (15e and Ig alization and the neutralization se	ete with the well-characterize tere distinct but share a commolex – the MAb 48d has the element on that more closely resemble b12, and in most cases of glyanti-V3 MAb 694/98D were ci-C5 MAb 1331A was used to envelope glycoproteins from HIV vaccines—2F5 bound to b12 and F105, A32 (C1-C4), n-neutralizing MAbs C11 and companies are involved, and detudy conformational changes as CD4—V3 mutants R298A ced 17b affinity in the present caused Env to become sensitivity profile of R2 is integrated to b12 and HNS2, a broad gG1b12), 2/2 CD4i MAbs (1) ensitivity profile of R2 is integrated to b12 and gamma of CD4 in D1D2Igαtp, which, unlike	d 17b CD4i MAb in an non element near isoleucine epitope most similar to the est the CD4 bound state of cycosylation site dependent not affected – viruses to track levels of cell surface in R5 strains YU2 and JRFL, to gp160\(\Delta\)CT with a C11 (C1-C5), and 39F (V3) d A32 bound with lower MPLs) to reduce eletion of the V1-V2 loops in the mutants—the affinity and R327A were not ce or absence of sCD4, tive to neutralization by ly neutralizing sera – 2/12 7b and 4.8D), and 2G12 and rmediate between the highly 4 retain the capacity to bind to CD4, does not enhance
969	21c	Env Ab type CD4i Doi References Xiang20 • 21c: Five CD4i MA non-progressor – 23 ELISA antigen captu	gp120 (IIIB, J62) nor James Robinson, Tule 202a, Xiang2002b bs were studied, 17b, 48d e and 21c were converted ure assay – critical bindin for CCR5 binding, and all	ane University, New and three new MAb to hybridomas to inc g residues are mappe	L Orleans, LA, USA s derived by Epstein-Barr virus to crease Ab production – all compe d and the CD4i MAb epitopes w 5 binding to a sCD4-gp120 comp	ete with the well-characterize ere distinct but share a comm	d 17b CD4i MAb in an non element near isoleucine

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Nei	utralizing I	Immunogen	Species(Isotype)
		gp120 closer to the 15e, IgG1b12, 21h neutralize either W	CD4-bound state, and is r and F91 was markedly red T or mutant, probably due	eadily bound by sCD4 luced – IgG1b12 failed to polymorphism in th	and CD4i MAbs (17b, 48d to neutralize this mutant, v	l, 49e, 21c ar while neutral nutant, 423 I/	nd 23e) but binding of the control o	s to favor a conformation of of anti-CD4BS MAbs (F105, s enhanced – 2F5 did not 20 bridging sheet, favored a
970	23e	References Xiang2  23e: Five CD4i MA non-progressor – 2: ELISA antigen cap 420, also important CCR5 binding site  23e: A series of mu gp120 closer to the 15e, IgG1b12, 21h neutralize either W	Abs were studied, 17b, 48d 3e and 21c were converted ture assay – critical binding for CCR5 binding, and al [Xiang2002a] attational changes were introposed to the control of the control	and three new MAbs of to hybridomas to increase gresidues are mapped I five can block CCR5 oduced into the YU2 geadily bound by sCD4 luced – IgG1b12 failed to polymorphism in the	derived by Epstein-Barr vir ease Ab production – all co and the CD4i MAb epitope binding to a sCD4-gp120 c p120 that favored different and CD4i MAbs (17b, 48d to neutralize this mutant, v	rus transform impete with t es were distin complex – the conformation 1, 49e, 21c ar while neutral nutant, 423 I/	the well-characterize nct but share a comme e MAb 48d has the e ons – 375 S/W seems nd 23e) but binding of lization by 2G12 was /P, disrupted the gp1:	ed 17b CD4i MAb in an an anon element near isoleucine epitope most similar to the s to favor a conformation of of anti-CD4BS MAbs (F105,
971	48d (4.8d, 4.8D)	References Thali 19 Poignard 1996a, Trl Mondor 1998, Parre Yang 2000, Salzwec 48d: 48d and 17b h 48d: Epitope is bet anti-CD4BS MAb 433A/L, 438 P/R at 48d: Called 4.8d — 48d: Binding of 48 48d: Poor cross-rea 48d: Poor cross-rea 48d: Called 4.8D — multi-laboratory str 48d: Studies using significant involver 48d: Formalin inac [Sattentau 1995c]	cola 1996a, Binley 1997a, Len 1998a, Sullivan 1998b, Ydel 2000, Kolchinsky 2001, have similar epitopes, and the ter exposed upon CD4 bind ICR 39.13g and linear antind 475 M/S confer decrease Neutralizes IIIB – reactived is much more influenced gp41, 582 A/T, confers reactivity with gp120 from mand to neutralize MN, lady involving 11 labs[D'Sea V1/V2 deletion mutant of the control of V2 – similar effect tivation of virus at 0.1% for milar affinity to monomer a	993d, Thali1994, Moo i,1997, Weinberg1997, ang1998, Binley1998, Verrier2001, Golding2 he pair are unique amoding to gp120 – compercy and season of the seaso	rleans, LA, USA re1994b, D'Souza1995, Sa Lee1997, Ugolini1997, W Stamatatos1998, Oscherwi 002b, Yang2002, Xiang200 ong human and rodent MAb tes with ICR 39.13, 15e an G3-508 – 113 D/R, 252 R/ dization [Thali1993] es not inhibit HIV-1 sera fr among molecular clones o on (also confers resistance of the subtype primary isolates, or need binding of 48d in the p	attentau 1995a yatt 1997, Par tz 1999a, Hor O2b, Xiang 20 os d 21h, anti-C W, 257 T/A or com binding of f LAI than is to MAbs F10 a D subtype presence of s	rren 1997c, Frankel1 ffman1999, Fortin20 002a, Edwards2002, CD4 binding site MA or G, 370 E/D, 382 I to IIIB gp120 [Moor s binding of 17b [Mo 05, 21h, 15e and 17b e primary isolate, by scD4 involves the V of virus while maint.	998, Wyatt1998a, 000, Ly2000, Park2000, Zhang2002  Abs – inhibited by F/L, 420 I/R, 421 K/L, re1993a] ore1993d] o) [Thali1994] most labs in a I/V2 loops, with more aining epitope integrity

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48d: Many MAbs inhibit binding (anti-C1, -C5, -C4, -CD4BS) – anti-C1-C4 discontinuous epitope MAbs A32 and 2/11c enhance binding – reciprocal enhanced binding with some anti-V2 MAbs [Moore1996]

- 48d: Binding resulted in gp120 dissociation from virion, mimicking sCD4, and exposure of the gp41 epitope of MAb 50-69, in contrast to CD4BS MAbs [Poignard1996a]
- 48d: Neutralizes JR-FL slightly inhibits gp120 interaction with CCR-5 in a MIP-1beta-CCR-5 competition study [Trkola1996a]
- 48d: One of 14 human MAbs tested for ability to neutralize a chimeric SHIV-vpu+, which expressed HIV-1 IIIB env all Ab combinations tested showed synergistic neutralization 48d has synergistic response with MAbs 694/98-D (anti-V3) and F105 [Li1997]
- 48d: 48d binds to the IIIB protein and not IIIB V3 peptide, while binding to the CanOA V3 peptide, suggesting CanOA V3 is a conformer that mimics the 48d, (but not 17b), epitope [Weinberg1997]
- 48d: Prefers CD4-gp120 complex to gp120 alone, but does not enhance fusion, in contrast to MAb CG10, in fact it inhibits syncytium formation [Lee1997]
- 48d: Viral binding inhibition by 48d was strongly correlated with neutralization (all other neutralizing MAbs tested showed some correlation except 2F5) [Ugolini1997]
- 48d: Binds efficiently to sgp120 but not soluble gp120+gp41, suggesting its gp120 epitope is blocked by gp41 binding [Wyatt1997]
- 48d: Neutralizes TCLA strains, but not primary isolates [Parren1997c]
- 48d: Summary of the implications of the crystal structure of the core of gp120 bound to CD4 and 17b with what is known about mutations that reduce NAb binding probable mechanism of neutralization of 48d is interference with chemokine receptor binding CD4 binding increases exposure of epitope due to V2 loop movement 88N, 117K, 121K, 256S, 257T, N262, delta V3, E370, E381, F 382, R 419, I 420, K 421, Q 422, I 423, W 427, Y 435, P 438, M 475 mutations in HXBc2 (IIIB) decrease binding [Wyatt1998a]
- 48d: Inhibits binding of Hx10 to both CD4 positive and CD4 negative HeLa cells [Mondor1998]
- 48d: The MAb and Fab binding to the oligomeric form of gp120 and neutralization were highly correlated authors suggest that neutralization is determined by the fraction of Ab sites occupied on a virion irrespective of the epitope [Parren1998a]
- 48d: CD4i MAbs 17b and 48d compete with MAb CG10, and the binding sites may overlap MAb A32 enhances binding of 17b, 48d and CG10 [Sullivan1998b]
- 48d: A neutralization assay was developed based on hemi-nested PCR amplification of the LTR (HNPCR) LTR-HNPCR consistently revealed HIV DNA and was shown to be a rapid, specific and reliable neutralization assay based on tests with 6 MAbs and 5 isolates [Yang1998]
- 48d: A panel of MAbs were shown to bind with similar or greater affinity and similar competition profiles to a deglycosylated or variable loop deleted core gp120 protein (Delta V1, V2, and V3), thus such a core protein produces a structure closely approximating full length folded monomer CD4i MAbs 17b and 48d bound better to the deleted protein than to wild type [Binley1998]
- 48d: Deleting the V2 loop of neutralization-resistant HIV-1 isolate SF162 does not abrogate its replication in PBMC or macrophages, but it enhances its neutralization sensitivity to sera from patients with B clade infection up to 170-fold, and also enhances sensitivity to sera from clades A through F deletion of V2 but not V1 enabled neutralization by CD4i MAbs 17b and 48d [Stamatatos1998]
- 48d: Infection of dendritic cells cultured from CD14+ blood cells or from cadaveric human skin was blocked by neutralizing MAbs IgG1b12, or 2F5 and 2G12 delivered together, but not by control non-neutralizing anti-gp120 MAb 4.8D, indicating that NAbs could interrupt early mucosal transmission events [Frankel1998]
- 48d: A CD4-independent viral variant of IIIB, IIIBx, was generated on CXCR4-expressing cells IIIBx exhibited greater exposure of the 17b and 48d epitopes and enhanced neutralization by CD4i MAbs and by polyclonal human sera [Hoffman1999]
- 48d: Called 4.8D host encoded intercellular adhesion molecule (ICAM-1) is incorporated by the HIV-1 virion and enhances viral infectivity ICAM-1 does not modify virus sensitivity to antibodies 0.5beta or 4.8D or sCD4, but neutralizing ability of F105 was diminished in ICAM bearing virions in the presence of lymphocyte function-association antigen-1 (LFA-1) Ab [Fortin2000]

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• 48d: SF162 is a neutralization-resistant HIV-1 isolate – N-linked glycosylation modifications in the V2 loop of the SF162 gp120 revealed that these sites prevent neutralization by CD4BS MAbs (IgG1b12 and IgGCD4), and protect against neutralization by V3 MAbs (447-D and 391-95D) – V2-region glycosylation site mutations did not alter neutralization resistance to V2 MAbs (G3.4 and G3.136) or CD4i MAbs (17b and 48d) – V2 glycosylation site modification allows infection of macrophages, probably due to glycosylated forms requiring fewer CCR5 molecules for viral entry [Ly2000]

- 48d: Six mutations in MN change the virus from a high-infectivity neutralization resistant phenotype to low-infectivity neutralization sensitive V3, CD4BS, and CD4i MAbs are 20-100 fold more efficient at neutralizing the sensitive form the mutation L544P reduced binding of all MAbs against gp120 by causing conformational changes [Park2000]
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- 48d: Mutations in two gloosylation sites in the V2 region of HIV-1 ADA at positions 190 and 197 (187 DNTSYRLINCNTS 199) cause the virus to become CD4-independent and able to enter cells through CCR5 alone these same mutations tended to increase the neutralization sensitivity of the virus, including to 48d only the CD4i antibodies 17b and 48d showed an increased affinity of the CD4 independent viruses relative to wild-type [Kolchinsky2001]
- 48d: Called 4.8d A panel of 12 MAbs was used to identify those that could neutralize the dual-tropic primary isolate HIV-1 89.6 six gave significant neutralization at 2 to 10 ug/ml: 2F5, 50-69, IgG1b12, 447-52D, 2G12, and 670-D six did not have neutralizing activity: 654-D, 4.8D, 450-D, 246-D, 98-6, and 1281 no synergy, only additive effects were seen for pairwise combinations of MAbs, and antagonism was noted between gp41 MAbs 50-69 and 98-6, as well as 98-6 and 2F5 [Verrier2001]
- 48d: The fusion process was slowed by using a suboptimal temperature (31.5 C) to re-evaluate the potential of Abs targeting fusion intermediates to block HIV entry preincubation of E/T cells at 31.5 C enabled polyclonal anti-N-HR Ab and anti-six-helix bundle Abs to inhibit fusion, indicating six-helix bundles form prior to fusion the preincubation 31.5 C step did not alter the inhibitory activity of neutralizing Abs anti-gp41 2F5, or anti-gp120 2G12, IG1b12, 48d, and 17b [Golding2002b]
- 48d: Uncleaved soluble gp140 (YU2 strain, R5 primary isolate) can be stabilized in an oligomer by fusion with a C-term trimeric GCN4 motif or using a T4 trimeric motif derived from T4 bacteriophage fibritin stabilized oligomer gp140 delta683(-FT) showed strong preferential recognition by NAbs IgG1b12 and 2G12 relative to the gp120 monomer, in contrast to poorly neutralizing MAbs F105, F91, 17b, 48d, and 39F which showed reduced levels of binding, and C11, A32, and 30D which did not bind the stabilized oligomer [Yang2002]
- 48d: A series of mutational changes were introduced into the YU2 gp120 that favored different conformations 375 S/W seems to favor a conformation of gp120 closer to the CD4-bound state, and is readily bound by sCD4 and CD4i MAbs (17b, 48d, 49e, 21c and 23e) but binding of anti-CD4BS MAbs (F105, 15e, IgG1b12, 21h and F91 was markedly reduced IgG1b12 failed to neutralize this mutant, while neutralization by 2G12 was enhanced 2F5 did not neutralize either WT or mutant, probably due to polymorphism in the YU2 epitope another mutant, 423 I/P, disrupted the gp120 bridging sheet, favored a different conformation and did not bind CD4, CCR5, or CD4i antibodies, but did bind to CD4BS MAbs [Xiang2002b]
- 48d: Five CD4i MAbs were studied, 17b, 48d and three new MAbs derived by Epstein-Barr virus transformation of PBMC from an HIV+ long term non-progressor 23e and 21c were converted to hybridomas to increase Ab production all compete with the well-characterized 17b CD4i MAb in an ELISA antigen capture assay critical binding residues are mapped and the CD4i MAb epitopes were distinct but share a common element near isoleucine 420, also important for CCR5 binding, and all five can block CCR5 binding to a sCD4-gp120 complex the MAb 48d has the epitope most similar to the CCR5 binding site [Xiang2002a]

No. MA	Ab ID	HXB2 Location	<b>Author's Location</b>	Sequence	Neutra	alizing Immunogen	Species(Isotype)
		the external Enveloe MAb 2G12 and the bearing the truncati expression of the m • 48d: Called 4.8D – neutralization by M neutralizing sera – and 4.8D), and 2G1 intermediate between	pe, enhancing binding of the anti-gp41 MAb 246D – it ion were more sensitive to the ion were more sensitive to the Arare mutation in the new IAbs directed against the Calla anti-V3 MAbs tested 12 and 2F5 – thus multiple	CD4i MAbs 17b and 48d in contrast, binding of the an eutralization by MAbs 42002] utralization sensitive R2-s CD4 binding site (CD4BS (19b and 694/98-D) neutralizations on R2 are functionally strain and the type of the contract of the con	and of CD4BS MAbs F105, anti-V2 MAb 697D and the 18d, b12, and 2G12 – the an train in the proximal limb o ), CD4-induced (CD4i) epit ralized R2, as did 2/3 anti-C	on that more closely resemble b12, and in most cases of gleanti-V3 MAb 694/98D were ti-C5 MAb 1331A was used ff the V3 region caused Envitopes, soluble CD4 (sCD4), a 2D4BS MAbs (15e and IgG11 on and the neutralization sensy strain [Zhang2002]	ycosylation site dependent not affected – viruses to track levels of cell surface become sensitive to nd HNS2, a broadly 012), 2/2 CD4i MAbs (17b
972 49e	2	References Xiang2  • 49e: Five CD4i MA non-progressor – 2 ELISA antigen cap 420, also important CCR5 binding site  • 49e: A series of mu gp120 closer to the 15e, IgG1b12, 21h neutralize either W	Abs were studied, 17b, 48c 3e and 21c were converted ture assay – critical binding for CCR5 binding, and al [Xiang2002a] attational changes were into a CD4-bound state, and is a rand F91 was markedly red T or mutant, probably due	d and three new MAbs der I to hybridomas to increas ng residues are mapped an Il five can block CCR5 bir roduced into the YU2 gp1 readily bound by sCD4 an duced – IgG1b12 failed to to polymorphism in the Y	ived by Epstein-Barr virus to e Ab production – all comp d the CD4i MAb epitopes withing to a sCD4-gp120 com 20 that favored different cord CD4i MAbs (17b, 48d, 49) neutralize this mutant, whi	HIV-1 infection  ransformation of PBMC from the with the well-characterized were distinct but share a complex – the MAb 48d has the endowned from the matter of the matter	d 17b CD4i MAb in an mon element near isoleucine epitope most similar to the s to favor a conformation of anti-CD4BS MAbs (F105, s enhanced – 2F5 did not
973 X5		for binding to purif C, D, E, F, and G, a enhanced by CCR5	b X5 was selected from a fied gp120-CD4-corecepto and neutralizes R5, X4, an	r complexes – the Fab net d R5X4 isolates – it binds Ab 17b binds the CCR5 b	ntralizes PBMC infection by to a conserved epitope on g inding site, X5 also compete	HIV-1 infection  donor with a highly neutraliz  a selection of HIV-1 primar  pp120 induced by CD4 bindir  es with Fab b12 which overla	v isolates from clades A, B, ag, its binding is slightly
974 T22	2	Ab type Env oligor References Earl19 T22: Generated du T22: Pulse label ex	94, Otteken1996, Sugiura ring a study of the influence	onal Institute of Allergy at 1999 ce of the oligomeric struct 0, D27, T20, and T22) bir	nd Infectious Diseases, NIH ure of Env in determining the ding to noncleavable gp140	Vaccine  , Bethesda, MD  ne repertoire of the Ab respon  ) revealed that these anti-CD-	

Env Antibodies Tables

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizing	Immunogen	Species(Isotype)
					was done – T22 is part of a grous, and could only partially block		
975	polyclonal	Ab type N-HR, C-H References deRosny A panel of Abs agai The fusion process ventry – preincubatio	IR, and six-helix bundle y2001, Golding2002b nst gp41 heptad repeats N was slowed by using a sub n of E/T cells at 31.5 C en	optimal temperature (31.5 Cabled polyclonal anti-N-HF	peptides  bled stable N-HR and C-HR six  bled to re-evaluate the potential of  the Ab and anti-six-helix bundle A  R Abs inability to inhibit fusion	Abs targeting fusion Abs to inhibit fusion, i	intermediates to block HIV
976	2A2	Env Ab type N-term References Weissen • Soluble gp41(21-16)		re that can be visualized wit	no h electron microscopy, and 2A2	HIV-1 infection  2 binds to one end of t	human (IgG1κ) he rod [Weissenhorn1996]
977	AC4	Ab type N-term References Dickey2 • AC4: Three MABs,	ID6, AC4, and AD3 that l	bind to a discontinuous N-te	yes rm first 204 aa of gp120 and ge n and are cross-reactive with vii		
978	AD3	<ul><li>Ab type N-term</li><li>References Dickey2</li><li>AD3: There may be</li><li>AD3: Three MABs,</li></ul>	two Abs with this name the ID6, AC4, and AD3 that	hat bind to the N-term regio bind to a discontinuous N-te	yes  n of gp120 [Cook1994, Dickey2  rm first 204 aa of gp120 and ge n and are cross-reactive with vi	nerate ADCC were el	
979	AD3	<ul><li>AD3: There may be</li><li>AD3: MAbs against against the N-termin</li></ul>	the glycosphingolipid Ga	hat bind to the N-term regio llCer block HIV infection of hibit gp120 binding to GalC	n of gp120 [Cook1994, Dickey] normally susceptible CD4 nega er – binding of GalCer to gp120	ative cells from the br	
980	ID6		gp120 (1–193 BH10) 93, Cook1994, Dickey200 wo Abs with this name th		of gp120 [Cook1994, Dickey2	000]	murine (IgG1)

No.	MAb ID	HXB2 Location	<b>Author's Location</b>	Sequence	Neut	ralizing	Immunogen	Species(Isotype)
		the N-terminal half		alCer block HIV infection of r p120 binding to GalCer – bin agent Program: 2343				
981	ID6	<b>Ab type</b> N-term <b>References</b> Dickey2	2000, Cook1994	HIV component: gp160 that bind to the N-term region	yes of gp120 [Cook1994, 1	Dickey2	Vaccine  000]	murine (IgG2a)
				bind to a discontinuous N-tern lo not depend on glycosylation				
982	11/68b	Env	gp120	Strain: BH10 HIV compone	L (H2		Vaccine Vaccine	rat (IgG1)
		<ul> <li>11/68b: Changes at 11/68b: 435 (Y/H) it</li> <li>11/68b: Cross-compresidue 185 – non-re</li> <li>11/68b: The most vadid not affect the abis substituted gp120 ha</li> <li>11/68b: UK Medica</li> </ul>	n C4 does not abrogate betes with MAbs 62c, 66 eciprocal inhibition of biariable amino acids in the lity of sCD4 or MAbs to a reduced response rel Research Council AID	b) within V2, 435 (Y/H) in C4, binding (John Moore, per comc, 66a, and CRA-4 – similar to a minimal of CRA-6 [le V3 loop were replaced with to V1/V2, C1 and C4 to bind – lative to wildtype, and no enhaloge.	m, 1996)  MAb 62c – HXB2 ne Shotton1995] serines to make the imi 11/68b was not affecte	utralizat nunodor d by V3	ion escape mutant had minant V3 loop less in serine substitutions – erved regions [Peet199	nmunogenic – these changes mice injected with serine 8]
983	62c	Ab type V1-V2 References Shotton • 62c: Cross-compete: CRA-3 and CRA-6- neutralize Hx10 [Shotton]	1995 s with MAbs 11/68b, 66 – substitutions 176-177	Strain: BH10 HIV components, 66a, and CRA-4 – same croffy/AT, 179-180 LD/DL, 183-eagent: ARP3075	ss-competition group a		-	_
984	CRA-6 (CRA6)	Env Ab type V1-V2 References Shotton • CRA-6: Called CRA		roup as CRA-3 [Shotton1995]	no			murine
985	L15	Env Ab type V1-V2 References Ditzel19	gp120 997, Parren1997c		P (we	ak)	HIV-1 infection	human (IgG1)

**Env Antibodies HIV Antibodies Tables** 

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neu	itralizing Immunogen	Species(Isotype)
		similar epitopes, L1 all compete with L1	15 and L17 – deletions in 1 15 [Ditzel1997]		ing, and rodent anti-V2 I		abs were obtained with very G3-136, BAT-085, and 52-684
986	T52	Ab type V1-V2 I References Earl199 T52: Generated dur T52: A comparison	Oonor P. Earl, National In 94, Sugiura1999 ring a study of the influence of 25 gp120 specific, con	formation dependent MA	ctious Diseases, NIH, Be are of Env in determining os was done – T52 is one	g the repertoire of the Ab resp	nat had limited cross-reactivity
987	T54	Ab type V1-V2 I References Earl199 T54: Generated dur T54: A comparison	Oonor P. Earl, National In 94, Sugiura1999 ring a study of the influence of 25 gp120 specific, com	formation dependent MA	ctious Diseases, NIH, Be are of Env in determining os was done – T54 is one	g the repertoire of the Ab resp	nat had limited cross-reactivity
988 <sub>F</sub>	polyclonal		n2000 ve great differences in sus			HIV-1 infection 2 and V3-V5 was measured by to neutralization [Gordon2000]	human  HTA in a set of viruses with a
989 1	1088	Env Ab type V2 References Berman • 1088: Binds weakly		kthrough cases from a MN	gp120 vaccine trial [Be	erman1997]	
990 1	110-B	Ab type V2 Done References Moore • 110-B: specific for	or Hybridolabs, Institute I 1993b BH10, does not bind to M		nding inhibited by delet	Vaccine ion of the V2 loop, and the fol S [Moore1993b]	murine llowing amino acid
991 1	1357	Env <b>Ab type</b> V2 <b>Don</b> e	gp120 or Susan Zolla-Pazner (Zo	ollas01@mcrcr6.med.nyu)	(NYU Med. Center)		human (IgG1κ)

References Nyambi1998, Gorny2000a, Nyambi2000

• 1357: 26 HIV-1 group M isolates (clades A to H) were tested for binding to 47 MAbs, including 5 anti-V2 MAbs, which showed weak and sporadic binding, with the most frequent binding to C and D clades [Nyambi2000]

No. MAb	ID HXB2 Locat	tion Author's Location	Sequence	Neutralizin	ng Immunogen	Species(Isotype)			
<ul> <li>1357: Using a whole virion-ELISA method, 18 human MAbs were tested for their ability to bind to a panel of 9 viruses from clades A V2 Abs 697-D, 1361, and 1357 tended to bind very weakly with a similar pattern of specificity to virions, but bound well to soluble g only to subtype D MAL [Nyambi1998]</li> <li>1357: Blocks binding of MAb 697-D to rgp120, and doesn't react with a protein from which V1V2 has been deleted – binding of pan soluble oligomeric gp140 versus gp41 or gp120 monomers was compared – no MAb was oligomer specific, though anti-V3 and CD4 better with the oligomer and V2 and C5 tended to favor the monomer – V2 MAbs 697-D, 1357 and 1361 favored the monomer by app [Gorny2000a]</li> <li>1357: 26 HIV-1 group M isolates (clades A to H) were tested for binding to 47 MAbs, including 5 anti-V2 MAbs, which showed weal binding, with the most frequent binding to C and D clades [Nyambi2000]</li> </ul>									
992 1361	Ab type V2 References II  1361: Using V2 Abs 697- B clade virus 1361: Blocks soluble oligo better with th [Gorny2000a 1361: 26 HIV	gp120 Vaccine human (IgG1κ) Vector/Type: protein HIV component: gp120 V2 Donor Susan Zolla-Pazner (Zollas01@mcrcr6.med.nyu) (NYU Med. Center) es Nyambi1998, Gorny2000a, Nyambi2000 ing a whole virion-ELISA method, 18 human MAbs were tested for their ability to bind to a panel of 9 viruses from clades A, B, D, F, G, and H 97-D, 1361, and 1357 tended to bind weakly with a similar pattern of specificity to virions, but bound well to soluble gp120: weak binding to 1 iruses (CA5), and also weak binding to a subtype D virus, MAL [Nyambi1998] ocks binding of MAb 697-D to rgp120, and doesn't react with a protein from which V1V2 has been deleted – binding of panel of 21 MAbs to digomeric gp140 versus gp41 or gp120 monomers was compared – no MAb was oligomer specific, though anti-V3 and CD4BS MAbs reacted the he oligomer and V2 and C5 tended to favor the monomer – V2 MAbs 697-D, 1357 and 1361 favored the monomer by approximately 2 fold 00a] HIV-1 group M isolates (clades A to H) were tested for binding to 47 MAbs, including 5 anti-V2 MAbs, which showed weak and sporadic with the most frequent binding to C and D clades [Nyambi2000]							
993 1393	A Env Ab type V2 References 1 • 1393A: 26 H	gp120	to H) were tested for bind	ling to 47 MAbs, including 5 ant	HIV-1 infection	owed weak and sporadic			
994 66a	Env Vaccine Vect Ab type V2 References S  66a: Substitut [Shotton1995]	gp120 cor/Type: recombinant protein S Shotton1995 ttions 176-177 FY/AT, 179-180 I	Strain: BH10 HIV comp	L (HXB2) onent: gp120	Vaccine  pinding – same compet	murine (IgG1) ition group as CRA4			
995 66c	Env <b>Vaccine</b> Vect <b>Ab type</b> V2 <b>References</b> S	gp120 for/Type: recombinant protein S Shotton1995	Strain: BH10 HIV comp	L (HXB2) onent: gp120	Vaccine	murine (IgG1)			

**HIV Antibodies Tables** 

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizing	Immunogen	Species(Isotype)
		• 66c: Substitutions 1 [Shotton1995]	76-177 FY/AT, 179-180 I	LD/DL, 183-184 PI/SG, ar	nd 191-193 YSL/GSS abrogate bin	nding – same comp	petition group as CRA4
996	684-238 (52-684-238, 52-684)	Ab type V2 Dono References Moorel • 684-238: Specific for following amino aci • 684-238: Weakly no • 684-238: Does not of	or Gerry Robey, Abbott L 1993b, Thali 1993, Gorny I 100 BH10 or HXB2, does not d substitutions: 176/177F 20 cutralizing, IC 50 = 84 mu 190 compete with IgG1b12, res	994, Ditzel1995, Moore 19 oot bind to MN, RF, or SF- FY/AT, 179/180LD/DL, 18 ag/ml [Gorny1994] eciprocal inhibition with M		SS [Moore1993b]	
997	830A		oup M isolates (clades A t	o H) were tested for bindi and D clades [Nyambi200	ng to 47 MAbs, including 5 anti-V	HIV-1 infection  72 MAbs, which sh	nowed weak and sporadic
998	CRA-3 (CRA3)	Ab type V2 Dono References Moore1  CRA-3: Conformation CRA-3: specific for substitutions: 176/1 [Moore1993b]  CRA-3: Many MAh [Moore1996]  CRA-3: Called CRA-3: Called CRA-3	or Mark Page, NIBSC All 993a, Moore1993b, Thal- onal, does not bind well to BH10 or HXB2, does no 77 FY/AT, 179/180 LD/D os enhance binding, includes	oL, 183/184 PI/SG, and 19 ding some anti-C5, C1, V4 coup as CRA6 [Shotton199	Bar, Herts, UK e1996, Ditzel1997 e1993a] gp120 – binding inhibited by delo 2-194 YSL/GSS – epitope probab , and C4 MAbs – enhances bindin	ly involves stem of	f V1/V2 loop structure
999		Ab type V2 Dono References McKeat • CRA-4: Changes at • CRA-4: Conformati • CRA-4: Specific for acid substitutions: 1 • CRA-4: Cross-comp [Shotton1995]	or Mark Page, NIBS, MRoing 1993b, Moore 1993a, iresidues 191/192/193 (Yonal, does not bind well to BH10 and HXB2, does 176/177 FY/AT, 179/180 I petes with MAbs 11/68b,	to denatured gp120 [Moorn not bind to MN, RF, or SF- LD/DL, 183/184 PI/SG, an 62c, 66c, 66a – similar to	y, ARP 325 Shotton1995, Moore1996 Y/H) in C4, abrogate binding – ty	eletion of the V2 lo Bb] bition by MAbs 12	pop, and the following amino b, 60b and CRA-6

No. MAb ID	<b>HXB2 Location</b>	<b>Author's Location</b>	Sequence	Neutralizi	ing Immunogen	Species(Isotype)
	• CRA-4: UK Medica	al Research Council AIDS	S reagent: ARP325			
000 L17	markedly different to > b13) and binding	r of Fab binding affinity to than Fab binding affinity to to oligomeric form and no	o the mature oligomeric for	2 > 3B3 > b12 = DO8i > b11 m (3B3 > b12 > DO142-10 > 1 for both Fabs and MAbs – a	Loop 2 > b11 > L17 > b6	> DO8i > b14 > DA48 > b
001 SC258 (52- 581-SC258)	Env Vaccine Vector/Typ Ab type V2 Done References Moore!  SC258: Called 52-5 amino acid substitu SC258: HIV-1 RF V SC258: Very poor r SC258: Does not co SC258: Several MA MAb F91 – reciprode SC258: Does not in SC258: Transgenic producing hybridon	gp120 e: purified protein Strain or Gerry Robey, Abbott L 1993b, Thali1993, Gorny 1 581-SC258 – binds to BH tions: 176/177 FY/AT, 17 V2 substitutions 177 Y/H reactivity with gp120 mole ompete with IgG1b12 – re Abs binding to various gp1 cal inhibition with V2 reg shibit gp120 interaction with mice carrying human gen	n: IIIB HIV component: gaboratories 994, Yoshiyama1994, Moo 10, MN, and RF gp120 – ne 9/180 LD/DL, 183/184 PI/S and 179 L/P in the V2 loop ecules outside of clade B [M ciprocal inhibition with MA 20 epitopes enhance bindin ion antibodies [Moore1996 ith CCR-5 in a MIP-1beta-C es allowing production of f HIV SF162 gp120 – the pr	L gp120 re1994b, Ditzel1995, Moore1 utralizes BH10 – binding inhi GG, and 192-194 YSL/GSS [N of RF reduce affinity – 177 Y loore1994b] Abs L39, L40, and L78 [Ditze g, but the only MAb that SC2	ibited by deletion of the V Moore1993b]  7H inhibits SC258 neutral  11995]  258 enhanced binding of w  sted as not neutralizing [Traction to rapidly create a panel of the steel of the ste	2 loop, and the following ization [Yoshiyama1994] vas anti-CD4 binding site kola1996a] f anti-HIV gp120 MAb
002 L25	• L25: gp120 immob obtained with with	995, Ditzel1997, Parren19 ilized on solid phase by ca sensitivity to substitutions	apture with anti-CD4 BS M	L (weak)  Ab L72 was used for selection ions – rodent anti-V2 MAb So 997c]		
.003 L39	Env Ab type V2-CD4B: References Ditzel1  L39: This Fab does sensitive to amino a binding) – does not	gp120 S 995 not inhibit sCD4 binding icid substitutions in the V3 compete with CD4BS MA	, but is inhibited by sCD4, p 3 loop (similar patterns wer Abs, but is sensitive to amin	no  probably due to conformations to observed for L39 and L78 g to acid changes at positions 30 th chain variable region seque	p120 amino acid substitut 58 and 370 – binding unaf	ions enhancing or reducing fected by deglycosylation
004 L40	Env Ab type V2-CD4B; References Ditzel1			no	HIV-1 infection	human (IgG1 $\kappa$ )

Env Antibodies Tables

No. MAb ID	HXB2 Location	Author's Location	Sequence	Neutral	izing Immunogen	Species(Isotype)
	sensitive to amino binding) – does no	acid substitutions in the V3 of compete with CD4BS MA	loop (similar patterns were Abs, but is sensitive to amin	e observed for L40 and L78 no acid changes at positions	onal changes – it is competed gp120 amino acid substituti 368 and 370 – binding only variable region sequence is a	ions enhancing or reducing partially affected by
1005 L78	binding, and some conformational ch but is sensitive to	1995 s at V2: (152/153 GE/SM, 1 c C4 and C5 substitutions en anges – it is competed by a amino acid changes at posit	thance binding – this Fab d nti-V2 MAbs, and sensitive ions 368 and 370 – Fab ne	oes not inhibit sCD4 bindin to amino acid substitutions	HIV-1 infection  W), CD4BS (257 T/R, 368 I g, but is inhibited by sCD4, in the V3 loop – does not coding unaffected by deglycosyailable [Ditzel1995]	probably due to ompete with CD4BS MAbs
1006	be strongly related	als with infections of HIV-	reflected the sum of react		HIV-1 infection  n primary PBMC cultures. Sable regions in the proteins.	
1007 110.J	<ul><li>References Thali</li><li>110.J: Inhibits sCI</li><li>110.J: Binds to car</li></ul>	D4-inducible anti-CD4 bind	ing site MAb 48d [Thali19/3 loop – reciprocal bindin	g inhibition with other anti-	V3 and anti-C4 MAbs – and	reciprocal enhanced
1008 1334-D (1 1334D)	Ab type V3 Doi References Zolla- 1334-D: This MA 1334-D: MAb per to be critical for re 1334-D: Called 13 subtypes – was su compared – no M. monomer – V3 M 1334-D: Called 13 tested, and of 494	eactivity in this group [Zolla 334 – binds to V3 peptides f ggested to be IgG1lambda h Ab was oligomer specific, th Abs 447-52D, 838-D, and 1 34D – A panel of 47 human	1999b, Gorny2000a, Nyam c gp160 from HIV451 [Zcered with immunological rap-Pazner1999b] from MN, SF2, NY5, RF, and rere – binding of panel of 2000 anti-V3 and CD4BS 334 bound with a 7-10 folion MAbs was tested againsted some viral binding – V3	bi2000 Ila-Pazner1999a] elated MAbs: 1334, 419, 50 and CDC4 strains as well as an Image of the MAbs to soluble oligome MAbs reacted better with the preference for the oligome 26 HIV-1 group M primary and MAbs tended to have the manage of MAbs t	HIV-1 infection  4, 447, 453 and 537 – the concentration of the concentr	om A, C, D, F, G, and H 120 monomers was tended to favor the ugh H – 19 V3 MAbs were
1009 2182	Env	(JRCSF) nor Susan Zolla-Pazner (Zo		P	HIV-1 infection	human (IgG1λ)

No. MAb ID	HXB2 Location	<b>Author's Location</b>	Sequence	Neutralizin	ng Immunogen	Species(Isotype)
	HIV-1-infected ind leukemia virus gp7 MAbs showed cros to CRF01(subtype well-characterized conformation-sensi of all clades) – 5/6 was infected abroad	on-dependent anti-V3 loop ividuals by selection of he 0 – the six new MAbs all is-clade binding to native, E, N=2) – the strength bin MAbs were used as control itive MAb control), 1331A MAbs were derived from d with clade A who is pres	eterhybridomas using a V3- bind to the tip of the V3 lo intact virions of clades A(lading was highly correlated ols: anti-V3 447-52D (anti- A (anti-C5 used as a linear individuals infected in the sently living in New York of	eactive, so six new V3 MAbs we -fusion protein (V3-fp), the HIV top and cross-compete with the N N=2), B(N=4), and F(N=2), limi I with percent neutralization using -V3 MAb for competition and no binding site MAb control), MAb US, presumably with clade B, a city – 2412 and 2456 were produce 82 bound to 8/16 of the diverse in	7-1 JRCSF V3 loop insert MAb 447-52D and are control with the difference of the diff	ted into a truncated murine onformationally sensitive — and D(N=3), and did not bind blast assay — five 4 (anti-CD4BS used as a at bound to primary isolates are from an individual who from the same individual,
1010 2191	Env	(JRCSF)		P	HIV-1 infection	human (IgG1λ)
	Ab type V3 Don References Gorny		ollas01@mcrcr6.med.nyu)	(NYU Med. Center)		
	MAbs showed cross to CRF01(subtype well-characterized conformation-sensition of all clades) – 5/6 was infected abroad	ss-clade binding to native, E, N=2) – the strength bin MAbs were used as control tive MAb control), 1331A MAbs were derived from d with clade A who is pres	intact virions of clades A(lading was highly correlated ols: anti-V3 447-52D (anti-A (anti-C5 used as a linear individuals infected in the sently living in New York of	op and cross-compete with the N=2), B(N=4), and F(N=2), limid with percent neutralization using -V3 MAb for competition and number of the MAb control), MAb US, presumably with clade B, a city – 2412 and 2456 were producted by the diverse production of the diverse production of the diverse of the manufacture of the diverse of the manufacture of the diverse of the manufacture of the diverse of the diverse of the manufacture of the diverse	ited binding to C(N=3) a ing the ghost cell or PHA eutralization studies), 65 o 246 (anti-gp41 MAb th and one, 2182, was derivated from cells obtained	nd D(N=3), and did not bind blast assay – five 4 (anti-CD4BS used as a at bound to primary isolates ed from an individual who from the same individual,
1011 2219	Env <b>Ab type</b> V3 <b>Don</b>	(JRCSF) or Susan Zolla-Pazner (Zo	ollas01@mcrcr6.med.nyu)	P	HIV-1 infection	human (IgG1λ)
	HIV-1-infected ind leukemia virus gp7 MAbs showed cros to CRF01(subtype well-characterized conformation-sensi of all clades) – 5/6 was infected abroad	on-dependent anti-V3 loop ividuals by selection of he 0 – the six new MAbs all is-clade binding to native, E, N=2) – the strength bin MAbs were used as control itive MAb control), 1331A MAbs were derived from d with clade A who is pres	eterhybridomas using a V3- bind to the tip of the V3 lo intact virions of clades A(lading was highly correlated ols: anti-V3 447-52D (anti- A (anti-C5 used as a linear individuals infected in the sently living in New York of	eactive, so six new V3 MAbs were-fusion protein (V3-fp), the HIV op and cross-compete with the N=2), B(N=4), and F(N=2), limit with percent neutralization using V3 MAb for competition and nobinding site MAb control), MAb US, presumably with clade B, a city – 2412 and 2456 were produted by bound to 13/16 of the diverses	7-1 JRCSF V3 loop insert MAb 447-52D and are counted binding to C(N=3) and the ghost cell or PHA eutralization studies), 65 to 246 (anti-gp41 MAb thand one, 2182, was derivated from cells obtained	ted into a truncated murine onformationally sensitive – and D(N=3), and did not bind blast assay – five 4 (anti-CD4BS used as a at bound to primary isolates deform an individual who
1012 2412	Env	(JRCSF)  or Susan Zolla-Pazner (Zo		P	HIV-1 infection	human (IgG1λ)

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No. MAb ID	HXB2 Location	<b>Author's Location</b>	Sequence	Neutral	izing Immunogen	Species(Isotype)	
	HIV-1-infected indi- leukemia virus gp7- MAbs showed cros to CRF01(subtype) well-characterized conformation-sensi of all clades) – 5/6 was infected abroad	ividuals by selection of he 0 – the six new MAbs all s-clade binding to native, E, N=2) – the strength bin MAbs were used as controlive MAb control), 1331A MAbs were derived from I with clade A who is presibs were each generated from	eterhybridomas using a V3- bind to the tip of the V3 loc intact virions of clades A(N dding was highly correlated ols: anti-V3 447-52D (anti- a (anti-C5 used as a linear b individuals infected in the sently living in New York c	fusion protein (V3-fp), the Inp and cross-compete with the I=2), B(N=4), and F(N=2), with percent neutralization V3 MAb for competition are inding site MAb control), Now, presumably with clade in the Input III and	using the ghost cell or PHA and neutralization studies), 65	ted into a truncated murine conformationally sensitive – and D(N=3), and did not bind blast assay – five 4 (anti-CD4BS used as a at bound to primary isolates and from an individual who from the same individual,	
1013 2442	References Gorny2  • 2442: Conformation HIV-1-infected indipleukemia virus gp7 MAbs showed crost to CRF01(subtype) well-characterized conformation-sensition of all clades) – 5/6 was infected abroad	2002 n-dependent anti-V3 loop (viduals by selection of he 0 – the six new MAbs all s-clade binding to native, E, N=2) – the strength bin MAbs were used as contre tive MAb control), 1331A MAbs were derived from I with clade A who is pres	eterhybridomas using a V3- bind to the tip of the V3 loo intact virions of clades A(N dding was highly correlated ols: anti-V3 447-52D (anti- a (anti-C5 used as a linear b individuals infected in the sently living in New York c	active, so six new V3 MAbs fusion protein (V3-fp), the I op and cross-compete with t I=2), B(N=4), and F(N=2), with percent neutralization V3 MAb for competition arinding site MAb control), MUS, presumably with clade ity – 2412 and 2456 were proposed to the six of	using the ghost cell or PHA and neutralization studies), 65 MAb 246 (anti-gp41 MAb th B, and one, 2182, was derive roduced from cells obtained	ted into a truncated murine onformationally sensitive – and D(N=3), and did not bind blast assay – five 4 (anti-CD4BS used as a at bound to primary isolates ed from an individual who	
1014 2456	while the other MAbs were each generated from different subjects – 2442 bound to 13/16 of the diverse isolates [Gorny2002]  4 2456  Env (JRCSF) P HIV-1 infection human (IgC Ab type V3 Donor Susan Zolla-Pazner (Zollas01@mcrcr6.med.nyu) (NYU Med. Center)  References Gorny2002  • 2456: Conformation-dependent anti-V3 loop Abs may be more cross-reactive, so six new V3 MAbs were generated from cells of asymptomatic HIV-1-infected individuals by selection of heterhybridomas using a V3-fusion protein (V3-fp), the HIV-1 JRCSF V3 loop inserted into a truncated leukemia virus gp70 – the six new MAbs all bind to the tip of the V3 loop and cross-compete with the MAb 447-52D and are conformationally sen MAbs showed cross-clade binding to native, intact virions of clades A(N=2), B(N=4), and F(N=2), limited binding to C(N=3) and D(N=3), and did to CRF01(subtype E, N=2) – the strength binding was highly correlated with percent neutralization using the ghost cell or PHA blast assay – five well-characterized MAbs were used as controls: anti-V3 447-52D (anti-V3 MAb for competition and neutralization studies), 654 (anti-CD4BS use conformation-sensitive MAb control), 1331A (anti-C5 used as a linear binding site MAb control), MAb 246 (anti-gp41 MAb that bound to primary of all clades) – 5/6 MAbs were derived from individuals infected in the US, presumably with clade B, and one, 2182, was derived from an individual was infected abroad with clade A who is presently living in New York city – 2412 and 2456 were produced from cells obtained from the same individual while the other MAbs were each generated from different subjects – 2456 bound to 12/16 of the diverse isolates [Gorny2002]						
1015 39F	Env	gp120	ne University, New Orleans.	no			

**Ab type** V3 **Donor** James Robinson, Tulane University, New Orleans, LA, USA **References** Yang2002, Grundner2002

No. MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizi	ng Immunogen	Species(Isotype)		
	trimeric motif deri and 2G12 relative and C11, A32, and • 39F: HIV-1 gp160 JRFL, and X4 stra a reconstituted me	to the gp120 monomer, in a 130D which did not bind the deltaCT (cytoplasmic tail-cin HXBc2, were made in a mbrane ten-fold better than	e fibritin – stabilized oligo contrast to poorly neutrali ne stabilized oligomer [Ya deleted) proteoliposomes physiologic membrane so n the same protein on beac	stabilized in an oligomer by fus mer gp140 delta683(-FT) showed zing MAbs F105, F91, 17b, 48d ng2002] (PLs) containing native, trimeric etting as candidate immunogens ls – anti-CD4BS MAbs IgG1b12 ltaCT expressed on the cell surfa	ed strong preferential r l, and 39F which show e envelope glycoprotei for HIV vaccines – 2F 2 and F105, A32 (C1-6	recognition by NAbs IgG1b12 yed reduced levels of binding, ans from R5 strains YU2 and F5 bound to gp160deltaCT with		
1016 55/68b	did not affect the a	variable amino acids in the ability of sCD4 or MAbs to	V1/V2, C1 and C4 to bin	rith serines to make the immuno d, and anti-V3 MAb 55/68b bin esponse relative to wildtype, and	ding was abrogated by	V3 serine substitutions in the		
1017 5G11	References Moore • 5G11: Binds to co	nformation sensitive epitor	be in the V3 loop – recipro	SA ocal inhibition of other V3 loop of d enhances binding of V2 MAbs		hancement of some C1-C5		
1018 6.1	Env	gp120 (SF162)		no	Vaccine	human from transgenic mice ( $IgG2\kappa$ )		
	Ab type V3 Dor References He200 • 6.1: Transgenic mi panel of anti-HIV	nor Dr. Abraham Pinter, Pu )2 ice (strain XenoMouse G2) gp120 MAb-producing hyl	blic Health Research Inst carrying human genes al oridomas by immunization	ponent: gp120 Adjuvant: Ribi itute, Newark, NJ, pinter@phri.dlowing production of fully human with HIV SF162 gp120 – 3/4 VE11/A8 could weakly neutralize	org an IgG2kappa MAbs v V3 MAbs bound a sim	M)  were used to rapidly create a nilar linear epitope between		
1019 6.7	Env	gp120 (SF162)		no	Vaccine	human from transgenic mice $(\operatorname{IgG2}\kappa)$		
	Vaccine Vector/Type: recombinant protein Strain: SF162 HIV component: gp120 Adjuvant: Ribi adjuvant (MPL+TDM)  Ab type V3 Donor Dr. Abraham Pinter, Public Health Research Institute, Newark, NJ, pinter@phri.org  References He2002  • 6.7: Transgenic mice (strain XenoMouse G2) carrying human genes allowing production of fully human IgG2kappa MAbs were used to rapidly create a panel of anti-HIV gp120 MAb-producing hybridomas by immunization with HIV SF162 gp120 – 3/4 V3 MAbs bound a similar linear epitope between positions 11-30 of the MN V3 loop (8E11/A8, 6.1, and 6.7), but only 8E11/A8 could weakly neutralize autologous strain SF162 [He2002]							

Env Antibodies Tables

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizing	Immunogen	Species(Isotype)					
1020	8.27.3	Env	gp120 (SF162)		L	Vaccine	human from transgenic mice (IgG2\kappa)					
		Ab type V3 Dono References He2002	or Dr. Abraham Pinter, P	ublic Health Research Institu	nent: gp120 Adjuvant: Ribi ac te, Newark, NJ, pinter@phri.org							
		• 8.27.3: Transgenic mice (strain XenoMouse G2) carrying human genes allowing production of fully human IgG2kappa MAbs were panel of anti-HIV gp120 MAb-producing hybridomas by immunization with HIV SF162 gp120 – 1/4 V3 MAbs, 8.27.3, bound a dis was broadly cross-reactive with B clade R5 and X4 strains (not E clade) and could neutralize autologous strain SF162 [He2002]										
021	8E11/A8	Env	gp120 (SF162)		L	Vaccine	human from transgenic mice $(\operatorname{IgG2}\kappa)$					
		<ul> <li>Vaccine Vector/Type: recombinant protein Strain: SF162 HIV component: gp120 Adjuvant: Ribi adjuvant (MPL+TDM)</li> <li>Ab type V3 Donor Dr. Abraham Pinter, Public Health Research Institute, Newark, NJ, pinter@phri.org</li> <li>References He2002</li> <li>8E11/A8: Transgenic mice (strain XenoMouse G2) carrying human genes allowing production of fully human IgG2kappa MAbs were used to rapidly creat a panel of anti-HIV gp120 MAb-producing hybridomas by immunization with HIV SF162 gp120 – 3/4 V3 MAbs bound a similar linear epitope between positions 11-30 of the MN V3 loop (8E11/A8, 6.1, and 6.7), but only 8E11/A8 could weakly neutralize autologous strain SF162 [He2002]</li> </ul>										
022	9305	Env Ab type V3 Dono References McDou	gp120 or Du Pont, Wilmington ggal1996	DE	L		murine					
	AG1121 (1121)	Env gp120 L  Ab type V3 Donor AGMED, Inc, Bedford, MA, USA or ImmunoDiagnostics, Inc, Woburn, MA, USA  References Sullivan1995, Cao1997b, Si2001  • AG1121: Recognizes monomeric gp120 from T-cell adapted line HXBc2 and primary isolate 89.6 equally well, but 89.6 was three-fold less sensitive to neutralization by AG1121 than HXBc2 [Sullivan1995]										
		<ul> <li>AG1121: Called 1121 – Virus with the V1-V2 loop deleted was viable and more susceptible to neutralization by CD4i MAb 17b, and anti-V3 MAbs 1121, 9284, and 110.4, but not to and CD4BS MAb F105 or sCD4 [Cao1997b]</li> <li>AG1121: SHIV-HXBc2 is a neutralization sensitive non-pathogenic virus, and several in vivo passages through monkey's yielded highly pathogenic SHIV KU-1 – HXBc2 and the KU-1 clone HXBc2P3.2 differ in 12 amino acids in gp160 – substitutions in both gp120 and gp41 reduced the ability of sCD4, IgG1b12, F105 and AG1121 to Env achieve saturation and full occupancy, and neutralize KU-1 – 17b and 2F5 also bound less efficiently to HXBc2P3.2, although 2G12 was able to bind both comparably [Si2001]</li> </ul>										
1024	D47	Ab type V3 Dono References Earl 199 D47: Generated dur D47: Used for captu	ring a study of the influer ure of oligomeric Env for	NIH eken1996, Wyatt1997, Earl199 nce of the oligomeric structure	e of Env in determining the repeal ding of this antibody to oligom							

No. MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizing Immunogen	Species(Isotype)
•	through chase period by D47: Binds both go D47: Used for cordependent anti-gp D47: sCD4 can ac	iod [Otteken1996] gp120 and soluble gp120+gp mparison in a study of gp41 a 41 MAbs [Earl1997] ctivate fusion between effector n specific and can inhibit sCI	41 complex efficiently, so antibodies – D47 binds to or cells expressing Env a	evealed that this anti-V3 MAb bound immediately an algesting its gp120 epitope is not blocked by gp41 be a greater extent to cell surface expressed Env than and target cells expressing coreceptor (CCR5 or CXCI at only of the closely related LAV Env, while anti-CD	inding [Wyatt1997] ny of 38 conformation R4) alone without CD4 – V3
1025 F5.5	References Altme F5.5: A Semliki F recognized by the and 694/98D and	orest virus (SFV) expression anti-V3 MAbs K24 and F5.:	n system carrying BX08 e 5, while gp120 at the plas n rat brain also showed th	env was used to study the conformation of gp120 Environment of the small membrane was detected only by conformation do not surface-expressed Environment only by the	ependent MAbs 2G12, 670-D
1026 G3-1472		e1996 o carboxy-terminal side of th		nding inhibition with other anti-V3 and anti-C4 MAl ling inhibited by anti-C4 MAbs [Moore1996]	bs – reciprocal enhanced
1027 K24	References Altme K24: A Semliki For recognized by the and 694/98D and	orest virus (SFV) expression anti-V3 MAbs K24 and F5.:	a system carrying BX08 e 5, while gp120 at the plas n rat brain also showed th	env was used to study the conformation of gp120 env sma membrane was detected only by conformation do nat surface-expressed Env was recognized only by the	ependent MAbs 2G12, 670-D
	Ab type V3 Doi References D'Sou TH1: Found to ne involving 11 labs TH1: A neutraliza	gp120  nor Michael Fung, Tanox Bi nza1995, Yang1998 utralize MN and JRCSF, but [D'Souza1995] ttion assay was developed ba	osystem, USA not two B subtype prima	L (MN, JRCSF)  ary isolates, nor a D subtype primary isolate, by most amplification of the LTR (HNPCR) – LTR-HNPCR passed on tests with 6 MAbs and 5 isolates [Yang1998]	consistently revealed HIV DNA
1029 anti-gp120/V3		nor Intracel Co	rus-like particle Strain:	Vaccine A clade 94UG018 HIV component: Gag, Pol, Nef,	murine (IgG) gp120

Env Antibodies Tables

No. MAb ID	HXB2 Location	<b>Author's Location</b>	Sequence	Neutr	alizing Immunogen	Species(Isotype)
	created using a Bac	culovirus expression syster	n to package additional Ol		nes as well as gp120 of the clad 3 and anti-p24 antibodies were VLP [Buonaguro2001]	
1030 polyclonal	Ab type V3 References Truong • Antibodies raised a regions of gp120 w	g1996 gainst recombinant anti-p	55 virus-like particles with ng responses, weak Env, a	nd strong Gag responses w	Vaccine B, CD4BS, p55 eleted, bearing inserts of either were elicited – the major homol	
1031 polyclonal	Pol LAI, rgp120 SF Ab type V3 References Verrier • Serum Abs elicited not react with V3 p	2000 by this vaccine reacted wieptides from clades E and	ith V3 peptides from clade O – neutralizing activity a	es B, C, and F, reacted weal	Vaccine HIV component: gp120 MN, g  sly with V3 peptides from class ates tested was observed, inclu  000]	les A, D, G, and H, and did
1032 polyclonal					in vitro stimulation	human (IgM) formation: they react with
1033 polyclonal					independent predictors of motl	human ner to infant transmission of
1034 polyclonal	virus, gp120 Adju Ab type V3 References Kawam • Vaginal fluids were IIIB neutralization	want: concavalin A-immo nura2002 collected after intravagina	abilized polystyrene nanos al immunization of BALB/ G was undetectable but ant	pheres  orange of the control of the	Vaccine n A-NS Strain: IIIB HIV co	using a IIIB-V3 ELISA and
1035 polyclonal	Env			L	Vaccine ha, IL-12, and IL-18 or GM-C	human (IgG1, IgG2a, IgA)

No. MAb ID	HXB2 Location	<b>Author's Location</b>	Sequence	Neut	ralizing Immunogen	Species(Isotype)
		ant combination IL-1alph		re found to stimulate potent m safe for use in humans [Bradi		upon intranasal immunization
1036 polyclonal	Vaccine Vector/Typ Ab type V3 References Hewer.  • A synthetic peptide found amino acids	2002 e immunogen designated a (>10%) from the C subtyp	multiple epitope immi	n HIV component: V3 Ad munogen (MEI) was generate netic peptide – when injected s – sera from eight HIV posit	d by synthesizing peptides vinto mice, the C subtype M	
1037 11/75a/21/	Ab type V3 discon References McKea • 11/75a/21/41: The changes did not aff	ating 1992a, Peet 1998 most variable amino acids ect the ability of sCD4 or ions – mice injected with s	MAbs to V1/V2, C1 at	eplaced with serines to make and C4 to bind, but anti-V3 MA and a reduced response rela	Ab 11/75a/21/41 binding wa	as dramatically diminished by
1038 41.1 (ICR41.1i, ICR41)	Ab type V3 discon References McKea  41.1: The gp41 mu neutralizing MAbs  41.1: Called ICR41 neutralization medi [McLain1994]  41.1: Called ICR41 [Armstrong1996a]  41.1: Called ICR41 41.1: Deletion of th	ating 1992a, McKeating 1994 tation 582(Ala to Thr) res – neutralization efficiency 1.1i – Kinetics of neutralization by 3 molecules of Ign 1.1i – IgG2c? – Neutralization occur the V1V2 regions did not a	Il, Institute for Cancer 23b, Klasse 1993a, McI ults in conformational of 41.1 is not affected ation studied – no lag of G per virion – most effected if the as by blocking a post-fuffect anti-V3 Abs ability	L (Hz) component: gp120 Research, Sutton, Surrey, UK Lain1994, Armstrong1996a, A changes in gp120 that confer [Reitz1988, Klasse1993a] for 39.3b, while ICR 39.13g a icient at neutralization of the e Ab was added after the virus asion internalization event, in ty to bind when compared to eutralization (all other neutral	Armstrong 1996b, Jeffs 1996, neutralization resistance to and ICR 41.1i have lags of 5 three MAbs studied – acts v bound to the host cells at 2 contrast to MAb F58 [Arms intact rec gp120 [Jeffs 1996]	conformationally sensitive and 15 min respectively – with multi-hit kinetics 4 degrees C or below strong 1996b]
1039 55/45a/11	Env Ab type V3 discon References Peet19					

Env Antibodies Tables

No. MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizing	Immunogen	Species(Isotype)
	changes did not aff	ect the ability of sCD4 or Mons – mice injected with so	MAbs to V1/V2, C1 and	d with serines to make the immund C4 to bind, and anti-V3 MAb 55/4 and a reduced response relative to v	5a/11 binding was only	ly marginally diminished by
1040 1108	• 1108: Selected with 386, 268, 311, 257,	Pazner 1999a, Zolla-Pazner n peptide 987, a mimotope 694.8 – the amino acids H	of anti-V3 MAb 447-D II tended to be critical fo	– MAb peptide reactivity pattern cl r reactivity in this group [Zolla-Paz AWRSVHLGPGRGSGSGMGK [	zner1999b]	human (IgG1λ) logical related MAbs: 1108,
1041 polyclonal	Env Ab type V3, V4 References Skott19 IgA and IgG from a primarily directed to	999 45 HIV+ individuals was st oward Env – peptide ELIS.	tudied – people with low A studies indicated that t	CD4+ cell counts had decreased length dominant IgA eptiopes were the etip of the loop (aa 308-325) [Sko	HIV-1 infection evels IgA in saliva – see V4 region (aa 385-40	
1042 polyclonal	Ab type V3-C4 References Zinckg  Nasal mucosal imn	raf1999 nunization and boosting of	HIV peptide and was su	V3/C4 Adjuvant: mucosal adjuv perior for inducing serum IgG and ing resulted low serum IgG and vag	vaginal secretory IgA	
1043 D27	<ul> <li>Ab type V3-CD4B</li> <li>References Earl19</li> <li>D27: Generated du</li> <li>D27: Pulse label exand that the epitope</li> <li>D27: A comparison</li> </ul>	94, Otteken1996, Sugiural ring a study of the influence periments of 4 MAbs (D20) formed with a t 1/2 of about of 25 gp120 specific, considerations.	al Institute of Allergy and 1999 be of the oligomeric struct, D. D27, T20, and T22) bit out 10 minutes [Otteken Information dependent MA	d Infectious Diseases, NIH, Bethes ture of Env in determining the reponding to noncleavable gp160 revea	ertoire of the Ab responded that these anti-CD	4 MAbs bound with a delay,
1044 D56	Ab type V3-CD4B References Earl19	94, Sugiura1999	al Institute of Allergy and	L meric gp140 d Infectious Diseases, NIH, Bethesture of Env in determining the repe		murine (IgG) onse [Earl1994]

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizi	ng Immunogen	Species(Isotype)			
	•		locked CD4 binding, and the		Abs was done – D56 is one of tw p abrogated binding – 12.5 ug/m	C 1	, , , , ,			
1045	2G12 (c2G12)	Env	gp120		LP	HIV-1 infection	human (IgG1κ)			
		Ab type carbohydrates at glycosylation residues in C2, C3, C4, and V4 Donor Herman Katinger, Inst. Appl. Microbiol. or Polymun Scientific Inc., Vienna, Austria, MRC AIDS reagent project  References Buchacher1994, Trkola1995, Moore1995b, McKeating1996b, McKeating1996a, Trkola1996b, Moore1996, Poignard1996b, Trkola1996a, Sattentau1996, D'Souza1997, Mo1997, Binley1997a, Fouts1997, Li1997, Moore1997, Mascola1997, Ugolini1997, Burton1997, Parren1997c, Andrus1998, Wyatt1998a, Mondor1998, Parren1998a, Sullivan1998b, Connor1998, Binley1998, Trkola1998, Fouts1998, Takefman1998, Parren1998b, Li1998, Wyatt1998b, Frankel1998, Kunert1998, Schonning1998, Montefiori1999, Beddows1999, Altmeyer1999, Poignard1999, Parren1999, Mascola1999, Mascola2000, Binley1999, Robert-Guroff2000, Baba2000, Grovit-Ferbas2000, Park2000, Si2001, Mascola2001, Zwick2001c, Barnett2001, Moore2001, Poignard2001, Zeder-Lutz2001, Verrier2001, Stiegler2001, Spenlehauer2001, Hofmann-Lehmann2001, Xu2001, Savarino2001, Golding2002b,								
			vards2002, Grundner200							
	•		b generated by electrofusion		volunteers with CB-F7 cells [Buo	chacher1994]				

- 2G12: Highly potent Cross-clade neutralizing activity [Trkola1995]
- 2G12: Conformationally sensitive epitope destroyed by mutations altering the N-linked glycosylation sites near the base of the V3 loop and the amino-terminal flank of the V4 loop [Trkola1996b]
- 2G12: Binding weakly enhanced by some anti-C1, -C4, -V3, and CD4 binding site MAbs unusual in that 2G12 binding neither enhanced or inhibited the binding of other MAbs included in the study [Moore1996]
- 2G12: Review: binding site is distinct from CD4BS MAbs epitope and is unique among known gp120 MAbs, human or rodent [Moore1995b]
- 2G12: Review: exceptional capacity to neutralize primary isolates in terms of both breadth and potency one of three MAbs (IgG1b12, 2G12, and 2F5) generally accepted as having significant potency against primary isolates [Poignard1996b]
- 2G12: Neutralizes JR-FL inhibits gp120 interaction with CCR-5 in a MIP-1beta-CCR-5 competition study [Trkola1996a]
- 2G12: Neutralizes primary isolates, HXB2, and chimeric virus with gp120 from primary isolates in an HXB2 background [McKeating1996b]
- 2G12: Review: Only four epitopes have been described which can stimulate a useful neutralizing response to a broad spectrum of primary isolates, represented by the binding sites of MAbs: 447-52-D, 2G12, Fab b12, and 2F5 [Sattentau1996]
- 2G12: In a multilab evaluation of monoclonal antibodies, only IgG1b12, 2G12, and 2F5 could neutralize at least half of the 9 primary test isolates at a concentration of < 25 mug per ml for 90% viral inhibition neutralized 6 of 9 primary isolates [D'Souza1997]
- 2G12: A JRCSF variant that was selected for IgG1b12 resistance remained sensitive to MAbs 2G12 and 2F5, for combination therapy [Mo1997]
- 2G12: Study shows neutralization is not predicted by MAb binding to JRFL monomeric gp120, but is associated with oligomeric Env binding 2G12 bound monomer, and weakly bound oligomer and neutralized JRFL [Fouts1997]
- 2G12: One of 14 human MAbs tested for ability to neutralize a chimeric SHIV-vpu+, which expressed HIV-1 IIIB Env 2G12 was a strong neutralizer of SHIV-vpu+ all Ab combinations tested showed synergistic neutralization 2G12 has synergistic response with MAbs 694/98-D (anti-V3), 2F5, F105, and b12 [Li1997]
- 2G12: Review: MAbs 2F5, 2G12 and IgG1b12 have potential for use in combination with CD4-IgG2 as an immunotherapeutic or immunoprophylactic –
  homologous MAbs to these are rare in humans and vaccine strategies should consider including constructs that may enhance exposure of these MAbs'
  epitopes [Moore1997]
- 2G12: Using concentrations of Abs achievable in vivo, the triple combination of 2F5, 2G12 and HIVIG was found to be synergistic to have the greatest breadth and magnitude of response against 15 clade B primary isolates [Mascola1997]

Env Antibodies HIV Antibodies Tables

No. MAb ID HXB2 Location Author's Location Sequence Neutralizing Immunogen Species(Isotype)

• 2G12: Viral binding inhibition by 2G12 was strongly correlated with neutralization (all other neutralizing MAbs tested showed some correlation except 2F5) [Ugolini1997]

- 2G12: Review that discusses this MAb reacts with residues at the base of the V3 loop and V4, and most of the changes that reduce binding are glycosylation sites it is not clear whether the binding site is peptidic or direct carbohydrate [Burton1997]
- 2G12: Neutralizes TCLA strains and primary isolates [Parren1997c]
- 2G12: Post-exposure prophylaxis was effective when MAb 694/98-D was delivered 15 min post-exposure to HIV-1 LAI in hu-PBL-SCID mice, but declined to 50% if delivered 60 min post-exposure, and similar time constraints have been observed for HIVIG, 2F5 and 2G12, in contrast to MAb BAT123 that could protect delivered 4 hours post infection [Andrus1998]
- 2G12: The MAb and Fab binding to the oligomeric form of gp120 and neutralization were highly correlated authors suggest that neutralization is determined by the fraction of Ab sites occupied on a virion irrespective of the epitope [Parren1998a]
- 2G12: Summary of the implications of the crystal structure of gp120 combined with what is known about mutations that reduce NAb binding probable mechanism of neutralization by 2G12 is unknown, but dependent on proper glycosylation and 2G12 is predicted to be oriented toward the target cell when bound, so neutralization may be due to steric hindrance mutations in positions N 295, T 297, S 334, N 386, N 392 and N 397 HXBc2 (IIIB) decrease 2G12 binding, and the binding region is 25 angstroms from the CD4 binding site probably the Ab binds in part to carbohydrates, which may account for both its broad reactivity and the scarcity of Abs in the same competition group [Wyatt1998a]
- 2G12: Enhances Hx10 binding to CD4 positive or negative HeLa cells, but inhibited binding to CD4+ T-cell line A3.01 neutralizes Hx10 infection of the HeLa cells [Mondor1998]
- 2G12: Ab from gp120 vaccinated individuals prior to infection, who subsequently became HIV infected, could not achieve 90% neutralization of the primary virus by which the individuals were ultimately infected these viruses were not particularly refractive to neutralization, as determined by their susceptibility to neutralization by MAbs 2G12, IgG1b12, 2F5 and 447-52D [Connor1998]
- 2G12: Does not compete with binding of MAb generated in response to gp120-CD4 complex, CG10 [Sullivan1998b]
- 2G12: A panel of MAbs were shown to bind with similar or greater affinity and similar competition profiles to a deglycosylated or variable loop deleted core gp120 protein (Delta V1, V2, and V3), thus such a core protein produces a structure closely approximating full length folded monomer MAb 2G12 was the only exception to this, showing reduced binding efficiency [Binley1998]
- 2G12: A wide range of neutralizing titers was observed that was independent of co-receptor usage [Trkola1998]
- 2G12: Notes that 2G12 and 2F5, potent neutralizing antibodies, were identified by screening for cell surface (oligomeric Envelope) reactivity [Fouts1998]
- 2G12: Induces Complement-mediated lysis in MN but not primary isolates primary isolates are refractive to CML [Takefman1998]
- 2G12: MAbs 2G12, 2F5 and b12 are broadly neutralizing, as are some human polyconal sera, but this paper describes a set of primary isolates that are resistant to all three MAbs and 2 broadly neutralizing sera results indicate that resistance levels of pediatric isolates might be higher than adult isolates resistance in general did not seem to be conferred by a loss of binding affinity for gp120 or gp41, rather by a more global perturbation of oligomeric Envelope [Parren1998b]
- 2G12: Neutralization synergy was observed when the MAbs 694/98-D (V3), 2F5 (gp41), and 2G12 (gp120 discontinuous) were used in combination, and even greater neutralizing potential was seen with the addition of a fourth MAb, F105 (CD4 BS) [Li1998]
- 2G12: Discussed in a review of the antigenic and receptor binding-domains of gp120 in relation to the structure of the molecule antibodies are discussed by category (anti-V2, anti-V3, CD4i, CD4BS...), however as 2G12 binds to a rarely immunogenic region, and it is dependent on glycosylation, it was discussed individually [Wyatt1998b]
- 2G12: The complete V, J and D(H) domain was sequenced unlike non-neutralizing anti-gp41 MAb 3D6, five neutralizing MAbs (2F5, 2G12, 1B1, 1F7, and 3D5) showed extensive somatic mutations giving evidence of persistent antigenic pressure over long periods 2G12 D(H) has the best homology to a D(H) segment between D3-22 and D4-23, a region not usually considered for heavy-chain rearrangement because it lacks associated recombination signals in the flanking regions, Kunert et al. suggest this may be why Abs that compete with 2G12 are rare [Kunert1998]
- 2G12: In a study of the influence of the glycan at position 306 of the V3 loop on MAb recognition, 2G12 was found to neutralize an HIV-BRU mutant virus that lacks the V3 loop glycan and has a mutation at the tip of the loop more efficiently than it neutralizes HIV-BRU [Schonning1998]

No. MAb ID HXB2 Location Author's Location Sequence Neutralizing Immunogen Species(Isotype)

• 2G12: Infection of dendritic cells cultured from CD14+ blood cells or from cadaveric human skin was blocked by neutralizing MAbs IgG1b12, or 2F5 and 2G12 delivered together, but not by control non-neutralizing anti-gp120 MAb 4.8D, indicating that NAbs could interrupt early mucosal transmission events [Frankel1998]

- 2G12: A meeting summary presented results regarding neutralization –MAbs 2G12 and 2F5 tested for their ability to neutralize primary isolate infection of genetically engineered cell lines (cMAGI and others, presented by T. Matthews, A. Trkola, J. Bradac) an advantage of such cells lines over PBMCs is that markers (X-Gal) can be added for staining to simplify the assay the consensus of the meeting was that these engineered cell lines did not improve the sensitivity of detection of primary isolate neutralization D. Burton and J. Mascola presented results concerning passive immunization and protection of hu-PBL-SCID mice and macaques, respectively, and both found combinations of MAbs that were able to achieve 99% neutralization in vitro corresponded to efficacy in vivo [Montefiori1999]
- 2G12: rgp120 derived from a R5X4 subtype B virus was used to vaccinate healthy volunteers and the resulting sera were compared with sera from HIV-1 positive subjects and neutralizing MAbs 2G12 was able to bind with low affinity to the rgp120 monomer HIV-1 W61D [Beddows1999]
- 2G12: A Semliki Forest virus (SFV) expression system carrying BX08 Env was used to study the conformation of gp120 Env intracytoplasmic gp120 was recognized by the anti-V3 MAbs K24 and F5.5, while gp120 at the plasma membrane was detected only by conformation dependent MAbs 2G12, 670-D and 694/98D and not V3 MAbs expression in rat brain also showed that surface expressed Env was recognized only by the conformation-dependent antibodies and not by anti-V3 antibodies [Altmeyer1999]
- 2G12: Hu-PBL-SCID mice were infected with HIV-1s JRCSF and SF162 to study the effect of NAbs on an established infection no significant differences in the initial rate of decrease in viral load or the plateau levels of viral RNA between the b12 treated and control mice were seen in most of the Ab treated mice b12 escape mutants were observed with varying patterns of mutations a combination of b12, 2G12 and 2F5 protected 1/3 mice, and an isolate from one of the other two was resistant to neutralization by all three MAbs [Poignard1999]
- 2G12: Review of the neutralizing Ab response to HIV-1 [Parren1999]
- 2G12: Combinations of HIVIG, 2F5, 2G12 were administered in passive-transfer experiments 24 hours prior to challenge with pathogenic SHIV 89.6PD 3/6 animals given HIVIG/2F5/2G12 were completely protected, the others had reduced viremia and normal CD4 counts 1/3 monkeys given 2F5/2G12 showed transient infection, the other two had reduced viral load all monkeys that received HIVIG, 2F5, or 2G12 alone became infected and developed high-level plasma viremia, although animals that got HIVIG or 2G12 had a less profound CD4 T cell decline [Mascola1999]
- 2G12: Because HIV-1 is most often transmitted across mucosal surfaces, the ability of passive transfer of infused HIVIG/2F5/2G12 to protect against mucosal exposure of macaques to pathogenic SHIV 89.6PD was studied HIVIG/2F5/2G12 protected 4/5 animals against vaginal challenge, 2F5/2G12 combined protected 2/5 animals, and 2G12 alone protected 2/4 animals in contrast, Mascola and co-workers had previously shown single MAbs could not protect against intervenous challenge Ab treated animals that got infected through vaginal innoculation had low viral loads and only modest declines in CD4 counts the infused Abs were detected in the nasal, vaginal, and oral mucosa [Mascola2000]
- 2G12: Combinations of HIVIG, 2F5, 2G12 were administered in passive-transfer experiments 24 hours prior to challenge with pathogenic SHIV 89.6PD –
   3/6 animals given HIVIG/2F5/2G12 were completely protected, the others had reduced viremia and normal CD4 counts 1/3 monkeys given 2F5/2G12 showed transient infection, the other two had reduced viral load all monkeys that received HIVIG, 2F5, or 2G12 alone became infected and developed high-level plasma viremia, although animals that got HIVIG or 2G12 had a less profound CD4 T cell decline [Mascola1999]
- 2G12: The MAbs with the broadest neutralizing activity, IgG1b12, 2G12 and 2F5, all have high affinity for the native trimer, indicating that they were raised in an immune response to the oligomer on the virion surface rather than dissociated subunits a disulfide linked gp120-gp41 (SOS gp140) was created to mimic the native conformation of Env and explore its potential as an immunogen SOS gp140 is recognized by NAbs IgG1b12, 2G12, and CD4-IgG2, and also by anti-V3 MAbs 19b and 83.1 SOSgp140 is not recognized by C4 region MAbs that neutralize only TCLA strains, G3-42 and G3-519 nor did it bind C11, 23A, and M90, MAbs that bind to gp120 C1 and C5, where it interacts with gp41 MAbs that bind CD4 inducible epitopes, 17b and A32 were very strongly induced by CD4 in SOS gp140 anti-gp41 MAbs that bind in the region that interacts with gp120, 7B2, 2.2B, T4, T15G1 and 4D4, did not bind to SOSgp140, in contrast to 2F5, which binds to the only gp41 epitope that is well exposed in native gp120-gp41 complexes [Binley1999]
- 2G12: A mini-review of observations of passive administration of IgG NAbs conferring protection against intervenous or vaginal SHIV challenge, that considers why IgG MAbs might protect against mucosal challenge [Robert-Guroff2000]

Env Antibodies HIV Antibodies Tables

No. MAb ID HXB2 Location Author's Location Sequence Neutralizing Immunogen Species(Isotype)

• 2G12: A triple combination of 2F5, F105 and 2G12 effectively neutralized perinatal infection of macaque infants when challenged with SHIV-vpu+ – the mean plasma half-life was 14.0 +/- 7.9 days, the longest of the three Abs [Baba2000]

- 2G12: To determine the antigenicity of virus killed by thermal and chemical inactivation, retention of conformation-dependent neutralization epitopes was examined, and exposure of CD4BS epitopes was found to be enhanced (MAbs IgG1b12, 205-46-9, and 205-43-1) binding to 2G12 and 447-52D epitopes was essentially unaltered the 17b CD4i epitope was also exposed [Grovit-Ferbas2000]
- 2G12: Six mutations in MN change the virus from a high-infectivity neutralization resistant phenotype to low-infectivity neutralization sensitive V3,
   CD4BS, and CD4i MAbs are 20-100 fold more efficient at neutralizing the sensitive form 2G12 was an exception and could not neutralize MN in either form [Park2000]
- 2G12: SHIV-HXBc2 is a neutralization sensitive non-pathogenic virus, and several in vivo passages through monkey's yielded highly pathogenic SHIV KU-1 HXBc2 and the KU-1 clone HXBc2P3.2 differ in 12 amino acids in gp160 substitutions in both gp120 and gp41 reduced the ability of sCD4, IgG1b12, F105 and AG1121 to Env achieve saturation and full occupancy, and neutralize KU-1 17b and 2F5 also bound less efficiently to HXBc2P3.2, although 2G12 was able to bind both comparably [Si2001]
- 2G12: Neutralization synergy between anti-HIV NAbs b12, 2G12, 2F5, and 4E10 was studied a classic fixed-ratio method was used, as well as a method where one Ab was fixed at a low neutralization titer and the other was varied using primary isolates, a two-four fold enhancement of neutralization was observed with MAb pairs, and a ten-fold enhancement with a quadruple Ab combination no synergy was observed with any MAb pair in the neutralization of TCLA strain HXB2 there was no evidence for cooperativity of binding between b12 and 2G12 to envelope spikes expressed on the cell surface of TCLA or primary isolates [Zwick2001c]
- 2G12: Review of studies in macaques that have shown immune control of pathogenic SHIV viremia, improved clinical outcome, and protection, and the implications of the observations for HIV vaccines [Mascola2001]
- 2G12: SF162DeltaV2 is a virus that has a 30 amino acids deletion in the V2 loop that does not abrogate its infectivity but renders it highly susceptible to neutralization when incorporated into a codon-optimized DNA vaccine with a CMV promoter and delivered by gene gun, SF162DeltaV2 gave higher neutralizing Ab titers against SF162 than did SF162 itself, and Abs that cross-neutralized non-homologous primary isolates were obtained only when SF162DeltaV2, but not intact SF162, was used as the immunogen Control MAbs 2F5 and 2G12 could neutralize all of the following primary isolates: 91US056(R5), 92US714(R5), 92US660(R5), 92HT593(R5X4), and BZ167(R5X4), while after the first protein boost, the sera from two SF162DeltaV2 immunized macaques could neutralize 91US056(R5), 92US714(R5), 92US660(R5) and ADA(R5), but not 92HT593(R5X4) or 92US657(R5) the pattern of cross-recognition shifted after the second boost [Barnett2001]
- 2G12: Moore and colleagues review structural aspects of gp120 and how they relate to antigenic domains, and review the data concerning the lack of a clear relationship between genetic subtype and serotype an exception exists for human MAb 2G12, which does not recognize CRF01 envelopes because of an unusual additional disulfide bond in the V4 loop region that appears to be unique to the subtype E, CRF01 gp120 protein [Moore2001]
- 2G12: Structural aspects of the interaction of neutralizing Abs with HIV-1 Env are reviewed Env essentially has three faces, one is largely inaccessible on the native trimer, and two that exposed but have low immunogenicity on primary viruses neutralization is suggested to occur by inhibition of the interaction between gp120 and the target cell membrane receptors as a result of steric hindrance and it is noted that the attachment of approximately 70 IgG molecules per virion is required for neutralization, which is equivalent to about one IgG molecule per spike the 2G12, 17b and b12 epitopes are discussed in detail although it is potently neutralizing, 2G12 does not interfere with CD4 and coreceptor binding, and this Ab specificity is uncommon in sera from HIV-1-infected individuals [Poignard2001]
- 2G12: Neutralizing synergy between MAbs 1b12, 2G12 and 2F5 was studied using surface plasmon resonance to determine the binding kinetics for these three MAbs with respect to monomeric and oligomeric Env protein gp160 IIIB the 2G12 epitope is highly accessible on both monomeric and oligomeric Envs, 1b12 is highly accessible on monomers but not oligomers, and 2F5 on neither form binding of 2G12 exposes the 2F5 epitope on gp160 oligomers 2G12-gp160 oligomer interactions were best fitted to a two state model, with the first complex having a high association constant and fast dissociation, that is stabilized by conformational changes induced by the binding of a second MAb [Zeder-Lutz2001]
- 2G12: A luciferase-reporter gene-expressing T-cell line was developed to facilitate neutralization and drug-sensitivity assays luciferase and p24 antigen neutralization titer end points were found comparable using NAb from sera from HIV+ donors, and MAbs 2F5, 2G12 and IgG1b12 [Spenlehauer2001]

No. MAb ID HXB2 Location Author's Location Sequence Neutralizing Immunogen Species(Isotype)

• 2G12: A panel of 12 MAbs was used to identify those that could neutralize the dual-tropic primary isolate HIV-1 89.6 – six gave significant neutralization at 2 to 10 ug/ml: 2F5, 50-69, IgG1b12, 447-52D, 2G12, and 670-D six did not have neutralizing activity: 654-D, 4.8D, 450-D, 246-D, 98-6, and 1281 – no synergy, only additive effects were seen for pairwise combinations of MAbs, and antagonism was noted between gp41 MAbs 50-69 and 98-6, as well as 98-6 and 2F5 [Verrier2001]

- 2G12: A combination of MAbs IgG1b12, 2F5, and 2G12 was given postnatally to four neonates macaques that were then challenged with highly pathogenic SHIV89.6P one of the four infants remained uninfected after oral challenge, two infants had no or a delayed CD4(+) T-cell decline [Hofmann-Lehmann2001]
- 2G12: Twenty HIV clade C isolates from five different countries were susceptible to neutralization by anti-clade B MAbs in a synergistic quadruple combination of mAbs IgG1b12, 2G12, 2F5, and 4E10 [Xu2001]
- 2G12: Chloroquine reduces the HIV-1-infectivity of H9 IIIB cells, apparently through altering the conformation of envelope there is a reduction of reactivity of 2G12 to its epitope in chloroquine treated cultures [Savarino2001]
- 2G12: A phase I trial in seven HIV+ individuals was conducted with MAbs 2F5 and 2G12—no clinical or laboratory abnormalities were observed throughout the study—eight infusions were administered over a 4-week period (total dose 14 g)—the elimination half-life (t\_1/2) was calculated to be 7.94 (range, 3.46–8.31) days for 2F5 and 16.48 (range, 12.84–24.85) days for 2G12 [Armbruster2002].
- 2G12: The fusion process was slowed by using a suboptimal temperature (31.5 C) to re-evaluate the potential of Abs targeting fusion intermediates to block HIV entry preincubation of E/T cells at 31.5 C enabled polyclonal anti-N-HR Ab and anti-six-helix bundle Abs to inhibit fusion, indicating six-helix bundles form prior to fusion the preincubation 31.5 C step did not alter the inhibitory activity of neutralizing Abs anti-gp41 2F5, or anti-gp120 2G12, IG1b12, 48d, and 17b [Golding2002b]
- 2G12: The 2G12 epitope is composed of carbohydrates involving high-mannose and hybrid glycans of residues 295, 332, and 392, with peripheral glycans from 386 and 448 contributing on either flank, and with little direct gp120 protein surface involvement these mannose residues are proximal to each other near the chemokine receptor binding surface [Sanders2002]
- 2G12: Alanine scanning mutagenesis used in conjunction with competition and replacement studies of N-linked carbohydrates and sugars suggest that the 2G12 epitope is formed from mannose residues contributed by the glycans attached to N295 and N332, with the other N-linked carbohydrates in positions N339, N386, and N392 playing a role in maintaining conformation relevant to 2G12 binding N295A and N332A mutants showed essentially unchanged anti-CD4BS NAb b12 binding affinities, while N339A, N386A and N392A mutants displayed significantly lowered b12 affinity, presumably due to conformational changes [Scanlan2002]
- 2G12: Ab binding characteristics of SOS gp140 were tested using SPR and RIPA SOS gp140 is gp120-gp41 bound by a disulfide bond NAbs 2G12, 2F5, IgG1b12, CD4 inducible 17b, and 19b bound to SOS gp140 better than uncleaved gp140 (gp140unc) and gp120 non-neutralizing MAbs 2.2B (binds to gp41 in gp140unc) and 23A (binds gp120) did not bind SOS gp140 2G12 complexes with SOS gp140 or with gp120 had a very unusual linear structure [Schulke2002]
- 2G12: Uncleaved soluble gp140 (YU2 strain, R5 primary isolate) can be stabilized in an oligomer by fusion with a C-term trimeric GCN4 motif or using a T4 trimeric motif derived from T4 bacteriophage fibritin stabilized oligomer gp140 delta683(-FT) showed strong preferential recognition by NAbs IgG1b12 and 2G12 relative to the gp120 monomer, in contrast to poorly neutralizing MAbs F105, F91, 17b, 48d, and 39F which showed reduced levels of binding, and MAbs C11, A32, and 30D which did not bind the stabilized oligomer [Yang2002]
- 2G12: Passive immunization of neonate macaques with a combination of F105+2G12+2F5 conferred complete protection against oral challenge with SHIV-vpu+ or the combination b12+2G12+2F5 conferred partial protection against SHIV89.6 such combinations may be useful for prophylaxis at birth and against milk born transmission the synergistic combination of IgG1b12, 2G12, 2F5, and 4E10 neutralized a collection of HIV clade C primary isolates [Xu2002]
- 2G12: A modified gp140 (gp140deltaCFI), with C-term mutations intended to mimic a fusion intermediate and stabilize trimer formation, retained antigenic conformational determinants as defined by binding to CD4 and to MAbs 2F5, 2G12, F105, and b12, and enhanced humoral immunity without diminishing the CTL response in mice injected with a DNA vaccine [Chakrabarti2002]

human ( $IgG1\lambda$ )

#### No. MAb ID **HXB2** Location **Author's Location** Sequence **Neutralizing Immunogen** Species(Isotype) • 2G12: A combination of MAbs 2F5 and 2G12 given in multiple infusions was found to be safe and well tolerated even in high doses in a phase I study of seven HIV-1 infected healthy volunteers – the median elimination half-life was 7.94 days for 2F5, and 16.48 for 2G12 – no anti-2F5 or anti-2G12 IgM or IgG responses were detected – although there was some transient increases, overall plasma viral RNA levels decreased in 6/7 volunteers, by a median of 0.62 log\_10 [Armbruster2002] • 2G12: Truncation of the gp41 cytoplasmic domain of X4, R5, and X4R5 viruses forces a conformation that more closely resembles the CD4 bound state of the external Envelope, enhancing binding of CD4i MAbs 17b and 48d and of CD4BS MAbs F105, b12, and in most cases of glycosylation site dependent MAb 2G12 and the anti-gp41 MAb 246D – in contrast, binding of the anti-V2 MAb 697D and the anti-V3 MAb 694/98D were not affected – viruses bearing the truncation were more sensitive to neutralization by MAbs 48d, b12, and 2G12 – the anti-C5 MAb 1331A was used to track levels of cell surface expression of the mutated proteins [Edwards2002] • 2G12: HIV-1 gp160deltaCT (cytoplasmic tail-deleted) proteoliposomes (PLs) containing native, trimeric envelope glycoproteins from R5 strains YU2 and JRFL, and X4 strain HXBc2, were made in a physiologic membrane setting as candidate immunogens for HIV vaccines – 2F5 bound to gp160deltaCT with a reconstituted membrane ten-fold better than the same protein on beads, while such an affinity difference was not seen with F105 and 2G12 – anti-CD4BS MAbs IgG1b12 and F105, A32 (C1-C4), C11 (C1-C5), and 39F (V3) MAbs bound gp160deltaCT PLs indistinguishably from gp160deltaCT expressed on the cell surface [Grundner2002] 2G12: Rhesus macagues were better protected from vaginal challenge with SHIV89.6D (MAb 2G12, 2/4; MAbs 2F5/2G12, 2/5; and HIVIG/2F5/2G12, 4/5 infected) than from intravenous challenge (MAb 2G12, 0/3; MAbs 2F5/2G12, 1/3; and HIVIG/2F5/2G12, 3/6 infected) – the animals that were infected by vaginal challenge after Ab infusion had low or undetectable viral RNA levels and modest CD4 T-cell decline [Mascola2002] • 2G12: A rare mutation in the neutralization sensitive R2-strain in the proximal limb of the V3 region caused Env to become sensitive to neutralization by MAbs directed against the CD4 binding site (CD4BS), CD4-induced (CD4i) epitopes, soluble CD4 (sCD4), and HNS2, a broadly neutralizing sera – 2/12 anti-V3 MAbs tested (19b and 694/98-D) neutralized R2, as did 2/3 anti-CD4BS MAbs (15e and IgG1b12), 2/2 CD4i MAbs (17b and 4.8D), and 2G12 and 2F5 – thus multiple epitopes on R2 are functional targets for neutralization and the neutralization sensitivity profile of R2 is intermediate between the highly sensitive MN-TCLA strain and the typically resistant MN-primary strain [Zhang2002] • 2G12: Review of NAbs that notes 2G12 alone or in combination with other MAbs can protect some macaques against SHIV infection, that it has strong ADCC activity, and that it is safe and well tolerated in humans [Ferrantelli2002] 2G12: Review of NAbs that discusses mechanisms of neutralization, passive transfer of NAbs and protection in animal studies, and vaccine strategies [Liu2002] • 2G12: Alanine scanning mutagenesis was used to compare substitutions that affected anti-CD4BS NAb b12 – rec gp120s were engineered to contain combinations of Alanine substitutions that enhanced b12 binding, and while binding of b12 to these gp120 monomers was generally maintained or increased, binding by five non-neutralizing anti-CD4bs MAbs (b3, b6, F105, 15e, and F91) was reduced or completely abolished – 2G12 binding was largely unperturbed, indicating these proteins were not grossly misfolded [Pantophlet2003] • 2G12: CD4BS MAbs b12 (neutralizing) and 205-42-15, 204-43-1, 205-46-9 (nonneutralizing) all cross-competed for binding to monomeric gp120, indicating the topological proximity of their epitopes, however, the nonneutralizing CD4BS MAbs did not interfere with the neutralization activity of MAb b12 – 2G12 was used to normalize and as a control in these experiments [Herrera2003] • 2G12: UK Medical Research council AIDS reagent: ARP3030 • 2G12: NIH AIDS Research and Reference Reagent Program: 1476

1046 1367 Env gp41 HIV-1 infection

Ab type cluster I Popor Susan Zolla Pazner (Zollas 0.1 @mercr6 med nyu) (NVII Med Center)

**Ab type** cluster I **Donor** Susan Zolla-Pazner (Zollas01@mcrcr6.med.nyu) (NYU Med. Center) **References** Nyambi1998, Gorny2000b, Gorny2000a, Nyambi2000

• 1367: Using a whole virion-ELISA method, 18 human MAbs were tested for their ability to bind to a panel of 9 viruses from clades A, B, D, F, G, and H – anti-gp41 Abs 98-6, 1367 and 1342 were not able to bind detectably with any of the viruses from any clade [Nyambi1998]

No. MAb ID	HXB2 Location	<b>Author's Location</b>	Sequence		Neutralizing	g Immunogen	Species(Isotype)
	fusogenic form of g [Gorny2000b]  1367: Binding of pa MAb 50-69 bound [Gorny2000a]  1367: 26 HIV-1 gro	with a 5 fold preference for oup M isolates (clades A to eakly bound to the majori	eact with either of the perecent with either of the perecent of the oligomer, while other binds of the binds of the oligomer.	us gp41 or gp120 mo her gp41 MAbs (136)	dividually – M nomers was co 7, 98-6, 167-E uding 5 cluste	MAbs 50-69 and 1367 h ompared – no MAb was D, 1281, 1342, and 1379 er I anti-gp41 MAbs wh	
1047 126-6 (SZ-126.6)	References Robins  126-6: No enhancir  126-6: No enhancir  126-6: Specific for  126-6: Called SZ-1  126-6: One of sever that the construct had the construct had been sever that the construct had been sever that the sever that the sever that the construct had been sever that the construction of the sever that the construct had been sever that the construction of the sever that the seve	ral anti-gp41 MAbs that b as retained aspects of norm bus epitope recognizing res [6] II MAb binds to a conform t binds to a peptide N51-C MAb 126-6 was biotinylar [2000b] Toup M isolates (clades A toross clades, but usually we	Xu1991, Eddleston1993, [Robinson1990b] [Robinson1991] [Xu1991] ind to a gp41-maltose bin mal gp41 conformation [6 sidues between 649-668-mational epitope in the ref43 complex trimer of het ted and used as a probe to H) were tested for bindeakly, while 98-6 and 134	nding fusion protein Chen1995]  – designated cluster legion 644-663 – like terodimers that appropriate ding to 47 MAbs, inc	designed to st I – Fabs D5, I most cluster I eximates the ce- gp41 MAb 56	udy the leucine zipper of D11, G1, T3, M12, M15 I MAbs (126-6, 167-D, ore of the fusogenic for 0-69 bound the fusogen ter II anti-gp41 MAbs —	lomain of gp41, showing 5, S6, S8, S9, S10 block 1281, 1342, and 1379 all m of gp41, but not to C43 ic form of the protein in of these 2F5, 167-D, 126-6,
1048 1342	References Nyamb  1342: Using a who anti-gp41 Abs 98-6 1342: This cluster I	6, 1367 and 1342 were not II MAb is a conformationa t binds to a peptide N51-C	ay2000a, Nyambi2000 18 human MAbs were tea able to bind detectably val epitope that binds in the	sted for their ability t with any of the viruse the region 644-663 – li	o bind to a pa s from any cla ke most clusto	ade [Nyambi1998] er II MAbs (126-6, 167-	human (IgG1λ)  ades A, B, D, F, G, and H –  D, 1281, 1342, and 1379 alm of gp41, but not to C43

- nor to N51 alone [Gorny2000b] • 1342: Binds within the region gp41 647-682 – binding of panel of 21 MAbs to soluble oligomeric gp140 versus gp41 or gp120 monomers was compared –
- no MAb was oligomer specific, but gp41 MAb 50-69 bound with a 5 fold preference for the oligomer, while other gp41 MAbs (1367, 98-6, 167-D, 1281, 1342, and 1379) did not show a preference [Gorny2000a]

Env Antibodies Tables

No. MAb ID	HXB2 Location	Author's Location	Sequence	Neutraliz	ing Immunogen	Species(Isotype)
	and 1281 bound acr	oss clades, but usually we	eakly, while 98-6 and 1342 l	to 47 MAbs, including 6 clu and poor cross reactivity – Cl s, but 1342 did not bind to the	ade D isolates bound most	
1049 1379	Env Ab type cluster II References Gorny2		er (Zollas01@mcrcr6.med.	nyu) (NYU Med. Center)	HIV-1 infection	human (IgG1λ)
	• 1379: This cluster I	I MAb binds to a conform binds to a peptide N51-C		n 644-663 – like most cluster dimers that approximates the		
	no MAb was oligon		b 50-69 bound with a 5 fold	Abs to soluble oligomeric gpl preference for the oligomer,		
1050 Fab D11	Env  Ab type cluster II  References Binley  Fab D11: Rinds to		es with MAhs 126-6 Md-1	no and D50 – conformation sens	HIV-1 infection	human (IgG1 $\kappa$ )
1051 Fab D5	Env <b>Ab type</b> cluster II <b>References</b> Binley I	gp41 (LAI)		no  nd D50 – conformation sensi	HIV-1 infection	human (IgG1κ)
1052 Fab G1	Env Ab type cluster II References Binley I • Fab G1: Binds to cl		s with MAbs 126-6, Md-1 a	no  nd D50 – conformation sensi	HIV-1 infection tive – variable regions sequ	human (IgG1 $\kappa$ ) nenced [Binley1996]
1053 Fab M10		cluster II region - compet		no and D50 – conformation sen		human (IgG1κ) quenced [Binley1996]
1054 Fab M12	Env <b>Ab type</b> cluster II <b>References</b> Binley I	gp41 (LAI)		AI and MN rgp120 and rgp14  no  and D50 – conformation sen	HIV-1 infection	human (IgG1κ) quenced [Binley1996]
1055 Fab M15	Env <b>Ab type</b> cluster II <b>References</b> Binley	gp41 (LAI)		no and D50 – conformation sen	HIV-1 infection	human (IgG1 $\kappa$ )

No.	MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizing	Immunogen	Species(Isotype)
1056	Fab S10	Env Ab type cluster II	gp41 (LAI)		no	HIV-1 infection	human (IgG1 $\kappa$ )
		<ul><li>References Binley 19</li><li>Fab S10: Binds to cla</li></ul>		s with MAbs 126-6, Md-1 and	D50 – conformation sensitiv	e – variable regions sec	quenced [Binley1996]
1057	Fab S6	Env	gp41 (LAI)	· · · · · · · · · · · · · · · · · · ·	no	HIV-1 infection	human (IgG1 $\kappa$ )
		<b>Ab type</b> cluster II <b>References</b> Binley 19	996	with MAbs 126-6, Md-1 and			,
1058	Fab S8	Env Ab type cluster II References Binley19	gp41 (LAI)		no	HIV-1 infection	human (IgG1 K)
		Fab S8: Binds to cluster	ster II region – competes	with MAbs 126-6, Md-1 and	D50 – conformation sensitive	<ul> <li>variable regions sequ</li> </ul>	ienced [Binley1996]
1059	Fab S9	Env Ab type cluster II References Binley 19 • Fab S9: Binds to clus		with MAbs 126-6, Md-1 and	no  D50 – conformation sensitive	HIV-1 infection  – variable regions sequ	human (IgG1 $\kappa$ ) nenced [Binley1996]
060	Fab T3	Env Ab type cluster II References Binley 19 • Fab T3: Binds to clu		with MAbs 126-6, Md-1 and	no  D50 – conformation sensitive	HIV-1 infection  – variable regions sequ	human (IgG1 k)
1061	Md-1 (MD-1)	<b>Ab type</b> cluster II References Myers19	93, Chen1995, Binley19		no		human (IgG1 $\lambda$ )
		<ul> <li>Md-1: Called MD-1 gp41, showing that tl</li> <li>Md-1: Discontinuous trimers and tetramers</li> </ul>	<ul> <li>one of several anti-gp4</li> <li>he construct has retained</li> <li>s epitope recognizing res</li> </ul>	that binds in the N-terminal re 1 MAbs that bind to a gp41-rr aspects of normal gp41 confo idues between 563-672, does a ster II – Fabs D5, D11, G1, T eagent Program: 1223	altose binding fusion protein rmation [Chen1995] not recognize cluster I disulfid	designed to study the le	eucine zipper domain of s almost exclusively with
1062	1281 (1281-D	Ab type cluster II, si References Hioe199 • 1281: Called 1281-D	7b, Gorny2000b, Gorny2 D: Four primary isolates s	Susan Zolla-Pazner (Zollas01) 2000a, Verrier2001, Golding20 howed distinct patterns of sen	02b	lyclonal sera or plasma	

• 1281: Called 1281-D: Four primary isolates showed distinct patterns of sensitivity to neutralization by polyclonal sera or plasma and MAbs – BZ167 was the only isolate inhibited by all polyclonal sera and plasma tested, and was also neutralized by 8/17 MAbs, in particular anti-V3 loop (419-D, 447-52D, 782-D, and 838-D), anti-CD4bd (559/64-D, 654-D and 830-D and a cluster II of gp41 directed MAb (98-6) – isolates 92HT593 and 91US056 were neutralized by V3 loop (419-D, and 447-52D)and cluster II gp41 (98-6) MAbs at higher concentrations – US4 was neutralized by some of the polyclonal sera/plasma tested and not at all by MAbs individually or by a cocktail of ten MAbs consisting of 419-D, 447-52D, 782-D, 838-D, 559/64-D, 654-D, 450-D, 670-D, 1281-D and 98-6 [Hioe1997b]

Env Antibodies Tables

No. MAb ID	HXB2 Location	Author's Location	Sequence	Neutraliz ————————————————————————————————————	ing Immunogen	Species(Isotype)				
	nor to N51 alone [C  1281: Binds within no MAb was oligor 1342, and 1379) die 1281: A panel of 12 2 to 10 ug/ml: 2F5, synergy, only additi 98-6 and 2F5 [Verri 1281: The fusion produced bundles form prior after 1 hour, doesn'	reacted similarly) it binds to a peptide N51-C43 complex trimer of heterodimers that approximates the core of the fusogenic form of gp41, but not to C43 nor to N51 alone [Gorny2000b]  1281: Binds within the region gp41 647-682 – binding of panel of 21 MAbs to soluble oligomeric gp140 versus gp41 or gp120 monomers was compared – no MAb was oligomer specific, but gp41 MAb 50-69 bound with a 5 fold preference for the oligomer, while other gp41 MAbs (1367, 98-6, 167-D, 1281, 1342, and 1379) did not show a preference [Gorny2000a]  1281: A panel of 12 MAbs was used to identify those that could neutralize the dual-tropic primary isolate HIV-1 89.6 – six gave significant neutralization a 2 to 10 ug/ml: 2F5, 50-69, IgG1b12, 447-52D, 2G12, and 670-D six did not have neutralizing activity: 654-D, 4.8D, 450-D, 246-D, 98-6, and 1281 – no synergy, only additive effects were seen for pairwise combinations of MAbs, and antagonism was noted between gp41 MAbs 50-69 and 98-6, as well as 98-6 and 2F5 [Verrier2001]  1281: The fusion process was slowed by using a suboptimal temperature (31.5 C) to re-evaluate the potential of Abs targeting fusion intermediates to block HIV entry – preincubation of E/T cells at 31.5 C enabled polyclonal anti-N-HR Ab and anti-six-helix bundle Abs to inhibit fusion, indicating six-helix bundles form prior to fusion – 98-6 binds to a C-HR hairpin epitope and blocks fusion when added to a 2 hour E/T preincubation at 31.5 C, but if added after 1 hour, doesn't inhibit – this is in contrast to six-helix bundle Abs 167-D and 1281 that inhibit more efficiently when added after one hour of incubation [Golding2002b]								
1063 Fab A9	Env Ab type cluster III References Binley: • Fab A9: Binds to cl [Binley1996]		es with MAb Md-1, but not	no MAbs 126-6 and D50 – conf	HIV-1 infection  formation sensitive – variab	human ( $\operatorname{IgG1}\kappa$ )				
1064 Fab G15	Env Ab type cluster III References Binley: • Fab G15: Binds to [Binley1996]		tes with MAb Md-1, but no	no t MAbs 126-6 and D50 – cor	HIV-1 infection  formation sensitive – varia	human ( $\operatorname{IgG1}\kappa$ ) ble regions sequenced				
1065 Fab G5	Env Ab type cluster III References Binley: • Fab G5: Binds to cl [Binley1996]		es with MAb Md-1, but not	no MAbs 126-6 and D50 – conf	HIV-1 infection formation sensitive – variab	human (IgG1 $\kappa$ )				
1066 Fab L1	Env Ab type cluster III References Binley • Fab L1: Binds to cl [Binley1996]		s with MAb Md-1, but not	no MAbs 126-6 and D50 – confe	HIV-1 infection ormation sensitive – variab	human ( $\operatorname{IgG1}\kappa$ )				
1067 Fab L11	Env <b>Ab type</b> cluster III <b>References</b> Binley	gp41 (LAI)		no	HIV-1 infection	human (IgG1 $\kappa$ )				

No. MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizir	ng Immunogen	Species(Isotype)
	• Fab L11: Binds to ( [Binley1996]	cluster III region – compet	es with MAb Md-1, but	not MAbs 126-6 and D50 – confo	ormation sensitive – va	riable regions sequenced
1068 Fab L2	References Binley	1996, Earl1997		no h Institute, La Jolla, California ot MAbs 126-6 and D50 – confor	HIV-1 infection rmation sensitive – var	human ( $\operatorname{IgG1}\kappa$ ) iable regions sequenced
1069 Chessie 8	References Lewis1  Chessie 8: Used to [Rovinski1995]  Chessie 8: This Ab dendritic cells (FDC)	was used in an in vitro stu C)'s and extend the period	tovinski 1995, Smith-Fran inoblots in a study exami ady demonstrating that H of infectivity – blocking	nklin2002 ining the feasibility of using unpr IIV-1 antibody and Fcgamma rece the FDC-Fcgamma receptor killi ase gp120 shedding [Smith-Frank	eptors can trap virus or ng the FDC cell reduc	the surface of follicular
1070 8F101	Ab type gp120-CD References DeVice • 8F101: MAbs spec	o1995	ked gp120 and CD4 wer	omponent: gp120 e derived (8F101, 8F102) – confo	Vaccine  Ormation dependent – o	murine (IgG)
1071 8F102	Ab type gp120-CD References DeVice • 8F102: MAbs spec	o1995	ked gp120 and CD4 wer	omponent: gp120 e derived (8F101, 8F102) – confo	Vaccine  ormation dependent – o	murine (IgG)
1072 CG-10 (CG10)	Ab type gp120-CD References Gersho CG-10: Reacts exc. CG-10: Called CG [Wu1996] CG-10: Called CG infection of HeLa C CG-10: Called CG	10 – MIP-1alpha binding t 10 – Promotes envelope m CD4+ (MAGI) cells by HI 10 – disrupts gp120-CCR5	han Gershoni, Tel Aviv U 7, Rizzuto1998, Sullivan complex, not with sCD4 o CCR-5 expressing cell ediated cell fusion betwo V-1 LAI, ELI1, and ELI2 5 interaction and compete	Jniversity, Isreal	with either T-cell and r-fold in the presence conserved bridging sh	macrophage tropic viruses – of CG10 [Lee1997] eet of gp120 – mutations in

No. MAb ID	HXB2 Location	Author's Location	Sequence	Neuti	alizing Immunogen	Species(Isotype)
	compete and the bi  - CG-10 can bind g  HXBc2 mutations	nding sites may overlap – 1 gp120 with V1/V2 and V3 Delta 298-327 (V3), 384 Y	MAb A32 enhances bindin deleted – HXBc2 mutatio /E, 298 R/G, 435 Y/S enh	ng of 17b, 48d and CG10- ns Delta 119-205, 314 G/V ance recognition – the CD	ruption of CD4-gp120 by 15e  MAbs C11, 2G12 and 212A  W, 432 K/A, 183,184 PI/SG do  contribution to the CG10 ep  so in the context of cell surfa	do not affect CG10 binding ecrease CG-10 recognition, bitope maps to the CD4
1073 CG-25	<b>Ab type</b> gp120-CD <b>References</b> Gersho			L th gp120 [Gershoni1993]	Vaccine	murine (IgG1)
1074 CG-4 (CG4)	Vaccine Vector/Typ Ab type gp120-CD References Gersho	gp120 pe: sCD4-gp120 complex p4 complex <b>Donor</b> Jonath oni1993 gp120 and sCD4-gp120 co	nan Gershoni, Tel Aviv Uı	•	Vaccine	murine (IgG1)
1075 CG-76	Ab type gp120-CD References Gersho	-		L purified gp120 [Gershoni1	Vaccine 993]	murine (IgG1)
1076 CG-9	Ab type gp120-CD References Gersho			L n gp120 [Gershoni1993]	Vaccine	murine (IgG1)
1077 105-518	Ab type immunode References Scheffe			-		murine (IgG1 κ)
1078 31A1	Env Ab type p24+gp41 References Pollocl • 31A1: Denatured v		timulation to generate Ab	no s – Reacts with both p24 a	in vitro stimulation and gp41 [Pollock1989]	human ( $\operatorname{IgM}\kappa/\lambda$ )
1079 39A64	Env <b>Ab type</b> p24+gp41	gp41		no	in vitro stimulation	human ( $\operatorname{IgM}\kappa/\lambda$ )

No. MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizing	Immunogen	Species(Isotype)
	References Pollock • 39A64: Denatured		stimulation to generate Ab	s – Reacts with both p24 and gp-	41 [Pollock1989]	
1080 39B86	Env Ab type p24+gp41 References Pollock • 39B86: Denatured v		stimulation to generate Ab	no s – Reacts with both p24 and gp <sup>2</sup>	in vitro stimulation 41 [Pollock1989]	human (IgMκ/λ)
1081 9303	Env <b>Ab type</b> p24+gp41 <b>References</b> McDou			no		murine
1082 NC-1	Ab type six helix by References Jiang 19  NC-1: Ab elicited in infected cells only if formation and abolistrain N243, O grouten NC-1: A combination trimers (gp140-GNO) a fraction assumes a glycoprotein, consistent NC-1: Uncleaved so trimeric motif derivations.	andle <b>Donor</b> S. Jiang, N. 198, Yang2000, Yang2002 in response to immunization the presence of sCD4, resh membrane fusion activity strain GAB, or HIV-2 Fron of gp41 fusion with the C4) – approximately 16% a fusogenic gp41 six-helixistent with the expectation bluble gp140 can be stabiled from T4 bacteriophage	New York Blood Center, NY 2 on with N36(L6)C34, a pept ecognizing the fusogenic control of the fusogenic control of the fusogenic control of the fusogenic control of the fusogenic sequences of the gp140(-GNC4) stability of the fusogenic of the description of the fusogenic of the gp140(-GNC4) stability of the fusogenic of the	that folds into a six helix bundle, NY  ide that folds into a six helix bundle, re structure – binding affinity war.  C-1 can recognize discontinuous and disruption of the YU2 gp12/lized trimer recognized by poole 40(-) monomers were not able to the six helix bundle, fusogenic conformation of the YU2 gp12/lized trimer recognized by poole 40(-) monomers were not able to the six helix bundle, fusogenic conformation of the six-helix bundle, fusogenic conformati	adle like gp41 – NC-1 bin as decreased by point mu epitopes from B clade is 0-gp41 cleavage site resu d sera was precipitated b to bind to the NC-1, nor v f the six-helix bundle [Yamotif (gp140delta683(-/ GCN4 motif trimers, but	ntations that disrupt core solate SC, but not E clade solate SC, but not E clade ulted in stable gp140 by NC-1, indicating that at was gp130(-/GCN4) ang2000] (GCN4)) or using a T4

# **IV-C-15** Nef Antibodies

No. MA	Ab ID	HXB2 Location	<b>Author's Location</b>	Sequence	Neutralizing	Immunogen	Species(Isotype)
1083 4H	H4	References Otake1	994	MGGKWSKSSVVGWPTVRERMRRAPT- VRERMRRAEPAADGVGAA  Strain: IIIB HIV component: Nef		Vaccine	human (IgG1)
1084 pol	lyclonal	Nef (9–24)  Vaccine Vector/Typ  References Tahtine  BALB/c mice were gene gun, and DNA long-lasting (6 mor	Nef (9–24)  ne: DNA Strain: BRU  n2001  immunized with a pBN- A dissolved in saline was  nths) Ab, CTL and prolif  found in Nef using peption	th a Nef fusion protein, could not detect Nef p  SVIGWLTVRERMRRAE  HIV component: Nef  -vector expressing HIV-1 nef, rev, or tat genes given intradermally or intramuscularly – Nef erative responses – the highest IgG1/IgG2a ra de mapping, although some sera reacted only	no s – DNA loaded gene gun immu atio was observed	Vaccine onto gold micropart nized mice showed t d in the gene gun im	murine (IgG) icles was delivered using a the strongest and most munized mice – three Ab
1085 13/	/042	References Schnei		VGWPTVRERM  HIV component: Nef  capeptides – core: TVRERM [Schneider1991	]	Vaccine	murine
1086 13/	/035	References Schneid		TVRERMRRAE  HIV component: Nef  capeptides – core: TVRERM [Schneider1991	]	Vaccine	murine
1087 AN	M5C6	Vaccine Vector/Typ References Schneid  • AM5C6: Epitope n			Nef(78-92) [Sch		murine  SKDLE [Maksiutov2002]
1088 AM	M5C6	Vaccine Vector/Typ References Schneid  • AM5C6: Epitope n			rith Nef(28-43) [		murine  SKDLE [Maksiutov2002]
1089 25/	//03		Nef (30–43 BH10) be: recombinant protein der1991, Maksiutov2002	•		Vaccine	murine

No. MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizing	Immunogen	Species(Isotype)
			eptides – core: ASRDLEK [s f the human protein vascular	Schneider1991] endothelial growth factor C, AI	EPDAGEATAYASKDLE [M	laksiutov2002]
1090 26/76	References Schne • 26/76: Epitope ma		peptides – core: SRDLEK [So	hneider1991] endothelial growth factor C, AF	Vaccine  EPDAGEATAYASKDLE [Material of the content	murine  [Aaksiutov2002]
1091 3F2	<ul><li>References Ovod!</li><li>3F2: Reacted with</li><li>3F2: Faintly cross</li><li>3F2: This epitope</li></ul>	1992, Saito1994, Ranki199 Nef from different HIV-1: -reactive with astrocytes of	strains (BRU, IIIB, RF, MN) uninfected control samples [ the human protein vascular en	[Ovod1992]	Vaccine PDAGEATAYASKDLE [Ma	murine (IgG1) ksiutov2002]
1092 3D12	References Ovod  3D12: There is an  3D12: Reacted wi  3D12: Over-expre  3D12: One of four expression associa  3D12: This epitop	1992, Saito1994, Ranki199, anti-RT MAb that also has th Nef from different HIV-ssion of Nef in astrocytes for antibodies used in combinated with dementia [Ranki19]	this name (see [Chiba1997] I strains (BRU, IIIB, RF, MN rom postmortem pediatric CN ation to show HIV Nef prote [995] I the human protein vascular	nt: Nef ) [Ovod1992]	•	
1093 polyclonal	Nef (33–65)  Vaccine Vector/Ty References Moure  Nef encapsulated i after 7 months – th recognized by the an Ab response to	Nef (32–64 LAI, BRU pe: PLG, recombinant proteau2002, Maksiutov2002 in poly(DL-lactide-co-glycone response was predomina sera of mice immunized with conformational epitopes [N	J) ASRDLEKHGAITSSNT.  LEAQEEEE ein Strain: LAI, BRU HI  blide) (PLG) had a more prol ntly IgG1, a Th2 immune res th NefPLG or Nef-CFA, but  Moureau2002]	AATNAACAW—  V component: Nef Adjuvant:  onged Ab response than Nef in ponse – three linear epitopes, N not after immunization with Ne elial growth factor C, AEPDAG	PBS or in Freund's adjuvantef 32-64, 118-167, and 185 f in PBS, which seemed to p	at (CFA), still strong -205, were frequently preferentially stimulate
1094 polyclonal	Nef (49–64)	Nef (49–64) pe: DNA Strain: BRU	AATNAACAWLEAQEEE	no	Vaccine	murine (IgG)

No. MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizing	Immunogen	Species(Isotype)
	gene gun, and DNA long-lasting (6 mo	A dissolved in saline was nths) Ab, CTL and prolife found in Nef using peptid	given intradermally or intran erative responses – the highe	F, rev, or tat genes – DNA loaded muscularly – Nef gene gun immust IgG1/IgG2a ratio was observe era reacted only to complete Net	nized mice showed d in the gene gun im	the strongest and most munized mice – three Ab
1095 3G12	References Ovod1	992	TNAACAWLEAQEEEE  Strain: BRU HIV compon  1 strains (BRU, IIIB, RF, M	nent: Nef	Vaccine	murine (IgG2a)
1096 13/058	References Schne		AQEEEEVGFPVTPQ  HIV component: Nef  apeptides – core: EEVGFP	[Schneider1991]	Vaccine	murine
1097 26/028	References Schne		AQEEEEVGFPVTPQ  HIV component: Nef  apeptides – core: EEVGFP	√ [Schneider1991]	Vaccine	murine
1098 2E3	References Ovod1 • 2E3: There are two	992, Nilsen1996 MAbs with the name 2E	QEEEEVGFPVTPQVP Strain: BRU HIV comport 3 – the other one binds to in ntified, 2E3 reacted with the	nent: Nef	Vaccine strain specific (MN a	murine (IgG1) and BRU reactive, not IIIB or
1099 polyclonal	<ul><li>References Pialou</li><li>28 subjects were v adjuvant QS21 – F</li></ul>	x2001 accinated with six HIV-1 IIV-specific Ab responses	were detected in 10/28, pro		3/24 (54%) of testab	
1100 F14.11	• F14.11: The MAb protein [De Santis	1991]	on of Nef that is similar to a	region found in thymosin alpha		murine (IgG2a $\kappa$ ) binds to the natural Nef
1101 31/03	Nef (83–103) Vaccine Vector/Ty	Nef (82–103 BH10) pe: recombinant protein	AAVDLSHFLKEKGGI HIV component: Nef	EGLIHS	Vaccine	murine

No.	MAb ID	<b>HXB2</b> Location	<b>Author's Location</b>	Sequence	Neutralizing	Immunogen	Species(Isotype)
		References Schne  • 31/03: Epitope ma		ptides – mapping suggests complex	epitope in this region [	Schneider1991]	
1102	polyclonal	Nef (117–147)	Nef (117–147 LAI)	TQGYFPDWQNYTPGPGVRYPL' CYKLVP	FFGW- no	Vaccine	human (IgG)
		References Pialou	ux2001	I HIV component: Nef Adjuvan			
		adjuvant QS21 – I	HIV-specific Ab responses we	ptides that were selected to be particle of the particle of the period o	n 3/24, and CTL in 13/	24 (54%) of testable volu	nteers – 20/28 had
1103	polyclonal	Nef (118–133) Vaccine Vector/Ty References Tahtir	Nef (118–133) ppe: DNA Strain: BRU H	QGYFPDWQNYTPGPGV IIV component: Nef	no	Vaccine	murine (IgG)
		BALB/c mice wer gene gun, and DN long-lasting (6 mc	re immunized with a pBN-veo IA dissolved in saline was giv onths) Ab, CTL and proliferate found in Nef using peptide r	ctor expressing HIV-1 nef, rev, or taken intradermally or intramuscularly tive responses—the highest IgG1/Ignapping, although some sera reacte	y—Nef gene gun immu gG2a ratio was observed	nized mice showed the st d in the gene gun immuni	rongest and most zed mice—three Ab
1104	polyclonal	Nef (119–168)	Nef (118–167 LAI, BRU)	GYFPDWQNYTPGPGVRYPLTF( KLVPVEPDKVEEANKGENTSLI		HIV-1 infection, Vaccin	e murine (IgG1)
			*	in Strain: LAI, BRU HIV compe		PLG, complete Freund's	adjuvant (CFA)
		Nef encapsulated after 7 months – the recognized by the an Ab response to	in poly(DL-lactide-co-glycol he response was predominant sera of mice immunized with conformational epitopes [Monilar to a fragment of the hun	ide) (PLG) had a more prolonged A tly IgG1, a Th2 immune response — n NefPLG or Nef-CFA, but not after oureau2002] nan protein Bone-derived growth fa	three linear epitopes, Normalization with Normalization with Normalization	Nef 32-64, 118-167, and 1 of in PBS, which seemed	85-205, were frequently to preferentially stimulate
1105	F1		Nef (148–157 IIIB) 1993, Otake1994, Fujii1996c,				murine (IgM)
		• F1: Insect cells ex MHC restricted C	pressing myristylated Nef protection of the cell surface	s at the cell surface – stained IIIB/M oteins on their cell surface can indu of Nef expressing insect cells carry cell surface induces cytolysis of CD	ce cytolysis of unstimu Nef that can be recogn	lated CD4+ cells – this renized by MAbs E7 and E9	esponse is not due to
1106	2F2	Nef (151–170) <b>Vaccine</b> Vector/Ty	Nef (151–170 BRU)  wpe: recombinant protein H.	DKVEEANKGENTSLLHPVSL  IV component: Nef		Vaccine	murine (IgG1)

No. MAb ID	HXB2 Location	Author's Location	Sequence	Neutralizing Immu	nogen Species(Isotype)
	<ul><li>expression associate</li><li>2F2: This epitope is</li></ul>	d with dementia [Ranki19	95] ne human protein Hematop	n expressed in astrocytes from 7/14 brai oietic progenitor cell antigen CD34, TSI	•
1107 E9	<ul><li>E9: The C-term end</li><li>E9: A carboxy-term</li><li>E9: Insect cells expr MHC restricted CTI</li></ul>	inal domain of Nef on the ressing myristylated Nef production activity – the cell surface	s at the cell surface – stain cell surface induces cytoly roteins on their cell surface of Nef expressing insect of	02 ed IIIB/M10, but not MN/M10, cells [Ot sis of CD4+ T cells [Fujii1996b] c can induce cytolysis of unstimulated Cl	D4+ cells – this response is not due to MAbs E7 and E9 but not F1 [Fujii1996c
1108 3E6	<ul><li>References Ovod19</li><li>3E6: Reacted with N</li><li>3E6: Faintly cross-re</li><li>3E6: This epitope is</li></ul>	Nef (161–180 BRU) ex recombinant protein Si 92, Saito1994, Ranki1995 Nef from different HIV-1 si eactive with astrocytes of to similar to a fragment of the esearch Council AIDS rea	, Maksiutov2002 trains (BRU, IIIB, RF, MN uninfected control samples ne human protein Hematop	ent: Nef ) [Ovod1992]	
1109 2A3	References Ovod19	Nef (171–190 BRU)  2: recombinant protein Si 92  Nef from different HIV-1 s	-	ent: Nef	ne murine (IgG1)
1110 2E4	References Ovod19	Nef (171–190 BRU)  2: recombinant protein Si 92  Nef from different HIV-1 s		ent: Nef	ne murine (IgG1)
1111 2H12	References Ovod19  • 2H12: Reacted with • 2H12: Over-express • 2H12: One of four a	Nef (171–190 BRU) 2: recombinant protein S. 92, Saito1994, Ranki1995 Nef from different HIV-1 ion of Nef in astrocytes frontibodies used in combina d with dementia [Ranki19	strains (BRU, IIIB, RF, Mom postmortem pediatric Cotion to show HIV Nef prof	ent: Nef N) [Ovod1992] NS tissue [Saito1994]	ne murine (IgG1) ain samples from HIV+ individuals – Ne
1112 3A2	<ul><li>References Ovod19</li><li>3A2: Reacted with N</li></ul>	Nef (171–190 BRU) 2: recombinant protein S. 92, Saito1994, Ranki1995 Nef from different HIV-1 s on of Nef in astrocytes fron	trains (BRU, IIIB, RF, MN	ent: Nef  [) [Ovod1992]	ne murine (IgG1)

No. MAb ID	HXB2 Location	<b>Author's Location</b>	Sequence	No	eutralizing Immunogen	Species(Isotype)
	expression associate	ntibodies used in combination ed with dementia [Ranki1995 Research Council AIDS reago	5]	otein expressed in astroc	ytes from 7/14 brain samples from HIV	/+ individuals – Nef
1113 NF1A1	Nef (173–206)	Nef (173–206)	MDDPEREVLEWRFI LHPEYFKNC	OSRLAFHHVARE-		murine
	References Kamino NF1A1: Recognize	chik1990 s the Nef protein of the two i	solates BH10 and LA	V1 – low affinity [Kamir	nchik1990]	
1114 polyclonal	Nef (186–206)	Nef (185–205 LAI, BRU)	DSRLAFHHVARELI	HPEYFKNC	HIV-1 infection, Vaccine	murine (IgG1)
	Vaccine Vector/Typ References Mourea		Strain: LAI, BRU	HIV component: Nef	Adjuvant: PLG, complete Freund's ad	juvant (CFA)
	after 7 months – the recognized by the s	e response was predominantly	y IgG1, a Th2 immund NefPLG or Nef-CFA,	e response – three linear	than Nef in PBS or in Freund's adjuvan epitopes, Nef 32-64, 118-167, and 185- ion with Nef in PBS, which seemed to p	-205, were frequently
1115 E7	<ul> <li>E7: The C-term end</li> <li>E7: Insect cells exp</li> <li>MHC restricted CT</li> <li>E7: Nef forms a ho</li> <li>clusters on the surfa</li> <li>E7: A carboxy-term</li> <li>E7: Soluble Nef inl</li> </ul>	ressing myristylated Nef pro L activity – the cell surface of momeric oligomerizing structure of HIV-1 infected CD4+ of hinal domain of Nef on the ce	at the cell surface – stateins on their cell surf of Nef expressing insecture, and using E7 and cells [Fujii1996a] all surface induces cytells, and Nef cross-lin	o, Fujii1996d ained IIIB/M10, but not ace can induce cytolysis act cells carry Nef that ca d membrane immunofluc olysis of CD4+ T cells [ aking by MAbs may ind	uce anti-CD4 cytocidal activity – sera fi	onse is not due to at not F1 [Fujii1996c] by, was shown to
1116 AE6	Ab type C-term I References Chang I AE6: The light and complementarity de	heavy chains of three MAbs etermining regions (CDR) of AI and cross-competed AG1	Molecular Med and 7 (AG11, AE6, EH1) s AG11 and AE6 were	pecific to C-terminus of highly related (95.1% at	Vaccine  Vancouver, B. C. Canada  NEF were cloned and variable regions the DNA level) and bound LAI Nef, but similar to AG11) – single chain Abs we	nt not SF2 Nef – EH1
1117 AG11		Nef (LAI)  e: recombinant protein HIV  Donor Frank Jirik, Centre for 1998		Therapeutics, U. B. C., V	Vaccine Vancouver, B. C. Canada	murine (IgG1 $\kappa$ )

No. MAb ID	HXB2 Location Author's Location	Sequence	Neutralizing Immunogen	Species(Isotype)
	complementarity determining regions (CDR) bound to SF2 and LAI and cross-competed AG11 and EH1 and subcloned into a eukaryot	of AG11 and AE6 were high G11 and AE6 but had a disti- ic expression vector with a	rific to C-terminus of NEF were cloned and variable aly related (95.1% at the DNA level) and bound LAI netive CDR (57.9% similar to AG11) – single chain green fluorescent protein marker to allow intracellulate the role of Nef and as a gene therapy model [Chang	Nef, but not SF2 Nef – EH1 Abs were constructed from ar expression – the single
1118 EH1	complementarity determining regions (CDR) bound to SF2 and LAI and cross-competed AG11 and EH1 and subcloned into a eukaryot	for Molecular Med and Then bs (AG11, AE6, EH1) speci of AG11 and AE6 were high G11 and AE6 but had a disti- ic expression vector with a	Vaccine apeutics, U. B. C., Vancouver, B. C. Canada fic to C-terminus of NEF were cloned and variable r ally related (95.1% at the DNA level) and bound LAI nctive CDR (57.9% similar to AG11) – single chain green fluorescent protein marker to allow intracellula the role of Nef and as a gene therapy model [Chang	Nef, but not SF2 Nef – EH1 Abs were constructed from ar expression – the single
1119 6.1	Nef Nef (dis JRCSF) References Ranki1995  • 6.1: Raised against CNS primary isolates, stai • 6.1: NIAID Repository number 1123 [Ranki1		han other Nef MAbs – Nef expression associated wi	murine th dementia [Ranki1995]
1120 NF2B2	Nef Nef (20–78 BH10)  Vaccine Vector/Type: recombinant protein S References Kaminchik1990  NF2B2: Recognizes the Nef protein of the two NF2B2: NIH AIDS Research and Reference I	o isolates BH10 and LAV1 [		murine
1121 NF3A3	Nef Nef (20–78 BH10)  Vaccine Vector/Type: recombinant protein S References Kaminchik1990  NF3A3: Recognizes the Nef protein of the tw			murine
1122 NF8B4	Nef Nef (BH10)  Vaccine Vector/Type: recombinant protein S References Kaminchik1990  NF8B4: Does not recognize Nef CNBr cleava	-	Vaccine  ent: Nef  act BH10 Nef but not LAV1 Nef [Kaminchik1990]	murine
1123 AE6	Nef Nef Ab type C-term Donor James Hoxie, Div o References Greenway 1994, Tornatore 1994 • AE6: NIH AIDS Research and Reference Rea			murine

# **IV-C-16 HIV-1 Antibodies**

No. MAb ID	HXB2 Location	<b>Author's Location</b>	Sequence	Neutraliz	ing Immunogen	Species(Isotype)		
1124 polyclonal	HIV-1 References Fournie	er2002b			HIV-1 infection	human		
	• Purified B lymphocytes secret only a fraction of Ig and anti-HIV-1 Ab compared with unfractionated cells because monocytes and natural killer cells enhance both secretions by cell-to-cell contacts, involving adhesion and CD27, CD80 costimulatory molecules and IL-6 – cell-to-cell contacts and soluble factors induce maturation of activated B cells in vitro to allow prolonged survival and terminal differentiation [Fournier2002b]							
1125 polyclonal	HIV-1 References Fournie	er2002a			HIV-1 infection	human		
	<ul> <li>An early and sustain incomplete responderesponders, and wa</li> </ul>	ned fall in plasma viral loa ders – HIV-1 specific Ab se	ecretion decreased in para acreases of CD4 T-cell co	observed in 17 HAART respor llel with plasma viral load – Hl unts and higher levels of HIV-s	V-1 specific Abs became	negative in only six		
1126 polyclonal	HIV-1				HIV-1 infection	human		
	for NAbs but only 3	nts were used to study the r	e presence of complement	ralizing Abs (NAbs), ADCC-A - 60% had ADCC Abs – 72%				
127 polyclonal	HIV-1 <b>References</b> Battle-	M:H2002			HIV-1 infection	human (IgA, IgG1)		
	• In a study of HIV-1			(12/51) of cervicovaginal fluic on [Battle-Miller2002]	ds, and 56% (25/45) of serv	um samples – 3 women had		
1128 polyclonal	HIV-1				HIV-1 infection	human (IgA2, IgA1, IgM)		
	_		_	-1 infected individuals – there v	was no anti-gp41 IgA in sa	lliva, in contrast to plasma -		
1129 polyclonal	HIV-1 <b>References</b> Hioe19	997a		P	HIV-1 infection	human		
	<ul> <li>Four primary isolated by all polyclonal seanti-CD4bd (559/64) (419-D, and 447-52)</li> </ul>	tes showed distinct patterns era and plasma tested, and value. 4-D, 654-D and 830-D and 2D)and cluster II gp41 (98-	was also neutralized by 8/ l a cluster II of gp41 direc 6) MAbs at higher conce	ration by polyclonal sera or pla (17 MAbs, in particular anti-V3 ted MAb (98-6) – isolates 92H attrations – US4 was neutralized (419-D, 447-52D, 782-D, 838-I	B loop (419-D, 447-52D, 7 T593 and 91US056 were d by some of the polyclona	82-D, and 838-D), neutralized by V3 loop Il sera/plasma tested and no		
1130 polyclonal	HIV-1 References Oelema	ann2002		no	HIV-1 infection	human (IgA, IgG)		

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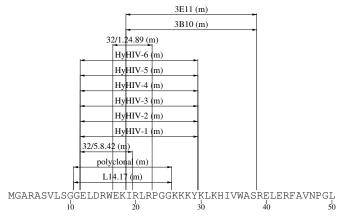
No.	MAb ID	HXB2 Location	<b>Author's Location</b>	Sequence	Neutral	izing Immunogen	Species(Isotype)		
					ation, Berkeley, CA was found vity), and 278/284 negative sam	1 .	E		
1131	polyclonal	HIV-1	HIV-1		no	HIV-1 infection	human (IgE)		
		References Secord1	996, Pellegrino2002						
		HIV-specific IgE found in clinically healthy HIV-1 infected children [Secord1996]							
		• Pediatric long term survivors (LTS) have been found to carry HIV-1 specific IgE – serum from these children inhibit HIV-1 production in culture, but this inhibition did not seem to be due to neutralization, rather due to a cytoxic event – serum lost the HIV-1 inhibitory effect when depleted of IgE							
		inhibition did not se [Pellegrino2002]	em to be due to neutraliza	ition, rather due to a cy	toxic event – serum lost the HI	V-1 inhibitory effect when d	epleted of IgE		

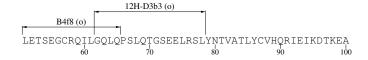
# **IV-D** Maps of MAb Locations Plotted by Protein

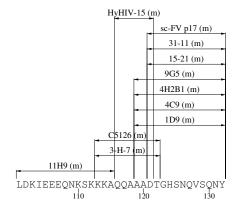
Linear epitopes less than twenty-two amino acids long are shown with their IV-D-1 p17 Ab Epitope Map antibody ID and the experimental species.

Key	Species
h	human
p	non-human primate
m	murine
О	other

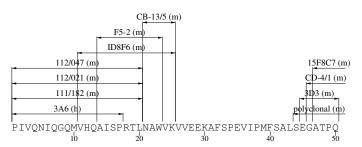
Table IV-D.1: The species for which the epitopes react

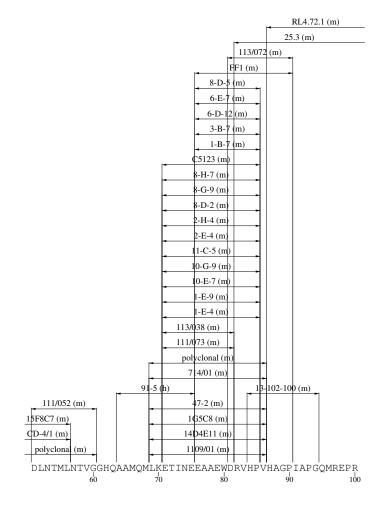


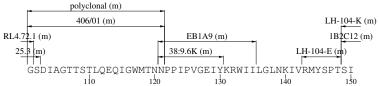


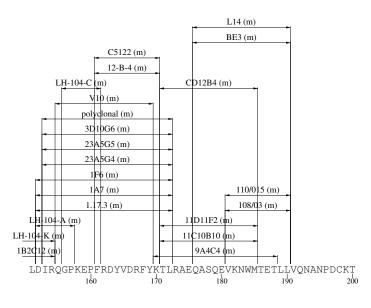


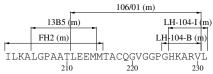
IV-D-2 p24 Ab Epitope Map





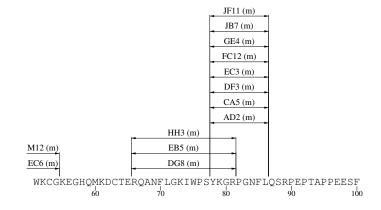




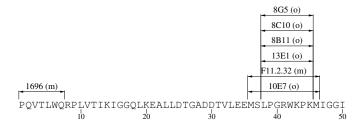


### IV-D-3 p2p7p1p6 Ab Epitope Map





#### **IV-D-4** Protease Ab Epitope Map

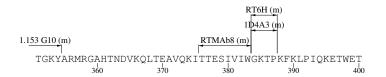


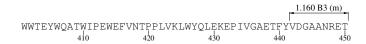
#### IV-D-5 RT Ab Epitope Map

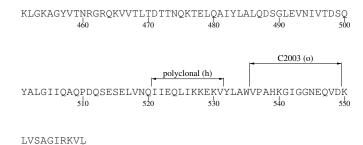
 $\begin{array}{c|c} & 1E8 \text{ (m)} \\ \hline \\ \text{GPENPYNTPVFAIKKKDSTKWRKLVDFRELNKRTQDFWEVQLGIPHPAGL} \\ & 60 & 70 & 80 & 90 & 100 \\ \end{array}$ 



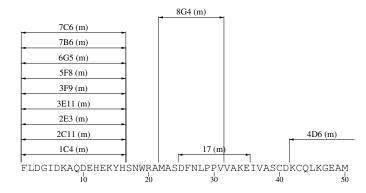






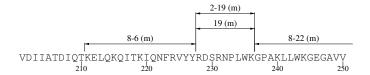


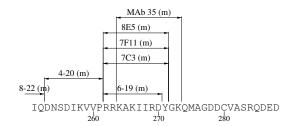
### IV-D-6 Integrase Ab Epitope Map





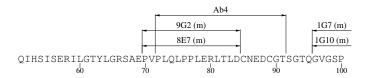


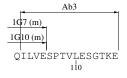




# IV-D-7 Rev Ab Epitope Map

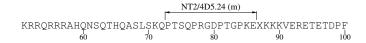






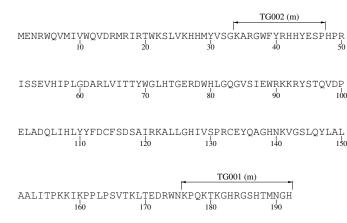
# **IV-D-8** Tat Ab Epitope Map





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# IV-D-9 Vif Ab Epitope Map



### IV-D-10 Vpr Ab Epitope Map

GDTWAGVEAIIRILQQLLF1HFRIGCRHSRIGVTRQRRARNGASRS 
$$\begin{matrix} 60 & 70 & 80 & 90 \end{matrix}$$

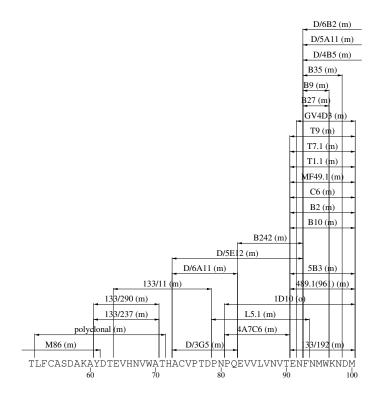
# IV-D-11 Vpu Ab Epitope Map

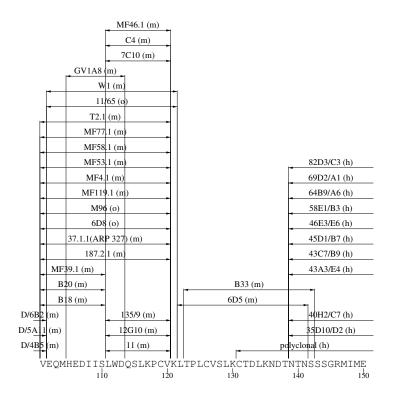
TQPIPIVALVVAIIIAIVVWSIVIIEYRKILRQRKIDRLIDRLIERA
10 20 30 40 50

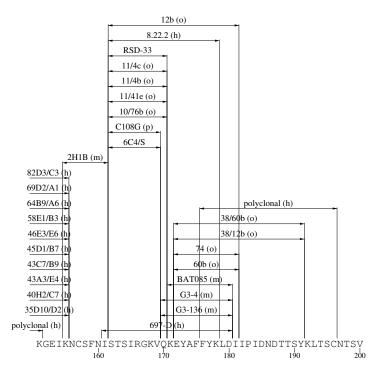
EDSGNESEGEISALVEMGVEMGHHAPWDVDDL
60 70 80

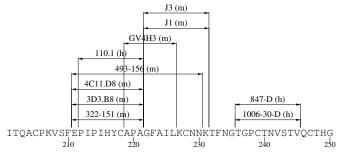
# IV-D-12 gp160 Ab Epitope Map

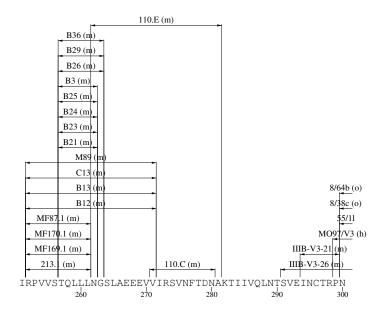


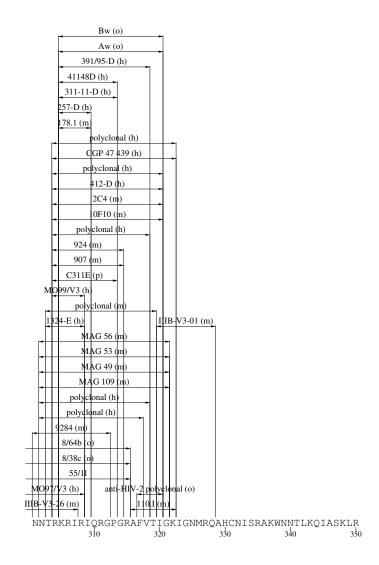


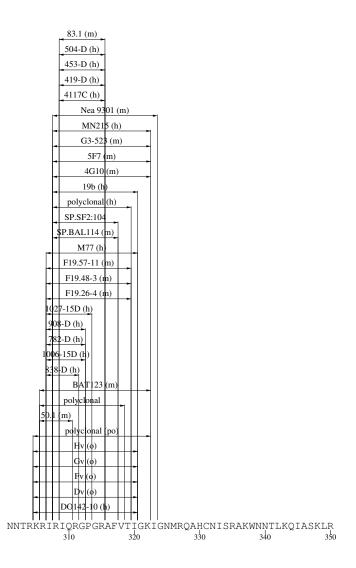


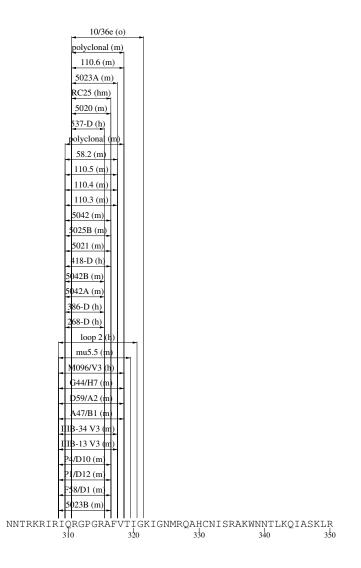


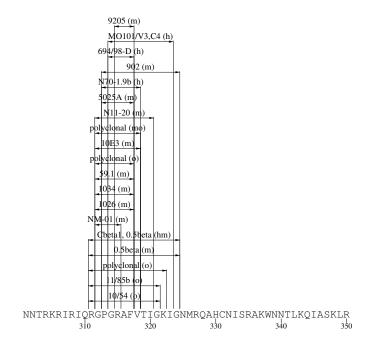


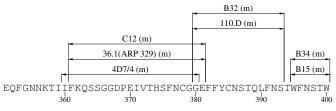


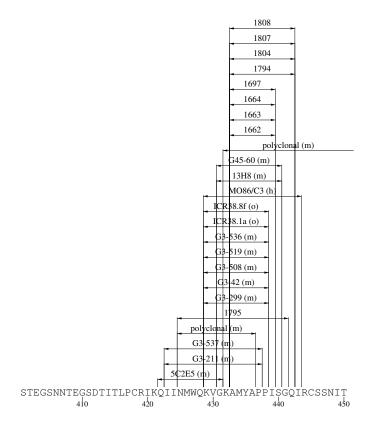


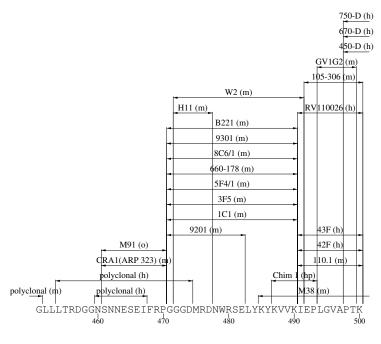


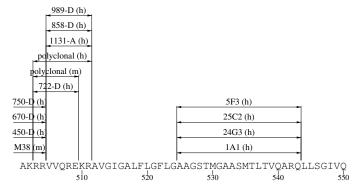


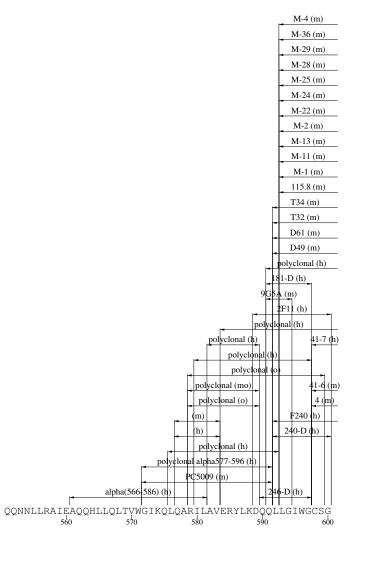


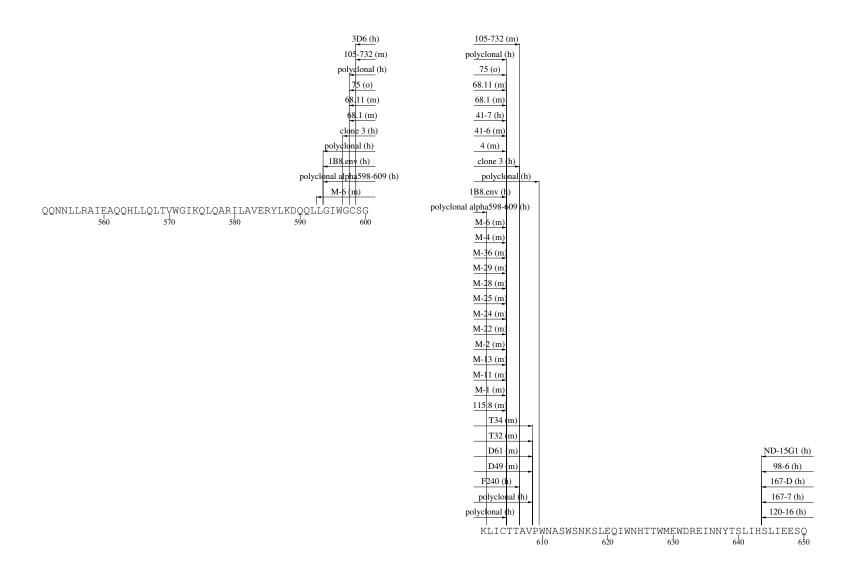




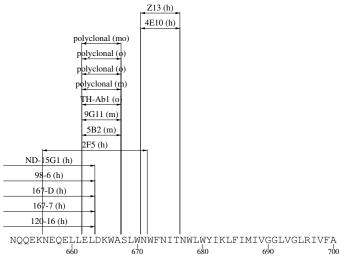


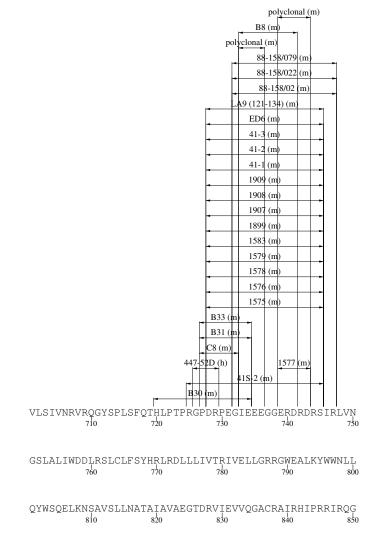






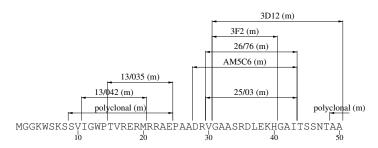


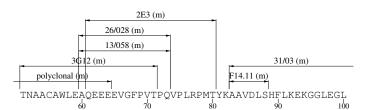


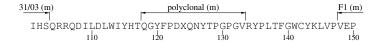


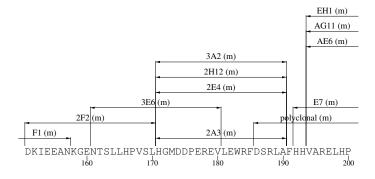
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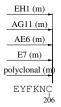
## IV-D-13 Nef Ab Epitope Map











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